

GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR

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GAM15 ACCTCTTTCTGATGGAGTCG 1 TGATGGAGTC 350 TTTCT- T TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT C GA GGAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA | ||||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT G CT TCTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCTCT T -- GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCCTTCGAT
 GGT

GAM16 ACCTCTTTCTGATGGAGTCG 2 TGATGGAGTC 351 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM17 ACCTCTTTCTGATGGAGTCG 3 TGATGGAGTC 352 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM18 ACCTCTTTCTGATGGAGTCG 4 TGATGGAGTC 353 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM19 ACCTCTTTCTGATGGAGTCG 5 TGATGGAGTC 354 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM20 ACCTCTTTCTGATGGAGTCG 6 TGATGGAGTC 355 TTTCT TG TC AAG CT TC TCTTC
T CTCACAA

TAAAAAAGTTTTATCTCTTT	GTAAAAAAGT	TC	GA	GAG	GTAAAA	TTTTAT	CTT	TC	GA
GGT A									
CTCTCTTCGATGGTCTCACA	TTTA								
AAAATATTAAACCTCTTTCT		AG	CT	TTC	TATTTT	AAAATG	GAG	AG	CTCCA A
GATGGAGTCGTAAAAAAGTT		CTTCT	CT	TC	GAA	CT	GT	TCTTT	- AATTATA
TTATCTCTTTCTCTCTTCGA									
TGGT									
GAM21 ACCTCTTTCTGATGGAGTCG 7	TGATGGAGTC 356	TTTCT	TG	TC	AAG	CT	TC	TCTTC	
T CTCACAA									
TAAAAAAGTTTTATCTCTTT	GTAAAAAAGT	TC	GA	GAG	GTAAAA	TTTTAT	CTT	TC	GA
GGT A									
CTCTCTTCGATGGTCTCACA	TTTA								
AAAATATTAAACCTCTTTCT		AG	CT	TTC	TATTTT	AAAATG	GAG	AG	CTCCA A
GATGGAGTCGTAAAAAAGTT		CTTCT	CT	TC	GAA	CT	GT	TCTTT	- AATTATA
TTATCTCTTTCTCTCTTCGA									
TGGT									
GAM22 ACCTCTTTCTGATGGAGTCG 8	TGATGGAGTC 357	TTTCT	TG	TC	AAG	CT	TC	TCTTC	
T CTCACAA									
TAAAAAAGTTTTATCTCTTT	GTAAAAAAGT	TC	GA	GAG	GTAAAA	TTTTAT	CTT	TC	GA
GGT A									
CTCTCTTCGATGGTCTCACA	TTTA								
AAAATATTAAACCTCTTTCT		AG	CT	TTC	TATTTT	AAAATG	GAG	AG	CTCCA A
GATGGAGTCGTAAAAAAGTT		CTTCT	CT	TC	GAA	CT	GT	TCTTT	- AATTATA
TTATCTCTTTCTCTCTTCGA									
TGGT									
GAM23 ACCTCTTTCTGATGGAGTCG 9	TGATGGAGTC 358	TTTCT	TG	TC	AAG	CT	TC	TCTTC	
T CTCACAA									
TAAAAAAGTTTTATCTCTTT	GTAAAAAAGT	TC	GA	GAG	GTAAAA	TTTTAT	CTT	TC	GA
GGT A									
CTCTCTTCGATGGTCTCACA	TTTA								
AAAATATTAAACCTCTTTCT		AG	CT	TTC	TATTTT	AAAATG	GAG	AG	CTCCA A
GATGGAGTCGTAAAAAAGTT		CTTCT	CT	TC	GAA	CT	GT	TCTTT	- AATTATA
TTATCTCTTTCTCTCTTCGA									
TGGT									
GAM24 ACCTCTTTCTGATGGAGTCG 10	TGATGGAGTC 359	TTTCT	TG	TC	AAG	CT	TC	TCTTC	
T CTCACAA									
TAAAAAAGTTTTATCTCTTT	GTAAAAAAGT	TC	GA	GAG	GTAAAA	TTTTAT	CTT	TC	GA
GGT A									
CTCTCTTCGATGGTCTCACA	TTTA								
AAAATATTAAACCTCTTTCT		AG	CT	TTC	TATTTT	AAAATG	GAG	AG	CTCCA A
GATGGAGTCGTAAAAAAGTT		CTTCT	CT	TC	GAA	CT	GT	TCTTT	- AATTATA
TTATCTCTTTCTCTCTTCGA									
TGGT									
GAM25 ACCTCTTTCTGATGGAGTCG 11	TGATGGAGTC 360	TTTCT	TG	TC	AAG	CT	TC	TCTTC	
T CTCACAA									
TAAAAAAGTTTTATCTCTTT	GTAAAAAAGT	TC	GA	GAG	GTAAAA	TTTTAT	CTT	TC	GA
GGT A									
CTCTCTTCGATGGTCTCACA	TTTA								
AAAATATTAAACCTCTTTCT		AG	CT	TTC	TATTTT	AAAATG	GAG	AG	CTCCA A
GATGGAGTCGTAAAAAAGTT		CTTCT	CT	TC	GAA	CT	GT	TCTTT	- AATTATA

TTATCTCTTTCTCTCTCGA
 TGGT
 GAM26 ACCTCTTTCTGATGGAGTCG 12 CGTAAAAAAG 361 TTTCT TG TC AAG CT C TTC--
 T CTCACAA
 TAAAAAAGTTTTATCTTTCT TTTTATCTTT TC GA GAG GTAAAA TTTTAT TTCT TC GA
 GGT A
 CTCTTCGATGGTCTCACAAA CTCT || ||| ||||| ||||| ||| || |||
 AATATTAAACCTCTTTCTGA AG CT TTC TATTTT AAAATG GAGG AG CT CCA
 A
 TGGAGTCGTAAAAAAGTTTT CTTCT CT TC GAA CT T TCTTT - AATTATA
 ATCTCTTTCTCTCTTCGATG
 GT
 GAM27 GATGGAGTCGTAAAAAAGTT 13 TGATGGAGTC 362 T TC AAG -- T TCCTTC T
 CTCACAA
 TTATCTCTTTCTCCTTCGAT GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTCT TC GA GGT
 A
 GGTCTCACAAAAATATTTAA TTTA ||||| ||||| ||||| ||| || |||
 CCTCTTTCTGATGGAGTCGT CT TCTC TATTTT AAAATG GAGG AG CT CCA A
 AAAAAAGTTTTATCTCTTTC T -- GAA CT T TCTTT- - AATTATA

 GAM28 GATGGAGTCGTAAAAAAGTT 14 TGATGGAGTC 363 T TC AAG -- T TCCTTC T
 CTCACAA
 TTATCTCTTTCTCCTTCGAT GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTCT TC GA GGT
 A
 GGTCTCACAAAAATATTTAA TTTA ||||| ||||| ||||| ||| || |||
 CCTCTTTCTGATGGAGTCGT CT TCTC TATTTT AAAATG GAGG AG CT CCA A
 AAAAAAGTTTTATCTCTTTC T -- GAA CT T TCTTT- - AATTATA

 GAM29 GATGGAGTCGTAAAAAAGTT 15 TGATGGAGTC 364 T TC AAG CT TC TCTTC T
 CTCACAA
 TTATCTCTTTCTCTCTTCGA GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTT TC GA GGT
 A
 TGGTCTCACAAAAATATTTAA TTTA ||||| ||||| ||||| ||| || |||
 ACCTCTTTCTGATGGAGTCG CT TCTC TATTTT AAAATG GAG AG CT CCA A
 TAAAAAAGTTTTATCTCTTT T -- GAA CT GT TCTTT - AATTATA
 C

 GAM30 GATGGTCTCATAAAAAAGT 16 ATAAAAAAG 365 G TCATAAAA TTTTAC ATTCT-
 CTCTCTT TG
 TTTACAAAAATATTTTTATT TTTTACAAAA AT GTC AAAG AAAAAATATTTTT CTTT
 TGA G
 CTCTTTCTCTCTTTGATGGT ATAT |||| ||| ||||| ||||| ||| |||
 CTCATAAAAAAAGTTTTACA TG TAG TTTC TTTTATAAAAA GAAA ACT /
 AAAATATTTTTATTCTCTTT G TTTCTCTC TCTTA- CATTTT AAAAT-- CT
 CTCTCTTTGATGGTC

 GAM31 GGAGTCATAAAATATTTTTA 17 TAAAAATATT 366 TC A T- T TCTCTTC T CTCACAA
 TTCTCTTTCTCTCTTCGAT TTATTCTCTT GGAG ATAAAAAT TTTTAT CTCT TC GA GGT
 A

GAAGAGAG

GAM43 CTTTTTTACGACTCCATCAG 29 CATCAGAAAG 378 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT I III III IIII III III IIII III IIII
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM44 CTTTTTTACGACTCCATCAG 30 CATCAGAAAG 379 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT I III III IIII III III IIII III IIII
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM45 CTTTTTTACGACTCCATCAG 31 CATCAGAAAG 380 A CTCCA G G T A G GACCA -
AAAG
AAAGAGGTTTAATATTTTTG AGGTTTAATA TT CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG A
TGAGACCATCGAAGAGAGAA TTTT II III III IIII III III IIII III IIII
AGATAAACTTTTTTACGAC AA GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTC T
TCCATCAGAAAGAGGTTTAA - ACCAG G A T G G ACCTC A AAAA
TATTTTTGTGAGACCATCGA
AGAGAG

GAM46 GTGTGCCTGAATCGTTTCGAT 32 TGAATAGAGT 381 C TTCGAT C C CAA
TAACCCTACTCATCCAATTT TATCGATTCA GTGTG CTGAATCG TAAC CTA TCATC T
CAGATGAATAGAGTTATCGA GACA IIII IIII IIII IIII IIII IIII
TTCAGACACAC CACAC GACTTAGC ATTG GAT AGTAG T
A T----- A A ACT

GAM47 TCAGAAAGAGGTTTAATATT 33 AGAGGTTTAA 382 AAA GTTT-- GAGACCA- GA
TTTGTGAGACCATCGAAGAG TATTTTTGTG TCAG GAG AATATTTTTGT TC A
AGAAAGAGAATAAAAAATATT AGAC IIII III IIII IIII II
TTATGACTCCATTGA AGTT CTC TTATAAAAATA AG /
AC- AGTATT AGAGAAAG AG

GAM48 TTTTATGAGACCATCAAAGA 34 AGAGAGAAAG 383 ACCA AAG AGA- AAAA A-
- GA
GAGAAAGAGAATAAAAAATAT AGAATAAAAA TCA AGAGAAAG ATAAAAATATTTTTGT
CTTTTTTT TGA C
TTTTGTAAACTTTTTTTAT TATT III IIII IIIIIIIIIII IIIII III

GAGACCATCAAAGAGAGAAA AGT TTTTTTC TGTTTTTATAAAAATA GAAAGAGA
 ACT /
 GAGAATAAAAAATATTTTTGT CCAG A-- AAAA AGA- GAA AC
 AAAACTTTTTTTATGAGACC
 ATCAAAGAGAG
 GAM49 TTTTATGAGACCATCAAAGA 35 GAAGAGAGAA 384 ACCA AAG AGA- AAAA---
 - A
 GAGAAAGAGAATAAAAAATAT AGAGAATAAAA TCA AGAGAAAG ATAAAAATATTTTTGT
 CTTTTTTTG TG G
 TTTTGTAACCTTTTTTTGT AATA ||| ||||| ||||||||| ||||| ||
 GAGACCATCGAAGAGAGAAA AGT TTTTTTC TGTTTTTATAAAAATA
 GAGAGAAGC AC A
 GAGAATAAAAAATATTTTTGT CCAG A-- AAAA AGAGAAA T C
 AAAACTTTTTTTATGAGACC
 ATCAAAGAGAG
 GAM50 TTTTCTTAGTACAAAAGTC 36 TCAATGTTTT 385 A- G- AT--- AAAA G
 AATGTTTTAAAATATATGGA AAAATATATG TTTTCTT GTACAAA TCA GTTTT
 TATATGGACAA A
 CAAGAATTTGTCTGTATAAA GACA ||||| ||||| || ||| |||||||
 AACTTGTGTGAAATTTTGTA AAAAGAA CATGTTTT AGT CAAAA ATATGTCTGTT A
 CCAAAGAAAA AC AA GTGTT --- T

 GAM51 ATGTAGTAATCGTTGTCGTG 37 ATGGTTCTTT 386 C TG GTGTTCC-- TCC TTCTCC -
 T TTCT
 TTCCTGTTTCCTACTTCTCC CCGTACAACA AT GT TC TGTT TAC AATCAT
 ATAGATATT TCT A
 AATCATATAGATATTTTCTT TACT ||| || ||| ||| ||||| ||||| |||
 TCTATCATGGATAATATTTG TATA AG ACAA ATG TTGGTA TGTTTATAA AGG /
 TAATGGTTCTTTCCGTACAA - GT ATTTGTCAT C-- CCTTTC A T TACT
 CATACTGTTTAGATGATATT
 GCGCAT
 GAM52 GAATGACTCGTCCCTTAATA 38 TGA CTGCTCC 387 GA G TAATA AGTAG - TCT
 GGCAGTAGGCTAGTATCTTT CTTAATAGGC GAAT CTC TCCCT GGC GCTA GTA T
 TTTACGTAGTAATCGTCGTA AGTA ||| ||| ||| ||| ||| |||
 GGGAGAGAATTC CTTA GAG AGGGA CTG TGAT CAT /
 A- - TG--- CTAA- G TTT

 GAM53 GAGATTGTATCAGTTTCGTA 39 GATTGTATCA 388 -- - T TA TGA G T
 GTCTTGAGTATTGGTATTAC GTTTCGTAGT GAGATTGTA TC AGT TCG GTCT GTATTG TAT A
 TATATAGTATATAGATGTCG CTTG ||||| || ||| ||| ||||| |||
 ACGCTAGATATACAGTCTC CTCTGACAT AG TCG AGC TAGA TATGAT ATA C
 AT A C TG TA- - T

 GAM54 GGCAAATCTTATCATTGGTC 40 TAACATCGAT 389 CTT - --- TG- TTGCTTT
 GGTGTTTGGTCTTGCTTTGT TCCCATATGA GGCAAAT ATCAT TGG TCGGTGTT GTC G
 GACTTTGATAATAACATCGA TGTT ||||| ||||| ||| ||||| |||
 TTCCCATATGATGTTTGT TTGTTG TAGTA ACC AGCTACAA TAG /

--- T CTT TAA TTTCAGT

GAM55 AGTATGTTGTACGGAAAGAA 41 TGATTGGAGA 390 -- A GAAAGAA ATTACAAA A- TG--
- AAGA

CCATTACAAATATTATCCAT AGTAGGAAAC AGTA TGTTGT CG CC TATT TCCA
ATAGA A
GATAGAAAGAAAATATCTAT AGGA ||| ||||| || || ||| ||| ||||
ATGATTGGAGAAGTAGGAAA TCAT GCAACA GC GG ATGA AGGT TATCT /
CAGGAACACGACAACGATTA TA - ACAA--- ACAAAGG- AG TAGTA ATAA
CT

GAM56 AAAATCGATTCCGTCCAAGA 42 TCGATTCCGT 391 C CCAAG AAAACA
TGATAAAACATTTACCGGC CCAAGATGAT AAAAT GATTCCGT ATGAT T
ATCATAAACACGGAGTTTAT AAAA |||| ||||| ||||
TTT TTTTA TTGAGGCA TACTA T
T CAAA- CGGCCAT

GAM57 CATGGAGATACTTTATTACT 43 TAATGTCCTG 392 ----- T TAAATA
CCATTAAATAATTTATCATG TTTCATTTGT CATGGAGAT AC TTATTACTCCAT A
GAGTGATAATGTCCTGTTTC TTCC ||||| || |||||
ATTTGTTTCCATG GTACCTTTG TG AATAGTGAGGTA /
TTTACTTTGTCC T CTATTT

GAM58 ACTGTATGCTCCTAGCGGAG 44 TGTATGCTCC 393 A - A AATCCTTCG T
TTAATCCTTCGTTGTTTCTA TAGCGGAGTT ACTGT TGCTC CT GCGGAGTT TTGT T
CAAAGTCTCTCGACTCCGCG AATC |||| |||| || ||||| |||
AGAGAGTAACAGT TGACA ATGAG GA CGCCTCAG AACAC
- A G CTCTCTGA- T

GAM59 ATACGGAATATCTACGTCCA 45 TCATCGGGTG 394 C C----- GT - T T
TGTCATTATTGTCATCGGGT TATTCTCATT ATA GGAATAT TAC CC ATG CA T
GTATTCTCATT CATATTCTC CATA ||| ||||| || || ||| ||
TAT TAT TCTTATA ATG GG TAC GT A
C CTTACTCTT TG C T T

GAM60 GCAATACTTCTGGTCTCGGA 46 TTCTGGTCTC 395 ACTTC A ----- C
TTAGGCGTCGTTACGTATAT GGATTAGGCG GCAAT TGGTCTCGGATT GG CGT G
ATCCACCAATCCGAGACCAT TCGT |||| ||||| ||| |||
TGATTGC CGTTA ACCAGAGCCTAA CC GCA T
GTT-- - ACCTATATAT T

GAM61 GCTTTGCAAATTGTATATTA 47 ATCGATCATA 396 TT ATT TAT C C CCGC AAT A
TTT
TTGACATCGACCGCGTAATA TCTATATCAT GCT GCAA GTATAT TGA AT GA GT ATAGT
GAG T

TAGTAGAGTTTTATTCTCAT	CCAT	
TATCGATCATATCTATATCA		TGA CGTT CATGTA ACT TA CT TA TATTA CTC /
TCCATGTACTTGCTTAGT		TT --- CCT A T ATAC GC- - TTA

GAM62	GTGTTCTCGTTCAGAATCT 48	TTGAAGACTC 397	T GTTC A TCG - G G
	TTCCAGAGAC	GTCGT CTC	AGA TCTT CAGC ATAAGTA TAT T
	TCGATATACTTATCGTTGAA	GAT	
	GA CTCTTCCAGAGACGAT	TAGCA GAG	TCT AGAA GTTG TATTCAT ATA C
	- ACCT C --- C - G		

GAM63	TAACAATATATTATTAGTTT 49	TTAATAATAT 398	----- TA
	ATATTACTGAATTAATAATA	AAAATTCCCA	TAACAA TATATTATTAGTTTA T
	TAA AATTCCCAATCTTGTTA	ATCT	
	ATTGTT	ATATAATAATTAAGT T	
	CTAACCCTTAAA	CA	

GAM64	TCTCAATAAGAAGATTAACG 50	TGGGGT TACT 399	C AA AACGAT-- CTA
	ATTTCCATGTCTACATTATA	CTAAATCGCT	TCT AATAAG GATT TTCCATGT C
	TGGGGT TACTCTAAATCGCT	TGTT	
	TGTTTAGA	AGA TTGTTC CTAA	GGGGTATA /
	T G- ATCTCATT	TTA	

GAM65	TGTATT CAGTCAGACAATGT 51	TTAGTAGCGT 400	A - AA TGACGTCG G C G
	CTGACGTCGGCCACGGTATT	GGCAATGACA	TGT TTCAGT CAGAC TGTC GCCACG TATT
AGG A	CAGGGAGTCCTTAGTAGCGT	GGGT	
	GGCAATGACAGGGTCTGAAC		ACA GGGTCA GTCTG ACAG CGGTGC ATGA TCC G
	TGGGCACA	C A GG TAA-----	G T T

GAM66	TTGATATTACTTATAATAAC 52	TTAATTGTAA 401	T T--- CG -TG -- TT T
	GATTTGTTTAATTTTTAGTT	ATGATATTAT	TTGATA TACTTA AATAA AT T TTTA ATT TAGT T
	TATACTATTAATTGTAAATG	TATT	
	ATATTATTATTTTTTTAAGT		GACTAT ATGAAT TTATT TA A AAAT TAA ATCA A
	ATTATCAG	T	TTTT AT TGT GT TT T

GAM67	TTTAAACTTTGGCATATACA 53	AGATAACATA 402	CTT CATATACAA-- ACT
	AGTCTATACTTTTAGTAGAT	CCACACCATT	TTTAAA TGG GTCTAT T
	AACATACCACACCATTTTTTT	TTTT	
AAA	AAATTT ACC	TAGATG /	
	TTT ACACCATACAA	ATT	

GAM68	TTTCTTTTTCACGATGCATCT 54	ATAAGTGGAC 403	TC- GA- ----- GA CGT
	TATTGAATGACGTTTTCTCA	ATATAGATGC	TTTCTTT AC TGCATCT TATT ATGA T

TAAGTGGACATATAGATGCA AGAA ||||| || ||||| ||| |||
GAAGTAATGAAGAAA AAAGAAG TG ACGTAGA GTGA TACT /
TAA AAG TATACAG A- CTT

GAM69 TCGATGATACATGTATTAAA 55 TGATACATGT 404 A--- TGTA T TCC
ATACTTTCCGAATAAGTCTT ATTAAAATAC TCG TGATACA TAAAA ACTT G
TTAAATATTGTATTAATTAT TTTC ||| ||||| ||||| |||
GA AGT ATTATGT AATTTT TGAA /
ATTA TATA C TAA

GAM70 TGATAATACTTAAAAAATA 56 TAAAAATTAA 405 A AAAAA ATCATTAC AA A
ATAATATCATTTACAATTAA ACAAATCGTT TGATA TACTT ATAATAAT AATT TAGT T
TAGTATAAACTAAAAATTAA ATTA ||||| ||||| ||||| ||| |||
ACAAATCGTTATTATAAGTA ACTAT ATGAA TATTATTG TTAA ATCA A
ATATCA A ----- CTAAACAAA AA A

GAM71 AGCAGCGAACAACAACATCA 57 ATGGATTCTG 406 AACAAAC T TAT CA
GATATTTTCATCGACATTTTT TGTTTATGCT AGCAGCG AACACAGA TTCATCGA T
GATGGATTCTGTGTTTATGC GTT ||||| ||| ||| |||||
TGTT TTGTCGT TTGT GTCT AGGTAGTT /
AT---- - T-- TT

GAM72 TAACAAGATTGGGAATTTTA 58 TAATATAAAC 407 GATTGGGAAT- AA
TATTATTAATTCAGTAATAT TAATAATATA TAACAA TTTATATTATT T
AAACTAATAATATATTGTTA TTGT ||||| ||||| |||||
ATTGTT AAATATAATGA /
ATATAATAATC CT

GAM73 TACATGCTGACATCTAATGC 59 TCTCTAGCGT 408 C ATCTAATGCC AA -- C- T
AATA
CTGTATAACCATGAGAGCAT GGATACAGTC TACATG TGAC TGTAT CCATG AGAG ATC
AC C
CTACAATACATACCGTCGAT ACCG ||||| ||||| ||||| ||||| ||| ||| |||
ATCTCTAGCGTGGATACAGT ATGTGC ACTG ACATA GGTGC TCTC TAG TG A
CACCGTGTA C ----- -- GA TA C CCAT

GAM74 TCCGTTTTTATCAGTATGTA 60 TATCAGTATG 409 T----- TGTA- C AT T
TATCTATATTAACGTCGTCG TATATCTATA TCCGTTTT ATCAGTA TAT TAT TAACG C
TTGTAGTGAATAGTAGTTAT TTAA ||||| ||||| ||| ||| |||||
TGATCTATTATATGAAACGG AGGCAAAG TAGTTAT ATA GTG GTTGC G
A TATATTATC TGATG A AT T

GAM75 TGCTAAATATGCGATGTATC 61 TATTATACAA 410 A- - T TCTAT A T- AACAAATAC

TATGTTATTTGTATTTATCT AAATTTT TGCT AATATGC GA GTA GTT TTTGTAT TATCTA
 C
 AAACAATACCTCTACCTCTA TTTC ||| ||||| ||| ||| ||||| |||||
 GATATTATACAAAAATTTT ATGA TTATACG CT TAT TAA AAACATA ATAGAT /
 TATTCAGCATATTAAAGTA AA A T TTTT- - TT CTCCATCT

GAM76 TTTTGATTACGATGTTATAA 62 TATAACATCG 411 ATGT TTAATT TG GAT
 GAATGTAGTTAATTGATGTA TAATCAAAA TTTTGATTACGATGTTATAAGA AG GA TAT G
 TGATGTTAATGTGTCCTCTT ||||| ||||| || || |||
 TCCTCTTATAACATCGTAAT AAACTAATGCTACAATATTCT TC CT GTA /
 CAAAA CCTT TC---- GT ATT

GAM77 GATTTTGTGATTTTCTTCC 63 ATAGTTAGAT 412 TTTT TTT TC A A
 TAAACTGTTTACGTAAATAG AGAATATTCA GA GTGA TTCT CTAA CTGTTT C
 TTAGATAGAATATTCATTAG TTAG || ||| ||| ||| |||||
 TTC CT TACT AAGA GATT GATAAA G
 TGAT TAT TA - T

GAM78 GCGTCAAATATTTCCCGTTT 64 TGGTATGTTT 413 CAA- CC TTA- GTCAAGA
 AATATCGCATTGTGCAAGAT ACGATAAGTA GCGT ATATTT CGT ATATCGCATT T
 AATAATAGAGTGTGGTATGT TAAT ||| ||||| ||| |||||
 TCACGATAAGTATAATAACG CGCA TATGAA GCA TATGGTGTGAG /
 C ATAA TA CTTG ATAATAA

GAM79 TATCTTTTAAGAATTGTGGA 65 TCTTTTAAGA 414 C A GATAT GA TA
 TATTAGGATATTATTACGTA ATTGTGGATA TAT TTTTA GAATTGTG TAG TAT T
 AACTATTACACAATTCTAAA TTAG ||| ||||| ||||| ||| |||
 ATATA ATA AAAAT CTTAACAC ATC ATG T
 T - ATT-- AA CA

GAM80 ATTTAGACTGATGTATGGGT 66 TTCTCATCAT 415 GA T T - GTTT
 AATAGTGTTTGAAGAGCTCG CAGAATAAAT ATTTA CTGATG ATGGG AAT AGT G
 TTCTCATCATCAGAATAAAT |||| ||||| ||||| ||| |||
 TAAAT GACTAC TACTC TTG TCG /
 AA - - C AGAA

GAM81 AGCCGCTGAGTGGTAAACAA 67 CCGCTGAGTG 416 C ---- CAACA- AG
 CAGAACAGATAGTTTATTAT GTAAACAACA AGC GCTGAG TGGTAAA GAAC A
 CTTTACCAACACCCTCAGCC GAAC ||| ||||| ||||| |||
 GCT TCG CGACTC ACCATTT TTTG /
 C CCACA CTATTA AT

GAM82 GACTAGATCCGTTAGTTTAA 68 CGTTAGTTTA 417 CCGTT T T CATC- TA

TATCCTCAGTCATCTTGTCT	ATATCCTCAG	GA	CTAGAT	AGTTTAA	ATCC	CAGT	TTGTC	G
AGAATGGCAAATCTAACTGC	TCAT							
GGGTTTAGGCTTTAGTTTAG		TTGATTTG	TCGGATT	TGGG	GTCA	AACGG	A	
TT	ATT--	-	C	ATCTA	TA			

GAM83	GGATGTAAAATGTTGATGAT	69	TTGATGATAT	418	AAAAT	A	CTACATCGTT	TTT
	ATCTACATCGTTTGGATTTT		CTACATCGTT		GGATGT	GTTG	TGATAT	TGGAT T
	TATGTATCCACTTTAATAAT		TGGA					
	ATCATAGCTGTAACATCC				CCTACA	CGAT	ACTATA	ACCTA A
			ATGT-	-	ATAATTC-	TGT		

GAM84	GTCCGTATCCAGTCAACACT	70	TAGCTTTCAC	419	C	CC	C	CA	TA	T
	ATGTTAGCATTCTGTGCGAT		TCATATGAC		GTC	GTAT	AGT	AA	CTATGT	GCA T
	ATAGCTTTCACATCATATGAC									
			CAG	TATA	TCA	TT	GATATA	TGT	T	
			-	C-	C	TC	GC	C		

GAM85	TAGCTTTCATAGTTAGATAC	71	CAGAAGTAGG	420	----	GTCTCA-	---	T	A	CT
	ATGGTCTCAGAAGTAGGATT		ATTATGTAAC		AGTTAG	ATACATG	GAA	GTAGGATTA		
	GTAAC TCAG TCG A									
	ATGTAACATCAGCTTCGATA		ATCA							
	AAATGACTGGGTTATTTAGT				TCAATT	TATGTAC	CTT	CATTCTGAT	TATTG	GGTC
	AGT A									
	CTTACACATTCGCTCATACA				GCCAG	ATACTCG	ACA	T	-	-- AA
	TGTATGACCGTTAACTACAG									
	AGTCTA									

GAM86	TCGTAAGATACTCCTTCATG	72	TATGAAGTAA	421	A	C--	GAAC	TCA	A
	AACATAATCAGTTACAAAAC		AGTATCTACG		TCGTA	GATACT	CTTCAT	ATAA	GTT C
	GTTTATATGAAGTAAAGTAT		A						
	CTACGA		AGCAT	CTATGA	GAAGTA	TATT	CAA	A	
			-	AAT	----	TG-	A		

GAM87	TTCACCGTTTGCATGTTACC	73	CCGTTTGCAT	422	C	C	TTACCACTATCA	AA
	ACTATCAACCGCATAATACA		GTTACCACTA		TTCAC	GTTTG	ATG	ACCGCAT T
	ATGCGGTGTTTCCTTTGTCA		TCAA					
	TCAAATTGTGAA		AAGTG	TAAAC	TAC	TGGCGTA	A	
			T	-	TGTTTCCTTTG-	AC		

GAM88	TTTCAGGAGATGATCTCGCC	74	GCTACAGTTC	423	-----	-	C	C	T	TACCA--	A	T
	GTAGCTACCATGATAGTAGA		CTTGTTTCGTC		TTTCAG	GAGAT	GAT	TCG	CG	AGC	TG	
	TAGTAGA G											
	TGCCTCTGCTACAGTTCCTT		GACA									
	GTTTCGTCGACATCTATCTTT				AAAGTC	TTCTA	CTA	AGC	GC	TTG	AC	ATCGTCT C
	GCATTCTGAAA		TTACGT		T	C	T	-	TTCCTTG	-	C	

GAM89 TGATGCATTAATTTTTGTAT 75 TGCATTAATT 424 C A A TTC CCTAAAA AAAA
AATAAG
TGATTCTCAATCCTAAAAAC TTTGTATTGA TGATG ATTA TTTTTGT TTGA TCAAT ACT
TATG T
TAAAATATGAATAAGTATTA TTCT ||||| ||||| ||||| ||||| ||||| ||||| |||||
AACATAGCGGTGTACTAATT ATTGT TGAT AAAAATA AATT AGTTA TGG ATAC /
GATTTAACATAAAAAATAGT - A C T-- ATCATG- CG-- AAATTA
TGTTA

GAM90 GTTGTTTTGCGATAGCCATG 76 TGTTTTGCGA 425 TG T A CCAT---- A CAG
TATCTACTAATCAGATCTAT TAGCCATGTA GT T TTGCG TAG GTATCT CTAAT A
TAGAGATATTATTAATTCTG TCTA || | ||||| ||||| ||||| |||||
GTGCAATATGAC CA A AACGT GTC TATAGA GATTA /
GT T G TTAATTAT - TCT

GAM91 ACTGATTCTGGACATAGCTT 77 TAAGTTTGGC 426 T GACA T C G----- AT
TCCGACTGGCGCATTTGGTG AGCTAGCAGA ACTGA TCTG TAGCT TC GACT GCGC T
TGATGGTTCCCATAAAGTTTG TTCA ||||| ||||| ||||| ||||| |||||
GCAGCTAGCAGATTCAGT TGACT AGAC ATCGA GG TTGA TGTG /
T G--- C T ATACCCTTGGTAG GT

GAM92 ATATGTGTATTATCAGATAT 78 TCCTCCTAGG 427 T T AAAATTTT ATG
CCAAAATTTTGTATGAAGAA ATATTTGTAA ATATG GTATTA CAGATATCC GT A
CTCCTCCTAGGATATTTGTA TATC ||||| ||||| ||||| ||||| |||||
ATATCTATGT TGTAT TATAAT GTTTATAGG CA /
C - ATCCTCCT AGA

GAM93 ATCATCATTTTTTTCACCATT 79 TGAGAATACT 428 A TTTTCACCATTAC TC - CA
ACTTCTTCCATGTCCAATAT AAAATTCCTA ATCATC TT TTCT CATG TC A
GATCATGTGAGAATACTAAA ACGA ||||| ||||| ||||| ||||| |||||
ATTCTAACGATGAT TAGTAG AA AAGA GTAC AG T
C TCCTTAAATCAT GT T TA

GAM94 GAAATTGTTGCTCCCATGGA 80 TAATAGTTAC 429 AA T TCC GAA CCAA T
ATGACCCAATAAGTAGATT CACGTGCTGT GA TTG TGC CATG TGAC TAAG A
AATAGTTACCACGTGCTGTA ACCA || ||||| ||||| ||||| |||||
CCAAAGTC CT AAC ATG GTGC ATTG ATTT G
GA C TC- ACC ATA- A

GAM95 TGGTTCTTTCCATAGTACAT 81 TCCATAGTAC 430 TCT GTACATAG GGTG
AGTTGTTGCGGTGCAGAAGC ATAGTTGTTG TGGT TTCCATA TTGTTGC C
AATAAATACAGAGTGTGGAA CGGT ||||| ||||| ||||| |||||
CACCA ACCA AAGGTGT AATAACG /

C-- GAGACATA AAGA

GAM96 TTAATAGTTTACACCTTTTA 82 TAGTAGGACT 431 TTTTA A C TA-- -- CAT CT
GAATTCCA
GTAGGACTAGTATCGTACAA AGTATCGTAC ACACC GT GGA TAG TCGT ACAATT AG
GTATTTT A
TTCATAGCTGTATTTTGAAT AATT ||||| ||||| ||| ||||| || |||||
TCCAATCACGCATAAAAATA TGTGG TA CCT ATC AGCA TGT TAA TC TATAAAA
T
TCTTCCAATTGTTGACGAAG CCTAC - A CAGA GT CCT -- ATACGCAC
ACCTAATCCATCATCCGGTG
TAATATTAA

GAM97 TTCATCCGATAAACTCCAAT 83 TTTGTGGTAT 432 - AACT A G GATA
AAAAAGATGATATATCTAGT TGGATAGAA TTC ATCCGATA CCA TAAAAA AT T
GTTTTTGTGGTATTGGATAG ||| ||||| ||| ||||| ||
AA AAG TAGGTTAT GGT GTTTTT TG A
A ---- - G ATCT

GAM98 TTAGTGACAGACCAGACCTA 84 TGACAGACCA 433 T ----- GA --- TC
GGAGCTATTCTACCATAGCA GACCTAGGAG TTAG GACAGA CCA CCTAGGA GCTAT T
AATCTTAGGCATGGACATAC CTAT ||| ||||| ||| ||||| |||||
TAATATCTGTCTTAA AATT CTGTCT GGT GGATTCT CGATA A
- ATAATCATACA AC AAA CC

GAM99 AACAAAGAAATGGAAATCGT 85 TTGAAATTGT 434 AG T TAATACC T
AATACCAGTTATGTTTAACT TTTTATTTT AACAA AAATGGAAA CG AGTTA G
TTGAAATTGTTTTTTATTTT CTTG ||||| ||||| ||| |||||
CTTGTT TTGTT TTTATTTT GT TCAAT T
CT T TAAAGTT T

GAM100 TTCCACTGTCCAAAATGATG 86 TCCAAAATGA 435 ACT A G - C CCTTTTTA
CCTCTGCCTTTTTTATACATG TGCCTCTGCC TTCC GTCCAA AT ATG C TCTG T
TTCCAGATGTCATAATATTG TTTT ||||| ||||| ||| |||||
GATTGGGAA AAGG TAGGTT TA TAC G AGAC /
GT- A A T T CTTGTACA

GAM101 CTGTGACCAAGATAGAGAGC 87 GTGAATCCAT 436 ACCA GCTCC-- TGAAT T CTA
AGTTT
TCCTTTGGTGAATCCATCTC CTCTATGTTT CTGTG AGATAGAGA TTTGG CCA CT
TGTTTC A
TATGTTTCAGTTTAACCAAG CAGT ||||| ||||| ||||| ||| ||| |||||
AAACAGTCAGCTGGTCTAAA GACAT TCTATCTCT AAATC GGT GA ACAAAG /
ATTTCCATCTCTATCTAATA AA-- ACCTTTA T---- C CTG AACCA
CAG

GAM102 GTTCTTTTAGAAGTGATTC 88 GAAGTGATTC 437 T-- GAA TT- A G
 TTTGATGGTGTGAGCATACG TTTGATGGTG GTTCT TTA GTGATTC TG TG T
 AATTACAATAATGCAGAAAC TCAG ||||| || ||||| |||
 CAAAGA AAT CATTAAG AC AC G
 CGT AA- CAT G T

GAM103 TTGATACGATATTTGTTGGA 89 TTTGTTGGAT 438 TACGA- - CCTG TT
 TTCCTGATTATTTACTATAA TCCTGATTAT TTGA TATTTGT TGGATT ATTAT A
 TATAATCTAGACAGATAGAT TTAC |||| ||||| ||||| ||||
 GATTCGA AGCT ATAGACA ATCTAA TAATA /
 TAGTAG G TA-- TC

GAM104 AATATCGGGCCAATAGTAGC 90 GGCCAATAGT 439 CG A AG - C
 TATTACCGTGCACACGTGTA AGCTATTACC AATAT GGCCA TAGT CTATTAC CGT G
 GTGGGAACATATGGCCAAATG GTCG |||| |||| |||| ||||| |||
 TT TTGTA CCGGT ATCA GGTGATG GCA A
 AA - AG T C

GAM105 AGACTTCTGGCGGTTGCCAT 91 TTATCCCAAT 440 ---- CG CCAT- ATA
 AGAATATACGTCGTTCTTAT TACCAACTAG AGACTTCT GG GTTG AGAAT C
 CCCAATTACCAACTAGAAGT AAGT ||||| || |||| ||||
 CT TCTGAAGA CC TAAC TCTTG /
 TCAA AT CCTAT CTG

GAM106 GAAGTTTTTGGAGAATAATA 92 GGAATTGGAG 441 GAATAAT ----- TATT CA
 ACA A G
 TGACTCATGATCTATTTTCGT GCGATGATCT GA ATGACTCAT GATC TCGTC TAA
 TCTA A
 CCATAACAATCTAGACATA TAAT || ||||| |||| ||||| ||||
 GGAATTGGAGGCGATGATCT CT TGCTGAGTA CTAG AGCGG GTT GGAT
 C
 TAATTTTGTGCAATGAGTCG AAC---- ACGTGTTTTAATT T--- AG AA-- A
 TCAATCCTATAACTTC

GAM107 TAATCCCTTTTTCAGATGCC 93 GCGCTCCCCT 442 - TTTTCA GCCTCTTTTA CA
 TCTTTTAGTTTATCAAAAAT AGTCGACTC TAATCC CT GAT GTTTAT A
 AAGCGCTCCCCTAGTCGTAC AGAG ||||| || ||||| |||||
 TCAGAGGATTA ATTAGG GA CTG CGAATA /
 A CTCATG ATCCCCTCG- AA

GAM108 TTAAATAGTTACGCAATATC 94 TTAGCTGTTT 443 TTAC T C----- T- T
 TCAATAGTTTCATAATTGTT TCATCAAGAT TTAAATAG GCAA ATCT AATAGTT CA A
 AGCTGTTTTTCATCAAGATTT TTGT ||||| |||| ||||| ||||| ||
 GTACCCTGTTTAA AATTTGTC TGTT TAGA TTGTCGA GT A
 CCA- - ACTACTT TT T

GAM109 TGCCGTTACTATTATTTATA 95 TATTATTTAT 444 C AT--- TAA TG A C
 ACTGATGTAACCCACGTAAC AACTGATGTA TGC GTTACTATT TTA C ATGT AC C
 ATTGGAATTAACATATCGATA ACCC ||| ||||| ||| | ||| ||
 GTAATGCA ACG TAATGATAG AAT G TACA TG A
 - CTATC TAA GT A C

GAM110 ACACGCGTGTCTAACTAGTG 96 ACGCGTGTCT 445 G - A TCGTCA T AGTT A
 GAGGTTTCGTCAGCTGCTCTA AACTAGTGGA ACAC CGTGTC TAACT GTGGAGGT GCTGC CT
 TGA T
 GTTTGAATCATCATCGGCGT GGTT |||| ||||| |||| ||||| |||| || |||
 AGTATTCCTACTTTTACAGT TGTG GCACAG ATTGA CATTTC A TGATG GG ACT C
 TAGGACACGGTGT - G - TCCTTA C CT-- A

GAM111 CAGCATCCGGCTTATCCGCC 97 CGAGGAGGAA 446 A T- - G C TCA
 TCCGTTGTCATAAACCAACG TATCGTCGGA CAGC TCCGGC TAT CC CCTC GTTG T
 AGGAGGAATATCGTCGGAGC GCTG |||| ||||| ||| || |||| ||||
 TG GTCG AGGCTG ATA GG GGAG CAAC A
 - CT A A - CAA

GAM112 CCATTAATATCTCTATTATA 98 TATACCAGAA 447 ATCTCTATTATAGCT AC TC
 GCTTCTGGACATAATTCATC TTAATGG CCATTAAT TCTGG ATAAT A
 TATTATACCAGAATTAATGG ||||| |||| ||||
 GGTAATTA AGACC TATTA T
 ----- A- TC

GAM113 CTTCAATTATGAATTGATTCT 99 TGAATTGATT 448 T T ---G TAT-- C-- CA TT TAG
 TT
 TGAGGTATAAACCTAACACA CTTGAGGTAT A GAAT GATTCT T AGG AAAC TAACA AA
 ATATTAT AC T
 AATTATATTATTAGACTTTT AAAC | |||| ||||| | ||| |||| ||| ||||| ||
 CGTATGTAATGTCTTTTCATG T TTTA CTAAGA G TCC TTTG ATTGT TT TGTAATG
 TG /
 TTATAAGTTTTTAATCCTGG - T TAA G TAATT AAT AC TC TA- CT
 AATAGAATCTATTTTAATGA
 GG

GAM114 GAAGAGATGTAACGGGAACA 100 ACGGGAACAG 449 -- ACG CAG TG
 GGGTTTGTTGATTTCGCAAAC GGTTTGTTGA GAAGAG ATGTA GGAA GGTTTG T A
 TATTCTAATACATAATTCTT TTCG ||||| ||||| |||| |||||
 C CTTCTT TACAT TCTT TCAAACG T
 AA AA- A-- CT

GAM115 GTTAATACGTCTTGACGTA 101 TGCACGTAAT 450 - C- CTAT CC
 ATCTATTATAGATGCCAAGA CTATTATAGA GTTAATA CGTCTTGCA GTAAT TATAGATG A

TATCTATATAATTATTTTGT TGCC ||||| ||||| ||||| |||||
AAGATGATGTTAAC CAATTGT GTAGAATGT TATTA ATATCTAT A
A TT AT-- AG

GAM116 GTTTTTGATATCGATCTGAT 102 TTCATATTTA 451 ATCG T CCTA A-
ATAACGTGCTC A TT
TGATCCTAGAACTAGATATA TTAGATACCG ATCTGAT GAT GAACT GATATATTA
ATTAGGC GT A
TTAATAACGTGCTCATTAGG CATT ||||| ||| ||||| ||||| ||
CAGTTTATGGCAGCTTGATA TAGATTA TTA CTTGA TTATATGAT TAGTTCG
CG /

ATTAGATATAGTATATTCCA CA-- T TA-- CC ATAGATTAA-- A GT
GTTTCATATTTATTAGATACC
GCATTGC

GAM117 TAATGGTGACAGGGTTAGCA 103 TATGATCCTC 452 T C GCA- CCAATCAATA TTT
TCTTTCCAATCAATAATTTT TCTCATTG TAATGG GA AGGGTTA TCTTT ATTTT A
TTTAGCCGGAATAACATCAT ||||| || ||||| ||||| |||||
CAAAAGACTTATGATCCTCT GTTACT CT TCCTAGT AGAAA TAAGG /
CTCATTG - C ATTC ACTACTACAA CCG

GAM118 TCGTTTAGATTTTCCATCTG 104 TAGGAGAGTT 453 TTA T TCCATCT TATCG A C CG-
A

CCTTATCGAATACTCTTCCG ACTAGGCCCA TCGT GA TT GCCT AAT CTCTT CGT
ATGTCT C
TCGATGTCTACACAGGCATA ACTG |||| ||| |||| ||| ||||| |||||
AAATGTAGGAGAGTTACTAG AGCA CT AG CGGA TTG GAGGA GTA TACGGA A
GCCCAACTGATTCAATACGA TAA T TCAACC- TCA-- A T AAA C

GAM119 TGATGTAGTACTTTGATGAT 105 TAAGTCTTCC 454 AGT T T TTCC CC
TTTTCCATGGCCCATTTCTAT AAGTTGGCAT TGATGT ACTT GA GATTT ATGG C
TAAGTCTTCCAAGTTGGCAT CA ||||| ||||| ||||| |||||
CA ACTACG TGAA CT CTGAA TATC A
GT- C T T--- TT

GAM120 TTGGTAACTCATTCTATATA 106 TAGAATATAC 455 A TC ----- G T GTT
TGCTTTCTTGTTGATGAAG TCAATAGAAT TTGGTA C ATTCTA TATAT CT TCCTT G
GATAGAATATACTCAATAGA TTGT ||||| || ||||| ||||| |||||
ATTTGTACCAA AACCAT G TAAGAT ATATA GA AGGAA /
- TT AACTC A T GTA

GAM121 TTTCTAAGATATGGGATTTT 107 TAAGATATGG 456 A-- A G ACT T A TC
ACTTAATATAATATTATTTT GATTTTACTT TTTCT AGAT TGG ATTTT TAATA AAT TTATT C
CCGTAATAAATTTTATTAGA AATA ||||| ||||| ||||| ||||| |||||
AATGCCAAATCTATAAGAAA AAAGA TCTA ACC TAAAG ATTAT TTA AATAA C
ATA A G --- T - TG

GAM122 TCTAGTTATCAATAACAGTT 108 TCAATAACAG 457 GTTA C-- - TTAG- TA
 AGTAGTTTAGTTATACATTG TTAGTAGTTT TCTA TCAATAA AGTTAGTA GT TTA C
 AATCATACATATTAATTTT AGTT |||| ||||| ||||| || |||
 TTATTGAGATAGA AGAT AGTTATT TTAATTAT CA AGT /
 AG-- TTT A TACTA TA

GAM123 TCCGCACTATCGATTTGATA 109 TAAAGCTATC 458 CACT T- - - T
 CTTTCTTTTCAGAGTAAAGC GTCATTGATC TCCG ATCGAT TGATA CTTT CTT T
 TATCGTCATTGATCATCGGA ATCG |||| ||||| ||||| |||| |||
 AGGC TAGTTA GCTAT GAAA GAG C
 TAC- CT C T A

GAM124 TTCTAGAGTAGTAGTCCTAA 110 TCTTATTGTC 459 T CT CATTCTCT--- TTAT- TCCT
 TT ATGT GT
 TCATTCTCTTAAATTTTATG TGATTTATTT TAG AGTC AAT TAAATT GTA AGT CA
 CTC A
 TATCCTAGTTTCAATGTCTC CTTT ||||| ||||| ||||| ||||| ||||| ||||| |||||
 GTAATGAGTTTGTGCTGCTC ATC TCGG TTA ATTTAG TAT TCG GT GAG /
 TTATTGTCTGATTTATTTCT - TT CCATTTTCTTT TCTGT TC-- TC GTTT TA
 TTTACCATTTTGGCTCTATT
 CTGAA

GAM125 GATCTATAGTCTTCGTATCT 111 TGTTACGAAA 460 - CTTC- CT T AA TAT TT
 GTTACGAAAATCAATATATT ATCAATATAT GATC TATAGT GTAT GTACGA ATCAA
 ATTCAGGA A
 CAGGATTATTTTCTGAATCA TCAG ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CTTGATTCGTCACATAATATA CTAG ATATCA TATA CA TGCT TAGTT TAAGTCTT /
 CATAACTATATGATC T ATACA AT C -- CAC TT

GAM126 TGTACGATTGTATTGCGTTA 112 TTAGTCAATG 461 A TATT - AC TAA
 CTAACGATAAATAATTCTT CTTTAAACGTA TGTACG TTG GCGTT ACTAA GA A
 AGTCAATGCTTTAACGTACA CA ||||| ||||| ||||| ||||| ||||| ||||| |||||
 ACATGC AAT CGTAA TGATT CT T
 - TT-- C -- TAA

GAM127 GCGTATCTACTACTCCAAAT 113 TCCAAATTGC 462 CTA CTCCA A TTC TAT
 TGCAGTTTCTGGTATCCATC AGTTTCTGGT GCGTATCTA AATTGC GT TGG C
 CATACGCGTAATTATCAAAT ATCC ||||| ||||| ||||| ||||| ||||| ||||| |||||
 AGATATGT TGTATAGAT TTAATG CG ACC /
 AA ACTA-- - CAT TAC

GAM128 TATATCCTACCGCTTTTTAT 114 TAATAAGATG 463 CG TTT C-- -- ATG TTTTATGTTAT
 TTA TTA
 CA ACTATGTAATGAGTTTTT CTAATACATC CT TAT AACT ATGTA AGT GTCTT
 GTTAGG A

ATGTTATGTCTTTTAGTTAG AGGT || ||| |||| |||| || |||| |||||
 GTTAATATTCTAATAAGATG GA ATG TTGG TACAT TCG TAGAA TAATCT /
 CTAATACATCAGGTAAAGT A- TT- AAA AC AA- ----- --- TAT
 ATTAGAATGGGATTATA

GAM129 ATCAGACCATATACTGAGTT 115 TGAGTTGGCT 464 AC TAT TT - ---- - CGT
 GGCTACTATCTTGTACGTAT ACTATCTTGT ATCAG CA ACTGAG GGCTA CTA TCT TGTA A
 ATTGCATGGAATCATAGATG ACGT ||||| || ||||| ||||| ||| ||| |||||
 GCCTTTTCAGTTGAACTGGT TGGTC GT TGA CTT CCGGT GAT AGG ACGT /
 AA --- TT A ACTA T TAT

GAM130 TAGTCACGACTGAAATAACC 116 CGGCATGGTT 465 ACT AA-- C -- TTT
 GCGTGATTATTTTTTGGTAT TCTGTGACTA TAGTCACG GAAAT CCG GT GATTAT T
 AATTCTACACGGCATGGTTT ||||| ||||| ||| ||| |||||
 CTGTGACTA ATCAGTGT CTTTG GGC CA TTAATA T
 --- GTAC A TC TGG

GAM131 TCATCCAATATTATTGAAAT 117 TGATGGACAG 466 CA TTGA- TT CAG TACAAATA
 A AC T C
 GACGTTGATGGACAGATGAT ATGATACAAA ATATTA AATGACG GATGGA ATGA AGA
 GGT GG AC T
 ACAATAAGAAGGTACGGTA TAAG ||||| ||||| ||||| ||| ||| ||| |||
 CCTTTGTCCACCATCTCCTC TGTAAT TTA CTTG TTATCT TACT TCT CCA CC
 TG T
 CAATTCATGCTCTATTTTGT -- TTCAA T- CG- TAACCTCC A -- - T
 CATTAACTTTAATGTATGA

GAM132 TCGTCGGTATTTTTTATGGC 118 CGGTATTTTT 467 CG A C TTTACTCT
 AAAC TTTACTCTTCCAGCAT TATGGCAAAC TCGT GTATTTTTT TGG AAAC T
 CCGTTTCTAAAAAATATTA TTTA |||| ||||| ||||| ||| |||
 ACGA AGCA TATAAAAAA ATC TTTG C
 AT - - CCTACGAC

GAM133 ACCATTCCAAGTCACTGTGT 119 TATCATAAGC 468 TTCCA CTG- TA GAT
 GTAAGAAGATTATATTCTAT TTGACTACAT ACCA AGTCA TGTG AGAA T
 CATAAGCTTGACTACATTTG TTGG |||| ||||| ||||| ||| |||
 GT TGGT TCAGT ATAC TCTT /
 TTACA TCGA TA ATA

GAM134 ATATCTTTAACTAAGTCAAT 120 TCAATGATTT 469 AACT ATTCATCAACCG-- TC
 GATTTTCATCAACCGTTAGAT CATCAACCGT ATATCTTT AAGTCAATG TTAGA T
 CTATTTTAAAGTTAATCATA TAGA ||||| ||||| ||||| ||| |||
 TAGGCATTGATTTTAAAAG TATGGAAA TTTAGTTAC AATTT /
 GTAT ATT- GGATATACTAATTGA TA

GAM135 CAGCCGAAACATATTCTACC 121 CATGGCTCCG 470 CC ATTCTACC GC A- T
 ATGGCTCCGTTTAATTTGTT TTTAATTTGT CAG GAAACAT ATG TCCGTTT ATT G
 GATGAAGATGGATTTCATCCT TGAT ||| ||||| ||| ||||| |||
 TAAATGTTTTCTCTG GTC TTTTGTA TAC AGGTAGA TAG T
 TC AATTCC-- TT AG T

GAM136 CCGTTTTTAGACCGAGACTC 122 TAACTCGGAT 471 TTT- - ACTCCA TAAA CA
 CATCCGTAAAAATGCATACT CTGCTATATG CCGT TAGA CCGAG TCCG AATG T
 CGTTAGTTTGGAATAACTCG G |||| ||| ||||| |||| ||||
 GATCTGCTATATGG GGTA GTCT GGCTC AGGT TTGC A
 TATC A AATA-- TTGA TC

GAM137 CGCTTCTATCTTGTTTAGAT 123 TGA CTAGATA 472 ---- GTTT TT TAAA TCTC--
 ACATA
 TTATTTTTATAAAGTTTAGT AACTATCAGT TCTATCTT AGATTTATT TA GTTTAGTC
 CTGCCA A
 CTCTCCTTCCAACATAATAA AAGT ||||| ||||| || ||||| |||||
 AAGTGGAAGTCATTTGACTA AGATAGAG TTTGAATGA AT TAGATCAG GAAGGT
 T
 GATAAACTATCAGTAAGTTT AAGC ATAT CT CAAA TTTACT GAAAA
 TATAGAGATAGACGAACAAT
 TAGCG

GAM138 GACATACATACTATCTTTAA 124 ACTATCTTTA 473 C TT----- CTCT C--- AAT--
 T
 TAGAACTCTTTTCATCCAGT ATAGAACTCT CATA TATCT AATAGAA TTTCAT CAGTTG
 GGA T
 TGAATGGATTGTCCTTAAC TTTC ||| |||| ||||| ||||| ||||| |||
 CAACTGATTAATGAGATCTT GTAT GTAGA TTATCTT AGAGTA GTCAAC CCT
 C
 CTATTTTATCATTTTCCAGA A CCTTTTACTATT CT-- ATTA CAATT G
 TGATATGTATGTC

GAM139 TACAAAGGAGATGATTTATC 125 TATGGTATTA 474 ----- TTATCTAT TT - C TC
 A
 TATGGTATTAAGAATTCGTT AGAATTCGTT ACAAAGGA GATGAT GGTA AAG AATT
 GTTTT GAC T
 TTTCGACATCCGTCAAAACC TTTC ||||| ||||| ||| ||| ||||| |||
 AATTCCTTTTGCCTGTATC TGTTTCCT CTACTA CCGT TTC TTAA CAAAA
 CTG C
 ATCCAGTTTTCCATCCTTTG ACCTTTTGAC TGT----- TT C C -- C
 TA

GAM140 TGTCAC TTTGTTATTGGCCA 126 TTCCTCGGCC 475 --- T-- AACC-- TT
 ACCTTTGTTGTACAAATTCC ATTTAATAT TGTCAC TT TGTTA TGGCC TTTG G
 TCGGCCATTTTAATATTTAA TTAA ||||| ||||| ||||| ||||
 GTGATA ATAGTGAA ATAAT ACCGG AAAC /
 TTT TTT CTCCTT AT

GAM141 TTGCTAGACACCTTTTCAAT 127 TTTGATAAAG 476 T ACAC- - T A T
 GTTTAATTTTTTTGAAATAA CCTTCCTCGC TTGC AG CTTT TCAA GTTTA TTT T
 GCTTTGATAAAGCCTTCCTC AA ||||| ||||| ||||| |||||
 GCAA AACG TC GAAA AGTT CGAAT AAG T
 C CTTCC T T A T

GAM142 CACCGCCTCTAGATATCGCC 128 CGCCTTTATT 477 CG ATCG-- TTTAT ACATT
 AAATCCA
 TTTATTTCCACATTAGATGG TCCACATTAG CAC CCTCTAGAT CC TTCC AGATGGT
 A
 TAAATCCAATAGTGAAACTA ATGG ||| ||||| || ||| |||||
 TCTTTTATAGGAATGTATGGA GTG GGAGATTG GG AAGG TCTATCA /
 CTCGCGTTTAGAGGAGTG A- CGCTCA TATGT ATTTT AAGTGAT

GAM143 GACACTTTGCCGGCGGTTGT 129 ACATATCCGT 478 CT CC T-- ATTTATCA
 AGATTTATCATATTTCTCCA TACAATTTGT GACA TTG GGCGG TGTAG T
 CTACATATCCGTTACAATTT T ||||| ||||| ||||| |||||
 GTT TTGT AAC TTGCC ACATC A
 TT A- TAT ACCTCTT

GAM144 GAGACTTGATAGATATTAGT 130 TCACCACGTG 479 - - TAG TA- TTGAA
 GATGAATTGAAAATTATTT TGTTCAGGA GA GA CTTGA ATAT GTGATGAA A
 TATCACCACGTGTGTTTCAG TCAT ||||| ||||| ||||| |||||
 GATCATC CT CT GGA CT TGTG CACTATTT A
 A A TTG CAC TTATT

GAM145 GGCTATTCTGGCGGCTAGAA 131 TGCTATTTCTG 480 C TA TAAT GA TGT
 TGGCATAATCCGGATGTTGT GCTGCCAGAG GG TATTCTGGCGGC GAATGGCA CCG TGT
 G
 GTAGTACAAGTGGCTGCTAT TGTC ||||| ||||| ||||| ||||| |||||
 TTCGGCTGCCAGAGTGTCC CC GTGAGACCGTCTG TTTATCGT GGT ACA T
 T GC C--- GA TGA

GAM146 TATATACGATAAGATATGTT 132 TAAGATATGT 481 C --- TTT A ----- -- AATT
 TATTCATAAACGCGTCAAAT TTATTCATAA TATATA GATAA GATATG ATTC TAAAC GCG
 TCA T
 TTTTCATGAATCGCTAAGGA ACGC ||||| ||||| ||||| ||||| ||||| |||||
 GTTTAAGAATCTCATGTCAA ATATAT CTGTT CTGTAC TAAG ATTTG CGC AGT /
 ATTGTCCTATATA C AAA TC- A AGGAAT TA ACTT

GAM147 TCTGGTTCTATGTTCTCTCGT 133 TCTATGTTCC 482 TC --- TT C TATT
 TTCCTGTATTCTTTTAAAGA TCGTTTCCTG TCTGGT TAT GTTCCTCG TC TG C
 TCGAGGAACGCCATAATATC TATT ||||| ||||| ||||| ||||| |||||

AGACTA ATA CAAGGAGC AG AT /
TA CCG T- A TTTT

GAM149 TTCCTTTTCGTTGATCTCTC 135 TCGTTGATCT 484 CGTT TCT TA G
ATAGATTTAGAAATAAATTC CTCATAGATT TTCCTTTT GATC CA GATTTA A
TTGCGATCCTCCAAAAGGAG TAGA ||||| ||| || |||||
GAGGAAAA CTAG GT TTAAAT A
CCTC C-- TC A

GAM151 GTATATCATCAGCTGAAAAA 137 TTCCTTCGGC 486 CA----- AAAC TT
CTATGTTTTACACGTATTCC ATTTCTTTTT GTATATCAT GCTGAA TATGT T
TTCGGCATTCTTTTAAATG AATG ||||| |||| ||||
ATATAT TATATAGTA CGGCTT ATGCA /
ATTTTTCTTTA CCTT CA

GAM153 GGATTTTAGAATTTCCAAAT 139 TGAAATCCAA 488 T AATT AAA--- --- T
TCACCAGCGATTTATCGGTT GGATTTATTA GGAT TTAG TCC TTCACCAG CGA T
TTGGTGAAATCCAAGGATTT ATGT |||| ||| ||||| ||
ATTAATGTCC CCTG AATT AGG AAGTGGTT GCT T
T AATT AACCTA TTG A

GAM154 ATGGTCGAAGTATAGCAGGA 140 TAGCAGGACA 489 ---- A CATT- GCTC CCG TA

CATTGATGCTCTAGACCGTG TTGATGCTCT ATGGT CGAAGTATAGC GGA GAT TAGA TG
 T
 TATAACAAAATCTACAAATT AGAC ||||| ||||| || || ||| ||
 TTTCATCCGCTATATTTTGT TATCA GTTTTATATCG CCT TTA ATCT AC /
 TTCACTAT CTTT - ACTTT AAC- AAA AA

GAM155 GGTGTTAATCCACTATATGT 141 TCCACTATAT 490 T - ----- - A--- C ATAACA
 CAT
 TTCTGTAGCGGCTGATAACA GTTCTGTAG GGTGT AATC CACT ATATGT TTCTGT GCGG
 TG CAG C
 CAGCATCCAACTGAGCATCC CGGC ||||| ||| ||| ||||| ||||| ||| || |||
 GCGTCCGCAGAGCACATATT CTACA TTGG GTGA TATACA GAGACG CGCC AC
 GTC /
 TTTAACAGTGAGGTTACATC - A CAATTTT C CCTG T GA---- AAC

GAM156 GTTAGCAAGAAATTAACATT 142 TTCCGCATAT 491 C A-- CATTG ATT C A T TCCC
 GGCATTCCGAACACTCTGGAT TTTAATGACT GTTAG AAGA ATTAA GC GAAC CTC GGA A
 CCCAACATTCTCGAGGTTCC CTC ||||| ||| ||||| || ||| ||| |||
 GCATATTTTAATGACTCTTC CAATC TTCT TAATT CG CTTG GAG TCT /
 TAAC - CAG TTATA C--- - C TACA

GAM157 TCAGTGGGTACTCCCGGAGG 143 GAGCTCAACA 492 TACTCCC-- A ----- GT
 CGGATCCCGTTTtagggagct CTTACTCCGC TCAGTGGG GG GGCGGA TCCC T
 CAACACTTACTCCGCCACCC CACC ||||| || ||||| |||
 ATATTTATCTCATTGA AGTTACTC CC CCGCCT AGGG /
 TATTTATAC A CATTCACTCG AT

GAM158 ACACGACTGTGGTAGATTTG 144 TGTGGTAGAT 493 C TG-- A T AGA C T
 TTCTATAGAGCCGTTGCGG TTGTTCTATA ACA GAC TGGTAG TTTGT CTAT GC GG T
 CAAATAGATAGAACTACCAA GAGC ||| ||| ||||| ||||| ||| |||
 TATGTCTGT TGT CTG ACCATC AGATA GATA CG CC /
 - TATA A - AA- - G

GAM159 ACAGTTTGAAAAATAACAGT 145 AACAGTATCA 494 AATA TCATTTAAACAT TG
 ATCATTTAAACATTTAACCTT TTTAAACATT ACAGTTTGAAA ACAGTA TTAAC C
 GCGGGGTTAATTTCACTACT TAAC ||||| ||||| ||||| |||||
 TTAAGCTGT TGTCGAATTTT TGTCAT AATTGG /
 ---- TTCAACACTTT- GG

GAM160 CCACCTGTTTTAACATATAA 146 TAATATTGAT 495 T- -- GA T TATCCGTCATTG- -----
 --- TT
 TAGGCAGGAGATAGATATCC AAAATCTCCA ATAATAG GCAG GA AGA CAATATT
 CCT T
 GTCATTGCAATATTCCTTTT TTCT ||||| ||| || ||| ||||| |||

CGTAGGCACACAATCTAATA TATTATT CGTC TT TCT GTTATAA GGA C
TTGATAAAATCTCCATTCTC TC TA TC C TACCTCTAAAATA TCTAACACAC TG
TTCTCTGCATTTATTATCTT
GTTTCGGTGG

GAM161 TACTTTTTCTTTACCTTGAG 147 TGAGAATATC 496 TTTACC -- T - CGT TGG
AATATCCATCGTTTGCTTGG CATCGTTTGC TACTTTTTTC TTGA GAA ATC CAT TTGCT T
TCAATAGCGATATGTGATT TTGG ||||| ||| ||| ||| |||
TTTATCAACCACTCGAAAAA ATGAAAAAG AACT TTT TAG GTA AGCGA C
GTA CTCACC AT T T T-- TAA

GAM162 TAGTACTAGACTGACTTCTA 148 TATTAAAGTC 497 TAC CT C-- A A CTCACCTG
ACAAACATCTCACCTGCCAT TTCTATTTCT TAG TAGA GACTT TA CAA CAT C
AAATAAATGCTTGATATTAA A ||| ||| ||| ||| |||
AGTCTTCTATTTCTA ATC ATCT CTGAA AT GTT GTA C
TTT T- ATT A C AATAAATA

GAM163 AAATTATTCTTATCATGCGT 149 ATTATTCTTA 498 T TATCAT TCC TCC T
CCATAGTCCCGTTCCGTATC TCATGCGTCC AAA TATTCT GCG ATAG CG T
TATTATCGTTAGAATATTTT ATAG ||| ||| ||| ||| |||
TTTATAAGA TGC TATC GC/
T T----- TAT TAT C

GAM164 ACATCCATTTTTTAAGTATTA 150 TTTTATAGATA 499 C TTA AAA- TC GTTTA
TATTAAAATTTAATCAATGT AAAAAATATAA ACATC ATTT AGTATTATATT ATTTAA AAT T
TTATTTTTAGTTTTTTTAGAT TATT |||| ||| ||||| |||| |||
AAAAAATATAATATTATGAG TGTAG TGAG TTATAATATAA TAGATT TTG /
TCGATGT C TA- AAAA TT ATTTT

GAM165 ATTTTATTACCGTGTGGGAT 151 TACCGTGTGG 500 TT G G ATAAA C TCCAT-- A
G
ATAAAAGTCCTTGATCCATT GATATAAAAG ATTTTA ACC TGTGG AT AGTC TTGA TG
TCTG A
GATCTGGAAACGGGCATCTC TCCT |||| ||| |||| ||| ||| |||
CATTTAAGACTAGATGCCAC TAAAAT TGG GCACC TA TCAG AATT AC GGGC A
GGGGTTTAAAAT T- G G GA--- - TACCTCT - A

GAM166 CTATCGGTTTACTATTTATT 152 GTTTACTATT 501 C T TTAT G A
GATAACGCAGATGTTTGAGT TATTGATAAC CTAT GG TTACTAT TGATAAC CAG T
TGTCATCCATGGTAATCCAT GCAG |||| ||| |||| |||
AG GATA CC AATGGTA ACTGTTG GTT G
- T CCT- A T

GAM167 GTACATGTGAAAATAGTCAT 153 CATGTGAAAA 502 CA- T- TCA - GAT AA AAAGT
CT

ATTCCTGATTAGGATAATCA TAGTCATATT GTA TGTGAAAA AG TATT CCT TAGGAT TC
 TAACAA A
 AAGTTAACAACACTACTTTGTT CCTG ||| ||||| || ||||| ||||| |||||
 ACGGACGATCTTATTAAGGT CAT ATACTTTT TC ATGA GGA ATTCTA AG ATTGTT
 /
 AGTACATCTTTTTTTCATAA TTA TT TAC T ATT GC GC--- TC
 TTTAC

GAM168 TGAAGAACATATTTAATTCA 154 TGAATACAAC 503 AACATATTTA GA AAAAT
 GATCTAAAAAATACATATAT GAATACTTCA TGAAG ATTCA TCTAA A
 TAGAATGAATACAACGAATA |||| |||| ||||
 CTTCA ACTTC TAAGT AGATT C
 ATAAGCAACA A- ATATA

GAM169 CAGCTACTTCTACCCAATCA 155 TTAATTGGTT 504 TC CAA GTAT T TTT---- --
 TA
 CCAGGCAATAAATGTATTTT TAATCGTTTA CAA ACCAGG TAAAT TTTATTTT AATAAAC
 CC TTGGCG T
 ATTTTAAATAAACTTTCCTT TTAA ||| ||||| |||| ||||| ||||| || |||||
 GCGTATTCTTGTTAATTGG GTT TGGTTC ATTTA AAATGAAA TTATTTG GG
 AATTGT T
 TTTAATCGTTTATTAAAGTA -- A-- ---- - CTAATTT TT TC
 AAATTTAACTTGGTTTGACG
 CTAATAGTTG

GAM170 TTGCAAGTTTCTGTTTCTGA 156 TTCCACAGAG 505 C TC T A- CG TCC
 GAGTAAACGAATCCCTGTTT CACTAATTTT TTG AAGTT TGTT CTG GAGTAAA AA C
 TATTTTATTCCACAGAGCAC CAA ||| ||||| ||||| ||||| ||||| ||
 TAATTTCCAA AAC TTAA ACGA GAC CTTATTT TT T
 C TC - AC TA TTG

GAM171 CCGCTTCTATTTACTCCCGC 157 CCGCAGCACA 506 C-- CTCCCG-- AC A AA
 AGCACAATGAACCAACACGG ATGAACCAAC CCGCTT TATTTA CAGC AATGA CC C
 GCTCGTTTCGTTGATCACAT ACGG ||||| ||||| ||||| ||||| ||
 TTAGATAAAAAGGCGG GGCGGA ATAGAT GTTG TTGCT GG A
 AAA TTACACTA CT C GC

GAM172 GTTAGGCAATGTATATTTAT 158 CAATGTATAT 507 - CA TATTTAT
 AAATTTAAAACATATT CT
 CCATCGTCAAATTTAAAACA TTATCCATCG GTTA GG ATGTA CCATCGTC TGAA T
 TATTTGAACTTAACTTCAGA TCAA ||| || |||| ||||| |||||
 TGATGGTGCATCCATAGC CGAT CC TACGT GG TAGTAG ACTT A
 A -- ----- CA

GAM173 ACTTTTTATGAAGAGCCGCG 159 TGAAGAGCCG 508 TAT A CG A--- C
 TTTAACAATGCTTTATTGTC CGTTTAAACAA ACTTTT GA GAGC CGTTT ACAATG T
 TCCGAACGTAGCTCTCTTAA TGCT ||||| ||||| ||||| |||||

GAGT

TGAGAA CT CTCG GCAAG TGTTAT /

TT- - AT CCTC T

GAM174 TCGTCATATCCCGTATAGTC 160 TTGAATTTAC 509 TATCCC ---- CA---- A
AGAGATAGGAATCTTGAATT TAATCTTGCC TCGTCA GTA TAGT GAGAT G
TACTAATCTTGCCCTTGTTG CTTG ||||| ||| ||| ||||
GCGG GCGGGT CGT ATCA TTCTA G
TGTTCC TCTA TTAAAG A

GAM175 CGCCTAATAGCTTGCGGCAG 161 TCCAATCGCA 510 ---- - CA- TGT
ATATGTTTTCTTATCCAATC TAGCTATAAA CGCCTA ATAGCT TGCGG GATA T
GCATAGCTATAAAATAGGCG ATAG ||||| ||||| ||||| ||||
GCGGAT TATCGA ACGCT CTAT T
AAAA T AAC TCT

GAM176 GCGCACTAATTGCCAATATA 162 TTGATGTTTT 511 C TAATT T A AAGAA
ATAACAAAGAATATAAGTGT GGCTGCTTGT GCG AC GCCAA ATA TAACA T
TGATGTTTTGGCTGCTTGTA ACGC ||| || ||||| ||| |||||
CGC CGCTG CGGTT TGT GTTGT /
A TTCGT T A GAATA

GAM177 AATACGAGTTATATTTTCGT 163 AGTTATATTT 512 AG-- C-- TATCCAT TTCA
CTATCCATTGTTTCACATTT TCGTCTATCC AATACG TTATATTTT GTC TGT C
ACATATTTTCGACAAAAAGAT ATTG ||||| ||||| ||| |||
ATAAAATGCGTATT TTATGC AATATAGAA CAG ACA /
GTAA AAA CTTTAT- TTAA

GAM178 GCCGATCTCTGAATGGATAC 164 TCTCTGAATG 513 ATCTCT - ACTA TA T- TA
TAGTTTTCTAAGTTCTAATG GATACTAGTT GCCG GAAT GGAT GTTTTC AG TC A
TGATTCTCTGAAAATGTAAA TTCT ||| ||| ||| ||||| || ||
TCCAATTCCTCCGGC CGGC CTTA CCTA TAAAAG TC AG T
CTC--- A AATG TC TT TG

GAM179 GCGGTATAATTAGTTTTTTTT 165 TGTGATGGAA 514 GG T - C ATT T
CTCTCAATTTCTATTTTTAG AAATGACTAA GC TA AATTAGTT TTTTCT TCA TCTA T
ATGTGATGGAAAAATGACTA TTTT || || ||||| ||||| ||| ||||
ATTTTGTAGC CG GT TTAATCAG AAAAAGG AGT AGAT T
AT T T T GT- T

GAM180 GTGGAAACGATAACTGTATT 166 GATAACTGTA 515 ACG-- A TTAATCAC- CA
TTTAATCACGTCAGCGGCAT TTTTAAATCA GTGGAA ATA CTGTATTT GT G
CTAAATTAAATATAGGTATA CGTC ||||| ||| ||||| ||
TTTATTCCAC CACCTT TAT GATATAAA CG /

GAM181 AAATTCATGTGAAACTTTGT 167 TTCATGTGAA 516 T T CTTT TTCCTACAAACT TAA
CCTTTCCTACAAACTTGATA ACTTTGTCCT AAAT CATG GAAA GTCCT TGA C
ACTATTTTCATCGGGACTTAT TTCC |||| |||| |||| |||| ||||
TTCTATGTGTTT TTTG GTAT CTTT CAGGG ACT T
T - ATT- CT----- TTA

GAM183 ACCGTCGATACTGCAGAGAT 169 TCGATACTGC 518 T C C- TC T TA
TCTAGTAATAATTTTCTTAA AGAGATTCTA ACCG CGATA TG AGAGAT TAG AA A
GATCTTTAACGATATTGTCG GTAA |||| |||| || |||| |||| ||||
GT TGGC GTTAT GC TTTCTA ATT TT /
T A AA GA C TT

GAM185 GGAGAAAGAATTACATTCTC 171 TTAGTTCATC 520 A T T AG----- AATAT CG
TCGT
TGGAGAAGCCATAAATATAT ATATGGAACT ATT CAT C CTGGAGA CCATA ATGA
TGATAGAG C
GACGTGATAGAGTCGTC AAT TTTT ||| ||| | ||||| |||| ||| |||||
TCCTTTATTAGTTCATCATA TAA GTG G GATCTCT GGTAT TACT ATTATTTC
A
TGGAAC TTTTTCATTGTCTC - T - GTTACTTTTTC AA AC--- TG CTTA
TAGGTGTGAATTCTATTTC

GAM186 GGATAAGTTATTTCATGACGG 172 TAAGTTATTC 521 T AT--- - - CATAA CGG GAA
TAGCATAATGTCTCGGATGA ATGACGGTAG GGA AAGTT TCAT GAC GGTAG TGTCT AT
A
AAAGAATAATGGATAGCAAA CATA ||| |||| |||| |||| |||| |||| ||
CTGCCAGTCGATGATATTAA CCT TTCAA AGTA CTG CCGTC ATAGG TA /
ACTTTCC - ATTAT G A AAACG TAA AGA

GAM187 GTATTTCTTTGACTTGAATA 173 CACTAGTTTA 522 TTCT C GAAT TCC CAC
 CTATCCGATCACAAATATCC GATTCAACAT GTAT TTGA TT ACTA GAT A
 ACTAGTTTAGATTCAACATA AC |||| |||| || ||||
 C CATA AACT AG TGAT CTA /
 C--- T ATT- CAC TAA

GAM188 GTTATCTATAGCATCTACTA 174 TCTATAGCAT 523 TA-- CTA AC CAT
 ACTGTACATTTTTTACATCT CTACTAACTG GTTATCTA GCAT CTA TGTA T
 AGACCATGTACCTTAGATAA TACA |||||| |||| || ||||
 T TAATAGAT TGTA GAT ACAT /
 TCCA CCA CT TTT

GAM189 TCCTTTACCATTCTCTAAAAT 175 TGTAAGCTCT 524 TTTCTAA- T CCATG TCTTTTTG
 A ATGA
 AGTCGTTGCCATGTAAGCTC TTTTGAAATT ACCA AATAG CGTTG TAAGC AAATTG
 TGGAGT C
 TTTTGGAAATTGATGGAGTA GATG |||| |||| |||| |||| ||||
 TGACCTACCACTTCAGCAGT TGGT TTATC GCAAT GTTTG TTTGAC ACTTCA
 C
 TTGTTTGATAGTTAACGCTA TTTTCAA - TGATA ----- G CCAT
 TTAACCTTTTTTGGTGACGGA

GAM190 TAGTGGCTTCTAATCAGATG 176 ATATCATTGA 525 TCTAAT T TAATAAATATTTTAAA
 ATCT A
 TTCTAATAAATATTTTAAAA CCATTGTCT TAGTGGCT CAGATG TC AATGA
 TGATT A
 ATGAATCTTGATTAATAATC GGCT |||||| |||| |||| ||||
 ATATCATTGACCATTGTCT GTCATCGG GTTTAC AG TTA CT ACTAA /
 GGCTACTG TCT--- C ----- AT-- A

GAM191 TTGATTTTCTTTCTAATACT 177 TGGAATAAAA 526 T TC A C ATAT TC A A TC
 ATATATTTCTCTCGAAGAAG ATACTACTGT TTGATTT CTT TA TA TAT TTCTC GA GA GT T
 TTCTTGACATCATCTGGGA TGAG |||||| || |||| |||| ||||
 ATAAATACTACTGTTGAGT GACTAAA GAG GT AT ATA AAGGG CT CT CA T
 AAATCAG T TT C C AAAT T- A A CG

GAM192 AGGTATCGGTCTCTACTGAA 178 TAGCTTCTAC 527 TAT TCTCT AATCTA TC
 TCTACTAACATGTCTCGTAT AGTCTTTCGT AGG CGG ACTG CTAACATG T
 GTTAGCTTCTACAGTCTTTC TTCC |||| |||| ||||
 GTTTCCT TCC GCT TGAC GATTGTAT /
 TTT TTC-- ATCTTC GC

GAM193 CGTCATTATTTTCAGCAGCC 179 TGAGAAAAGT 528 ATTATT CA- ---- T A
 TCTCTACCAGAAGGTTGAGA GTGTTCTGAA CGTC TTCAG GC C TCTC ACC G
 AAAGTGTGTTCTGAATCGCA TCGC |||| |||| || ||||

CGACG

GCAG AAGTC TG G AGAG TGG A
CACGCT TTG T AAA T A

GAM194 GGGTGTAGGATATAGTTTCA 180 TAGGATATAG 529 ----- TTTC AACAT AT---
CATTTC

TAATAGGAACATGATATTTT TTTCATAATA T GTAGGATATAG ATAATAGG GAT
TTTTTGTAC A
TTGTACCATTTTCACCAACAA GGAA | ||||| ||||| || |||||
GTATAGAAATGCAAATCTAT A CATTTTATGTT TATTATCT CTA AAAGATATG
C
ATCTATTATTTTGTATTTTA ATCTAC T--- ATAT- AACGT AACAAC
CCATCTAACCC

GAM195 GAATAGTTACATTTGATTCA 181 TATTACACAC 530 CATT ATCTTCG TTT TC ACTAT
CC A AT

TCTTCGATGTTTAATGTTCC GGAACGTTTA GTTA TGATTG ATG AATGTTCC TG AT
CC ACGTG A
TCTGACTATATCCCCAACGT TAAC ||| |||| | ||||| || || |||||
GATAATACGCGTAGGTTATT CAAT ATTAAG TAT TTGCAAGG AC TA GG
TGCGC A
ACACACGGAACGTTTATAAC T--- ACATCAA --- C- ACAT- TT A AT
TACAGAATTATTA ACTATTT

GAM196 GCTACCAAGGCGAACAACAA 182 TAACACGCTT 531 C - C-- ACA A- CCTGATC
AGCGATTATTGTTTTACCTG CTGTTCTCAT GCTA CA AGG GAACA AAGCG TTATTGTTTTA
C

ATCCCATAATATGGAACAAT CTAT ||| || |||| |||| |||||
AACACGCTTCTGTTCTCATC TGAT GT TCT CTTGT TTCGC AATAACAAGGT /
TATGATAGT A A ACT C-- AC ATAATAC

GAM197 TCAGGCATTTTCGTAATATGA 183 AGGCATTTTCG 532 G -- TATTCTTCC--- CA

TATTCTTCTTTAAGCAAAT TAATATGATA TCAGGCATTTTC TAAT ATGA TTTAAG A
CCTTAAGTACATTCACACCT TTCT ||||| |||| ||||
CGTTCGTTAAGAAGTGTCTG AGTCTGTGAAG ATTG TGCT GAATTC A
A A CT CCACACTTACAT CT

GAM198 AAGAATATAGAAATAATGAT 184 TATAGAAATA 533 AAATA TA TC TCATCG

AAGTCCATCATCGTGT TTTT ATGATAAGTC AAGAATATAG ATGA AG CA T
TTGCCTCTTCATAAGAACTA CATC ||||| |||| || ||
TATTTT TTTTATATC TACT TC GT G
AAGAA TC C- TTTT

GAM199 CTTGATAGTTGTTTCTAGAT 185 TACTAGGTAG 534 T - - A AAAAT

ATGTAAAATAATCCAACGTA CAAATTGTCT CT GATAGTT GTT CCTAG TATGT A
CTAGGTAGCAAATTGTCTAG AG || ||||| || |||||
GA CTGTAA CGA GGATC ATGCA /

T A T - ACCTA

GAM200 TAATATACTTGCGTGTGCGTC 186 TTCAATTTAT 535 AT TGCG TC TATAC
TTTCTATAGTTCT TAT
GTTCAATTTATACGGATTTT ACGGATTTCT TA ATACT TGTCGTGCGT AATT GGA
CTGT A
TATAGTTCTCTGTTATATAA ATAG || |||| |||||| ||| ||| |||
TACGGTTTTCCATCATGATT AT TGTGA ACAGCAGCA TTAG CCT GGCA T
AGACGACGACAATAGTGTTT CT TA-- GA TACTA TTT----- TAA
TA

GAM201 GCGGACACGGATACTCGTTT 187 ACTCGTTTAT 536 ACAC - GT--- G - A GGT
ATGACACCATAGGCATTGGT GACACCATAG GCGG GGAT ACTC TTAT ACAC CAT GGCATT
T
TAACGAATGCCGTGAGTGTA GCAT ||| ||| ||| ||| ||| ||| |||
ATAATTTGAGAGTCATCCTC CGCT CCTA TGAG AATA TGTG GTG CCGTAA A
GC ---- C AGTTT A A - GCA

GAM202 TTTCTGTTTGGACAAATAA 188 TTTCTAGTTC 537 - GGAC AATTC ATC CT
TTGGAATAATTCAGAAATAA TAATTATTTC TTTC CTGTTT AAATAATTGGAAT AGAAATA
GTTT T
TCGTTTCTTTCTAAACATGT AGAA ||| |||| |||||| |||| |||
TTCTAGTTCTAATTATTTCA AAAG GATAAG TTTATTAATCTTG TCTTTGT CAAA T
GAATAGAGAAA A AC-- A--- A-- TC

GAM203 CGGGATTGTCCGGCATATCA 189 CATCGTATAC 538 - T C C C AGT
TGTAAGATAGTTACCGTCTAC TCGACCATCT CG GGAT GTC GG ATAT ATGTAGAT T
ATCGTATACTCGACCATCTA ACG || ||| || ||| ||||||
CG GC TCTA CAG TC TATG TACATCTG /
A C C A C CCA

GAM204 GCCATTATAAAGTGACGTT 190 TATAAAGTGC 539 ATAAAGTGCA AC TC GGAG
TACATATCTACGTTCTGGAG ACGTTTACAT GCCATT CGTTT ATA TACGTTCT G
GAGTAAGAACGTGACTATTG ATCT |||| |||| || ||||||
AGACGAATGGC CGGTAA GCAGA TAT GTGCAAGA /
----- GT CA ATGA

GAM205 GCTCTTGAAACCAAGGTTTT 191 TGAGAAGTCT 540 CT CC GT TC A --- TC
CCAACCGGACTCATTGTGCGA TTTTCATTAG GCT TGAAA AAG TT CA CCG GAC A
TCGGTGAGAAGTCTTTTTCA C ||| |||| || || ||| |||
TTAGC CGA ACTTT TTC AA GT GGC CTG /
TT -- TG GA - TAG TT

GAM206 AATTCAGTAAATAGAGAGAT 192 CCGCACTAGC 541 GT--- ATA AG--- C C CC C
T TT

ATCAGCCGCACTAGCATCCC ATCCCCTTTC AATTCA AAATAGAGAG TC CCGCA TAG AT
CCTTT AA AG C
CTTTCAATAGTTCTCCCTTT AATA ||||| ||||| || ||||| || ||||| ||
TTAAAGGTATCTAATGCGGA TTAAGT TTTATCTCTC AG GCGGT ATC TA GGAAA
TT TC T
TTTAGAAAACCTCTCTATTTT AATTC AAA ATTTA A - T- T T CC
TTAATGAATT

GAM207 GAACGTAAACGTAGTAGCCA 193 TGATATACCT 542 C CG - GC- A CTC A
TACGTCTCAGAATTCTAAAT GTTTTTATTT GAA GTAAA TAG TA CAT CGT AG A
GATGATATACCTGTTTTTAT C ||| ||||| ||| ||| ||
TTC CTT TATTT GTC AT GTA GTA TC T
- TT C ATA - AA- T

GAM208 TATTAACGTATCGCATTAA 194 TAACGTATCG 543 T TATCGCATTAACT TAGCGA-
C C
ACTGTTTTCTTAGCGAATGA CATTAATACT TA TAACG GTTTTCT ATGATG AGA C
TGCAGACCCTTCTACGTCAT GTTT || ||||| ||||| ||||| |||
CAAAAATAGAAAACCTCGTTA AT ATTGC CAAAAGA TACTGC TCT C
TTA T T----- TAAAAAC A T

GAM209 TCAAAGACTAGACATTTACC 195 ACTAGACATT 544 GAC- CATTTACCA TGCT
ATGGGATGCTAATATTCCCA TACCATGGGA TCAAA TAGA TGGA A
AACATACATCTATAAATTTG TGCT ||||| ||||| |||||
A AGTTT ATCT ACCCT /
AAAT ACATACAA- TATA

GAM210 ATGTATAGATTGTTTTAGT 196 TAGATTGTTT 545 - TCA- ---- A G
GAGATGATTATTAGATTTAA TCAGTGAGAT ATGTA TAGATTGTTT GTGA GATG TTATTA A
TAGCATCTCGTTCACGTTTG GATT ||||| ||||| ||||| |||||
AACAGTTTATTGCGT TCGGT ATTTGACAAG CACT CTAC GATAAT T
T TTTG TGCT - T

GAM211 TAATGACGCATATTCTACTC 197 ACGCATATTC 546 G C AT TACTC- T TAG ATA
TTGGAATTAATAGTTTTGAT TACTCTTGGA TAAT ACG AT TC TTGGAA TAA TTTTG T
ATTAGTAAAAAATTTATTTT ATTA ||||| ||||| ||||| |||||
TAAATTTTGTATCATCGTAA ATTA TGC TA AG AATCTT ATT AAAAT /
TTA A - CT TTTTAA T TAA GAT

GAM212 TAATGGCGGAAAACCTTTTTA 198 TTCGTGTTCC 547 GC- A TTTTT GTTATAT
GAAATGTTATATATAAAAGA AAACATTA TAATG GGAA AC AGAAAT A
ATTTTTTCGTGTTCCAAACA ||||| ||||| |||||
TTA ATTAC CCTT TG TTTTAA /
AAA G CT--- AGAAAAT

GAM220 AGGATGAGTACATTTTCACAG 206 TGAAATAGCT 555 TG ACATTTTCAC ACT ATTG ATGT
 A
 AAACACTAGCATTGTTCAAT CGTTTCTATT AGGA AGT AGAAAC AGC TTCA
 GCTCTTTAC T
 GTGCTCTTTACATGGGTAAG TGT TCTT TTA TCTTTG TCG AAGT TGAGGAATG G
 GAGTTGAAATAGCTCGTTTC GT ----- C-- ATA- ---- G
 TATTTGTTCT

GAM221 GATGGCGGCGTCGTCGTTTT 207 AGATAATATC 556 G - TC C TTTG---- TTA
 TTGATCTTTATTAAATTTAG CTGAACAGCA GATG CG GCG GT GTTT ATCTTTA A
 AGATAATATCCTGAACAGCA TTGC TTTT TTTT TTTT TTTT
 TTGCTCGGCGTC CTGC GC CGT CG CAAG TAGAGAT /
 G T TA A TCCTATAA TTA

GAM222 GTTATAGCTTTCTGCTATTA 208 TAGTATAGCG 557 GCTT A T C- TTCAAA TT
 TACCCGCTATTTCAAATAGA TCGTTTAAGA GTTATA TCTGCT TTA AC CGCTAT TAGAC A
 CTTATACGTCTAGTATAGCG GCAG TTTT TTTT TTTT TTTT
 TCGTTTAAGAGCAGATATAT TAGTAT AGACGA AAT TG GCGATA ATCTG T
 GAT AT-- G T CT TG---- CA

GAM223 GTTTTTGAAGTTTCCAAATT 209 TTGAAGTTTC 558 T AA TTCCAA T- A TG
 TTGATAATATAGTCTAGATG CAAATTTTGA GTT TTG GT ATTTTGATAA AT GTCTAGA G
 GAATTTTAGACCATCTTTGT TAAT TTTT TTTT TTTT TTTT
 CAAATCGTTTACCGACAAC CAA AGC CA TAAACTGTT TA CAGATTT A
 C -- TTTGC- TC C TA

GAM224 AGGATCTAGATAATTAATAA 210 TTCTTTGTAT 559 --- --- TT T T
 TGATGGGTTTTCTATTCTTA TTTGGCATAT AGGAT CTAG ATAA AATAA GATGGG T
 TTCTTTGTATTTTGGCATAT CCT TTTT TTTT TTTT TTTT
 CCT TCCTA GGTT TGTT TTATT TTATCT /
 TAC TTA TC C T

GAM225 CAGAGTTGGGATAGTATTTT 211 TAGTATTTT 560 - - T T T- C TATTATAT G TC
 T
 TCTAACGTCGGTATTATATT CTAACGTCGG CAGA GTTGG GATAG ATTT TC AACGT GG
 TATTA GA TACGT C
 ATTAGGATCTACGTTTCATAT TATT TTTT TTTT TTTT TTTT
 GTATCATAATATTAATCATC GTCT CGATT CTATC TAAA AG TTGCA CC ATAAT CT
 ATGTA A
 CACGTTTTGATAAATCTATC T T - T TT - TACTAATT A -- T
 TTTAGCTTCTG

GAM226 CGTATAAATTTTAGAAATAA 212 AATTTTAGAA 561 AAA -- TA -- AAT
 CATTAGCGAATTGTTGTGCA ATAACATTAG CGTAT TTTTAGAA A ACATTA GCG T

TTGATGTCGTTATTCTGAAA	CGAA					
CAGTATG	GTATG	AAAGTCTT	T	TGTAGT	CGT	G
	AC-	AT GC	TA	GTT		

GAM227	TAGAGTTAAGAGAGATTAGA	213	TGGCTACAAA	562	GTAA--	ATT	ACATTA	A	GTC
	GTTTGTACATTAAGCAACAT		CTTTTCCTTT		TAGA	GAGAG	AGAGTTTGT	AGC	ACAT T
	GTCTCTAAATGTGGCTACAA		TCCA						
	ACTTTTCCTTTTCCACATCA				ATCT	CTTTT	TTTCAAACA	TCG	TGTA C
	TCTA		ACTACAC		CCT	-----	G	AAT	

GAM228	GAGTCATTCTGAAGCGTCAAT	214	TTTCCGGCTG	563	CG	GCGT	-----	T	CT
	AGAATATGTCTCTTAACAT		TTGTATATTT		GAGTCATT	AA	CAATAG	AATA	GT C
	TTCCGGCTGTTGTATATTTA		AAAT						
	AATGACTT		TTCAGTAA		TT	GTTGTC	TTAT	CA	T
			AT		ATAT	GGCCT	-	AT	

GAM229	GACTTGACTAGATCGTCAGT	215	TAGCATCGCT	564	---	----	G	T	TA -	CGTC	T
	ATCC										
	AGTAATTTGTGCATCGTCTA		TTGAGATTCT		ACTTGA	CTA	GATC	TCAG	AG	AT	TTGTGCAT
	TATTC GC G										
	TTCTGCATCCGCTTCGTCGA		CCAT								
	ATAATGTATAGCATCGCTTT				TGAACT	GAT	TTAG	AGTT	TC	TA	GATATGTA ATAAG
	TG /										
	GAGATTCTCCATAGCTATCA				ATC	ACCTC	-	-	GC	C	---- C CTTC
	AGTC										

GAM230	ATAATAGTGGCCGGAGAATC	216	TTCCTCTGGA	565	A	G	G	AA	A	---	GA	TA
	ATCATCTGGAAATAGATCTT		GATGACACTA		ATAAT	GT	GCCG	AG	TCATC	TCT	GGAAATA	
	TCTTCAT A											
	CATTAAGTTGTGAGGATATT		CGGC									
	TCCTCTGGAGATGACACTAC				TATTA	CG	CGGC	TC	AGTAG	AGG	CCTTTAT	AGGAGTG
	G											
	GGCGGCATTAT		-		G	A	AC	-	TCT	--	TT	

GAM231	GATAATGTTTATGACAATAA	217	TATTGTTTAA	566	AT	C-----	A	TT	----	TAA
	TAATCACGTTAGTGACGATA		TCGTTTTATA		GATA	GTTTATGA	AATAATA	TCACG	AGT	
	GACGA T									
	ATTTTTCGTTTTCTACTTTC		GATT							
	GTGATATTGTTTAATCGTTT				CTAT	TAGATATT	TTGTTAT	AGTGC	TCA	TTGCT /
	TATAGATTCTATC				CT	TTGCTAAT	-	TT	TCTT	TTT

GAM232	GTTGTTGACGTTGTTCCGAT	218	GGAGGTGGAG	567	T	GATATCAATA	CT	A
	ATCAATAACTCTCTACGAAA		TATCGTCAAT		GTTGTTGACG	TGTTCC	ACT	CTACG A
	CGTAGGAGGTGGAGTATCGT		AAT					
	CAATAAT		TAATAACTGC		ATGAGG	TGG	GATGC /	

T ----- AG A

GAM233 TAGTATTCTGGTAAAATTAT 219 TATCAGATGA 568 A C AT TCTAAATTA
ATTTTGTATTAGATC TC
CTAAATTATCAGATGATTTT TTTTGTATTA AGT TT TGGTAAA TA TCAGATG
GTTGATT T
GTATTAGATCGTTGATTTCT GATC ||| || ||||| || ||||| |||||
AAGATTAACCACTTCATCCT TCA AA ACTATTT AT AGTCTAC CAATTAG /
CCAACATCTGAATTCTTTTA - T CT TTTCTTA-- AACCTCCTACTTCAC AA
TCTTTATCATAAACTA

GAM234 ATAAAGTCTTGGTATGACTC 220 ACTACCTTTG 569 CT TA ----- TTT A
CTTTCTAATATAGTACGGAC TCACCCAAC ATAAAGT TGG TGAC TCC CTA T
TACCTTTGTCACCCAACTTT TTAT ||||| ||| ||| ||| |||
AT TATTTCA ACC ACTG AGG GAT /
-- C- TTTCCATC CAT A

GAM235 GCTGAAGTAATTAATTTTTTC 221 TGAAGTAATT 570 TG - TTTTTC C TTT ACTAGTT
TGCTCGTTTTTACTACAAC AATTTTTCTG GC A AGTAATTAA TGC TCGTT ACTACA T
TAGTTTTCATCAATGTAGTG CCTC || | ||||| ||| ||||| |||||
ACGATGTATTGTTTAGTTAC TG T TCATTGATT ATG AGCAG TGATGT /
TCTTGGT GT C TGTT-- T --- AACTACT

GAM236 GGGTATTAATAATATCTATA 222 ATTCACGTGA 571 AATATCTATATTT G A TAAC C
TTTCCAGCGTTAAGTGTAAC CGTGGTATCA GGGTATTAAT CCA CGTTA GTG ATTAAA
A
ATTAAACAGTTTTTAATTCAC ATTA ||||| ||| ||||| ||| |||||
GTGACGTGGTATCAATTAAA CCCGTAATTA GGT GCAGT CAC TAATTT G
TAATTAATGCCC ATAAATTA ACTAT - G T--- T

GAM237 GTTCTAGTACAATTAGACGT 223 TACAATTAGA 572 TAGTAC C TC C AATTTT- C
A
AAGTTCTGCTTGGAATTTT CGTAAGTTCT GTTC AATTAGA GTAAGT TG TTGGG
TTAACG TAA G
TTAACGCTAAAGAGTTAACG GCTT ||| ||||| ||||| ||| ||||| ||||| |||
TTAATCGTGCACCCAACGTA CAAG TTGATCT CATTTA GC AACCC AATTGC ATT A
TTTACATCTAGTTCTTTGAA TTTC-- A T- - ACGTGCT A G
C

GAM238 TGATTTTGGTTTACATGTAA 224 TACATGTAAT 573 - TTA A TT-TG C
TACATTTGAACTCTTTGAT ACATTTTGAA TGATT TTGGT CATGT ATACA T AA T
TTTGTATCACATGCGCCGGC CTCT ||||| ||||| ||||| ||| |||
AGTCA ACTGA GGCCG GTACA TATGT A TT /
C C-- C TTT GT C

GAM239 ACTACTATTTAATTTTACCA 225 TCGAAAACAA 574 CCAT T -- ---- GAT TTTT--
CA
TATCTTCGAAAACAAAAATA AAATAGATAT AATTTTA ATC TCGAA AACAAA AATA ATTAT
GCAGTA A
GATATTATTTTGCAGTACA TATT ||||| ||||| ||||| ||| |||| |||||
AACTATTGTTTTTATATGGT TTAAAAT TAG GGCTT TTGTTT TTAT TGGTA
TGTTAT /
TTATATTCCACTTTGTTCAT T--- C AC CACC ATT TATTTT CA
TCGGCGATTATAAAATTTTA
TTAGT

GAM240 GAAGAGTAATGTATAGAGGA 226 TGTATAGAGG 575 - AAT-- A CGTTT T
CGTTTTGATTTCGATCATTTT ACGTTTTGAT GAAG AGT GTAT GAGGA TGAT C
CCTCATATTAGAACTACTT TCGA ||||| ||||| ||||| |||||
C CTTC TCA TATA CTCCT ACTA /
A AAGAT - TTT-- G

GAM241 TCCTAGTTTATCTACAGACA 227 TTTATCTACA 576 T CAGA CT TTCGT AATT
GACTAATAATTCGTTGCATG GACAGACTAA TCCTAGT TATCTA CAGA AATAA TGCATGA
T
AAATTCCTATCATGTACTT TAAT ||||| ||||| ||||| ||||| |||||
TATTTCTTTGATGGATGTGC AGGATCG GTAGGT GTTT TTATT ATGTACT /
TAGGA T A--- CT TC--- ATCC

GAM242 AAAGAATTATACTTTTCTAT 228 TTTGTACAGA 577 TA T- ATAGCC TC- AA
AGCCGCAGAATCTGAAAATC CTAAGTAATT AAAGAAT TACTT TCT GCAGAA TGA A
TCAAACCTTTGTACAGACTA CTTT ||||| ||||| ||||| ||||| |||||
AGTAATTCTTT TTTCTTA ATGAA AGA TGTTTT ACT /
-- TC CA---- CAA CT

GAM243 AAGTAAAGATATTGACTTGG 229 AACATCTTTG 578 A TG CTT GTA TG
ATGGTATTTTCTGACAGAAA AAATCTTTAC AAGTAAAGAT T A GGATG TTTTC A
ACATCTTTGAAATCTTTACT TT ||||| ||||| ||||| ||||| |||||
T TTCATTTCTA A T TCTAC AAAAG /
AGT --- --- AC

GAM244 CCGTTATAAATGTCTTTGTC 230 TATCCAGAGA 579 - TCGAT TCAA TTC
GATGATATATTCAACGCTTC TATCTTGTA CCGTTATAA ATGTCTTTG GATATAT CGC C
CAATTGTGATATATCCAGAG TGG ||||| ||||| ||||| ||||| |||||
ATATCTTGTAATGG GGTAATGTT TATAGAGAC CTATATA GTG A
C ---- --- TTA

GAM245 TCATCTAATGCCGTAGCCGT 231 TACTTCTTTA 580 T C- GCCGT TAC TACA
AAGTACGTGGTTTACAACAT AAGTACTCGT TCATCTAA GC GTA AAG GTGGTT A
TAGCTACTTCTTTAAAGTAC TTTG ||||| ||||| ||||| ||||| |||||
TCGTTTTGGATGA AGTAGGTT TG CAT TTC CATCGA /

T CT GAAAT TT- TTAC

GAM246 TGTGATTGATTCCCACTAAT 232 TCTAAATTCG 581 GA CA - GA-- CCAC
GAAGATGCCACATATCCATC GCAGGAAAGT TGTGATT TTCC CT AAT AGATG A
TCTAAATTCGGCAGGAAAGT CACA ||||| ||| || ||| ||||
CACA ACACTGA AAGG GG TTA TCTAC /
-- AC C AATC CTAT

GAM247 AATGCTCGCAACATTAACAT 233 ATAAATTTAT 582 CT C ACATCT CCGT T AA
CTTGAACCGTTGGTACAATT AATGTTTCGCC AATG CG AACATTA TGAA TGG AC T
CCGTTCCATAAATTTATAAT ATT |||| || ||||| ||| ||| ||
GTTTCGCCATT TTAC GC TTGTAAT ATTT ACC TG T
C- - ----- AAAT T CC

GAM248 ATGGAGATTTTCTATTCTCG 234 TCCCTAATAA 583 TTTC T TCCATT ATAT C
TCCATTTTAGGATATGCTTT CTTCGTGAAT ATGGAGAT TATTC CG TTAGG GCTTT A
CATAAAGTCCCTAATAACTT AATG ||||| ||||| ||| ||||
CGTGAATAATGTTTCTAT TATCTTTG ATAAG GC AATCC TGAAA /
TA-- T TTCAAT C--- T

GAM249 TCTTTTTAGCCAGAGATATC 235 GTTTCAGCGT 584 T CCA- T A C--- T
ATAGCCGCTCTTAGAGTTTC GATTTTCCAA TCT TTTAG GAGA ATCAT GC GCTC T
AGCGTGATTTTCCAACCTAA CCTA ||| |||| ||| ||||| || |||
ATAGA AGA AAATC CTTT TAGTG CG TGAG /
T CAAC - - ACTT A

GAM250 TTGCTTCGCGTTTAGCCTCT 236 TAGCCTCTGG 585 TTCGCG CT GC A A C
GGCTTTTTATCAGCCTTTGT CTTTTTATCA TTGC TTTAGC CTG TTTTT TC GC T
AGAAAAAAATTTCAGTTGCTG GCCT |||| ||||| ||| ||||| |||
GAATTGCAA AACG AGGTCG GAC AAAAA AG TG T
TTA--- TT TT A A T

GAM251 ACACCAGAAAAGACGGCTTG 237 TGAGATCAAC 586 A AAAGAC T - CT TCTAAT
ATAA A
AGATCAACTTTATCTAATGG TTTATCTAAT AC CCAGA GGC TGAGA TCAA TTA GGTTT
AACGAAGG G
TTTATAAACGAAGGAGGCC GGTT || |||| ||| ||||| ||| |||| |||||
TTCGTTTCGAAATCTAATTTG TG GGTCT CCG ATTTT AGTT AAT CTA
TTGCTTCC /
ACTTTTACGCCTCTGGCGT C ----- C C T- ----- GC-- G

GAM252 TGTGAGAAGTTTGCCTCGTT 238 TGGAATAGTT 587 GA-- GC C T T -- TTA----- TT
T

AAGGTCTTCCATTAAATAT	TTTTACTAGT	TGA	AGTTT	CT GT AAGG CT	TCCAT	AATA
ATATAACA T						
TATATAAACATTTGTGTTTG	AAAG					
TATCTTATTCGTCTTTTATG		ATT	TCGAA	GA CA TTTT GA	AGGTA	TTAT
TATGTTTGT T						
GAATAGTTTTTTTACTAGTAA		AACG	AT T T	T TA	TTTTCTGC	TC G
AGCTGCAATTACA						

GAM253 ATAGATGCCATGTAAAAAT 239	GATGCCATGT 588	T	AAAAAT-	CG-	TCGA
GTCCGCCGTCGACTTTTTGG	TAAAAATGTC	ATAGATGCCA	GTT	GTC	CCG C
AACGATTGATAAAAGCTGGT	CGCC				
GTTTAT	TATTTGTGGT CGA	TAG	GGT /		
	- AAATAGT CAA	TTTT			

GAM254 ATAGCATCATCTTTAGATCA 240	AGCATCATCT 589	GC	CTTTA	C AA-	TACCTT
TTAATTGTTACCTTCCCAA	TTAGATCATT	ATA	ATCAT	GAT ATT	TTGT C
TACAACCAAATCATCATGAT	AATT				
ATAT	TAT TAGTA	CTATAA	AACA /		
	A- ----	C ACC	TAACCC		

GAM255 CTTTGGCTTATAAAATACAA 241	TAAAATACAA 590	AAT-----	CCC	TT--	C--	CT
TC						
ATGACATTCCCTTATGTTTA	ATGACATTCC	ATACA	GACATT	TTATG	TAAT	TTAAT
TT T						
ATCTTAATCTTTTCTTTAGT	CTTA					
TATTGAATCGTTACAATTAT		TATGT	TTGTAG	AATAT	ATTG	AGTTA GA /
AAAATGATGTTTTTTCCAAA			GAATCCAAAAACCTTTT	TAA	TAAC	CTA TT TT
AACCTAAGTGTATTTAAAAT						
AGATGCCATG						

GAM256 TACGACACTGATAAACCGCA 242	ACACTGATAA 591	C T	CGCA	----	G T
TTATCTGTGGACATTTTAAT	ACCGCATTAT	TACGA	AC GATAAAC	TTATCTG	T GACAT T
GTTGGTATCTAGATAACAAT	CTGT				
GTTTATCGTATTGTA		ATGTT	TG CTATTTG	AATAGAT	G TTGTA T
	A -	TAAC	CTAT G	A	

GAM257 TGTATCCTCAACATAATCAA 243	TTTATTGGGT 592	--- C	AA-	- AG-	AAT
TGAGCCAGGTAATCAAGACA	AGTGTTGATG	TGT	ATC TCAACAT	TCAATGAG	CC GT C
TCGGATTTATTGGGTAGTGT	ATTC				
TGATGATTCCGCA		ACG	TAG AGTTGTG	GGTTATTT	GG CA /
	CCT T	ATG	A CTA	GAA	

GAM258 GATTTGGCCAAATGTATCCA 244	TAAC TAGTGT 593	CC	G	CATCATAA---	GG ATAA G
GTAAC T					
TCATAATCTGGGTATAAAC	AGAAAACAGA	GG	AAAT TATC	TCTG	TT AC GGT
AAGAATATA G					
GGGTGTAAACAAGAATATAT	GATA				

GTTTATATTTTTTAACTAGT
GTAGAAAACAGAGATAGTAA
ATAGATAGTTTTTCCAGATC

CC TTTG ATAG AGAC AA TG TCA TTTTATAT T
TT - ATAAATGATAG AA GATG A AT---- T

GAM259 AGCGAAGCTATCATCGTCCA 245 ATATTATCTA 594 TATCAT CC-- C ATT
ATATCTCATTCCCTAGAAATA CGTCATTGTT AGCGAAGC CGT AATAT TC C
TTATCTACGTCATTGTTTTG TTGT ||||| || |||||
TT TTGTTTTG GCA TTATA AG /
TTACT- TCTA A ATC

GAM260 GTGGTATTATACTCATGCCT 246 TATTATACTC 595 A AT- TCAT-- A AA---- - G T
AGTAATAGTCTCTTTGCGTT ATGCCTAGTA GTGGT TT AC GCCT GT TAGTCT CTTT CG
T
GACGGAAAGCAGACTAGAAA ATAG ||||| || ||||| |||||
TAACAGGCTAAAATGTTTCAG TACCA AG TG CGGA CA ATCAGA GAAA GC G
ACACCAT C ACT TAAAT - ATAAAG C G A

GAM261 GGCAAATAATTAATCAGTGA 247 AACGATGTTA 596 TA AATCA AG T AGT
TAGATTGTTTACATACAGTA CCAATCGTTT GGCAAA ATT GTGAT ATTGTTTACA AC A
TGTCGTTTGTAACGATGTT GCT ||||| || ||||| |||||
ACCAATCGTTTGCT TCGTTT TAA CATTG TAGCAAATGT TG T
GC C---- -- T CTG

GAM262 GGAATTTTGACAATTCTCTT 248 AGTGAAAAGA 597 A - TTC----- GA C A
TGAGCCGATAGTATCAGTGA ATGTAACTT GG ATTT TGACAA TCTTT GC GAT G
AAAGAATGTAACTTTGTCA TGTC ||||| ||||| |||||
TAAGTACC CC TGAA ACTGTT AGAAA TG CTA /
A T TCAAATGTA AG A T

GAM263 ATATTACGCAGCAAGCATAA 249 TTAGGTTTGT 598 A --- T A--- TA
CCAGCATAATCTGTCTTAGG TCATTGTCGT ATATTACGC GCAA GCA AACC GCA A
TTTGTTTCATTGTCGTGTGGT GTGG ||||| ||||| |||||
GT TGTGGTGTG TGT TGT TTGG TGT /
C ACT - ATTC CT

GAM264 GATAAAAATGTAGTGTAATT 250 TATAGTGTA 599 - GTAATT TAT AA ATGC TT
TCG TG
GTTATATAGTGTAACACGAA CACGAATGCA ATGTAGT GTTA AGTGT CACGA AG
TGGGAGTAT TTG C
TGCAGTTTGGGAGTATTCGT GTTT ||||| ||||| ||||| |||||
TGTGCTACAAATATATTTCC TATATTA CGAT TTACG GTGCT TC ACCTTTATA
AAC /
ATTCTTCGTGGCATTTTTAG G AAATAT TT- -- --- TT TA- AT
CTATAAAATTATATGGGGTT
GTC

GAM272 ATTCGCGAAGCGACGTCATT 258 ACGTCATTTA 607 G CGTC AATAAA TTT
 TAATAAAAAAAGTATTTTTT ATAAAAAAG ATTCGCGAA CGA ATTT AAAAGTATT T
 TTTAATATTTTTTCACAAATA TATT ||||| ||| ||| |||||
 TCGTTCGCGGAT TAGGCGCTT GCT TAAA TTTTATAA /
 - A--- CAC--- TTT

GAM273 TATCTTGGCAATAACTAATT 259 TGGCAATAAC 608 CT AACT G A -- A T
 GAGATATTGATGCGAGTTCTG TAATTGAGAT TAT TGGCAAT AATT AG TATT GATGCG
 GTTCGGTA G
 GTATGCATATCGGACACGTA ATTG ||| ||||| |||| || ||||| |||||
 TCCGAGTACTGATTCCAAGT ATG ACCGTTG TTAG TC ATGA CTATGC CAGGCTAT C
 TGCCAGAGTA AG AACC - - GC A A

GAM274 ATAGATATGATAACAGGAAT 260 GATATGATAA 609 - A ATAA A TA- T AAATA
 AACATCTTTAGGTTTAAAAT CAGGAATAAC ATAGAT ATGAT ACAGGA C TCTT GGT TA A
 AATTATACACCAGTAGGA ATCT ||||| ||||| ||||| ||||| |||||
 GTCTTGTATCGTCATCTAT TATCTA TGCTA TGTCT G AGGA CCA AT /
 C C ---- TGA C ATATT

GAM275 GAGTCGTCCATATTTTATTC 261 CGTCCATATT 610 TC CATATT - CC ----- A
 TGAGGCCTAATAGACCTCTG TTATTCTGAG GAG GTC TTATTCT GAGG TA ATAG C
 TACATAAAATATTCCTCTAG GCCT ||| ||| ||||| ||||| ||| |||||
 AATAGTAGACATCTC CTC CAG GATAAGA CTCC AT TGTC C
 TA AT---- T TT AAAATACA T

GAM276 GGATATTCTTGATACATTCT 262 TATGGCAAAT 611 T T T TTCTTTTT A TACAT- -----
 - CA
 TTTTATACAGTGAATTGCAT CTGCAATCAC ATA TCT GA ACA ATACAGTGA TTGCA CC
 GATA G
 ACATCCGATACAGCATTATC TGTA ||| ||| ||||| ||||| ||| |||||
 CATATATGGCAAATCTGCAA TGT AGA TT TGT TATGTCACT AACGT GG CTAT
 C
 TCACTGTATTGTTTTTAGAT T T T ----- - CTAAAC TATATAC TA
 TGTCC

GAM277 GTAGTCACCGTAAATTTATC 263 CACCGTAAAT 612 A AA T TCACC A A
 ACCAGAAATACTAATATCTA TTATCACCAG GT GTCACCGT AT TA AGA AT C
 TCTTTATGTCCATGGTGATC AAAT || ||||| |||| ||| |||
 AC CATAGTGGTA TG AT TCT TA T
 C CC T TTCTA A A

GAM278 TATCTATCAGATTATTATGT 264 TAAGGTAATT 613 ----- AT AT-- GG - - ATAAA
 GTTATAAGGTACTTTTTCTC TTTCTCATAA TATCTATCA GATT TATGTGTT AA TACT TTTT
 CTCATA C

ATAATAAACTAGAGTATGAG TAAA ||||| ||| ||||| || ||| ||| |||||
 TAAGATAGTGTTTTTCAAAA GTAGGTAGT CTAA ATATACAA TT GTGA AGAA
 GAGTAT /
 CATATAAATCTAAAATTGAT TAAAAT -- AACT TT T T GAGAT
 GGATG

GAM279 AAAGTATTGGTAATCGTGTC 265 TTTGTTCTAT 614 - TAATCGT CA TA TAAAAAG
 TTATTTTT TA
 ATATTAGTATAAAAAGTGAT CAACTACCTA AAAGTATT GG GT TAT GTA TGAT
 ACAAAAT T
 TTATTTTTACAAAATTATGT TAAA ||||| || ||| || ||| |||||
 ATTTTGTTCTATCAACTACC TTTCATAA CC CA ATA CAT ACTA TGTTTTA /
 TATAAACTTTCCAAATACT A TTT---- AA TC CA---- TCT----- TG
 TT

GAM280 ATGGCAGATCCAATTTGTAA 266 ATCCAATTTG 615 CA - AA TAAAA C ---- GAA
 AAAATCAGCGGTTGAAAGAA TAAAAAATCA ATGG GAT CC TTTG AAT AGCGGT TGAA T
 TATATTTACGTTATCGTTA GCGG ||| ||| ||| ||| ||||| |||||
 GTTAGGCTCAAAGGTATCCC TACC CTA GG AAAC TTG TTGCTA ACTTT /
 AT -- T -- TCGGA A TTGC ATA

GAM281 CGTGAAGATATCATTTCCCA 267 TCATTTCCCA 616 AA TC CA---- - TT TT
 TGTATTTTTTTTATGATTGT TGTATTTTTT CGTG GATA ATTTCC TGT AT TT T
 AGCAGTTTATGAAATTTTA TTAT ||| ||| ||||| ||| |||
 TCACGCG GCGC CTAT TAAAGG ACG TG AG /
 A- TT TATTTG A TT TA

GAM282 CTTGGTATAATTATCAAAAT 268 TGGAATTGGG 617 TTATCAAAATA GA- CG-- C
 ACAAGACGTCGCTTTTAGCA CTCCTTATAC CTTGGTATAA CAA CGT CTTTAGA
 GCTAAAAGAATAATGGAATT CAAG ||||| ||| ||| |||||
 GGGCTCCTTATACCAAG GAACCATATT GTT GTA GAAAATC /
 CCTCGG---- AAG ATAA G

GAM283 TACCTTATCAAATGATCCTG 269 TATCAAATGA 618 TT- A- G C T CA T TA
 TTGGGCATTTTCTACATTGA TCCTGTTGGG TACC ATC AAT AT CTG TGGG TT TC C
 TGACATCCATTAGAATAATT CATT ||| ||| ||| ||| ||| |||
 GGGATTGTGGTA ATGG TAG TTA TA GAT ACCT AG AG A
 TGT GG A A T AC T TT

GAM284 TCGCTACTTGGTTAGTGTAT 270 TTAATAATTA 619 CTACTT T T C TGA
 TATTCAGTATGAAGACCTAT CTTATCTTTT TCG GGT AGTG ATTATT AGTA A
 TAATAATTACTTATCTTTTG GACG ||| ||| ||| ||||| |||||
 ACGA AGC CTA TCAT TAATAA TTAT G
 AGTTTT T - - CCA

GAM285 TTTTGGTAATCTATTATTAT 271 TATTATTATT 620 CT TATT CTCT- ACCG
 TGGCTCTGATCACCGCATCT GGCTCTGATC TTTTGGTAAT AT ATTGG GATC C
 AGATCTACACCTAATCTATT ACCG ||||| || |||| ||
 AATTACCAAGA AGAACCATTA TA TAATC CTAG A
 AT TC-- CACAT ATCT

GAM286 TTTGGTCGATGTAAAATTTT 272 TGTAAAATTT 621 CGA AAATTTTT - AAA
 TGTCGATAAAAATTAAAAA TTGTCGATAA TTTGGT TGTA GTCGATAA AAATTAA A
 TAACCTAATTTATTATTGAT AAAT |||| || ||||| |||||
 CTCGTGTGTACAACCGAA AAGCCA ACAT TAGTTATT TTAAATT T
 --- GTGTGCTC A CAA

GAM287 GATTCTCGTCGTACCCACCG 273 TCGTACCCAC 622 T C- CC G T TAA
 AGAGCGTGTGCGTAAAACAT CGAGAGCGTG GAT CTCGT GTAC ACCGAGA CGTG GCG A
 CGCCATGATTTGCGTTGTAC TGCG ||| |||| ||| ||||| |||||
 ACACGAGATC CTA GAGCA CATG TGGCTTT GTAC CGC A
 - CA T- A - TAC

GAM288 CGTATTATACGCATTATAAC 274 TTCGTTGTAT 623 CGCAT T C GTA
 TGACAGCGTCGTAAATAGAT ATAGTACG CGTATTATA TATAAC GA AGCGTC A
 GTTTCGTTGTATATAGTACG ||||| ||||| |||||
 GCATGATAT ATGTTG CT TTGTAG /
 ----- - - ATA

GAM289 GGTAGCAATTTATGGAACCT 275 TAACGGAGAT 624 --- T AAC GGTCATT CAC
 GAACAA
 ATATTGGTCATTATTTTGT TAAAAATATG GGT AGCAATT ATGG TTATATT ATTTTGT
 AG A
 CACAGGAACAACTAATACT ACGC ||| ||||| ||||| ||||| ||||| ||
 ATAACGGAGATTAAAAATAT CCG TTGTAA TACC AGTATAA TAGAGGCA TC /
 GACGCCATAATTGTTAACG CAA - CGC AAAT--- ATA ATAATC
 CC

GAM290 GTATCATAATTTTCAAAGAT 276 GTTGTTGTTT 625 T AAT A- A TTA- TACTTCC
 GGTCGTTTAGACAATAGTAC GCGACTGCTT GTA CAT TTTC AAG TGGTCGT GACAATAG
 A
 TTCCATTATTATTTGTTGT CCGA ||| ||| ||| ||||| |||||
 TGTTTGCGACTGCTTCCGAA CAT GTA AAAG TTC GTCAGCG TTGTTGTT T
 ATACATGTAC - CAT CC - TTTG TTATTAT

GAM291 TGTTCTCTATAGTTACATTA 277 TGTGACACCC 626 TA----- - TTA
 ATTAAAATTTTATATGTGAC ATTCATCTGG TGTTCTCTA GTTACAT TAA A
 ACCCATTCTCTGGAGAATA AGAA ||||| ||||| |||
 ATAAGAGGT CAGTGTA ATT A
 CTACTTACCCA T TTA

GAM292 CATCTTTTACCAACACAAAG 278 TCTTTTACCA 627 CT ACACAAA ATATTT TT -
 GATAAT ACA
 GGTGGATATTTGTTTCATTGG ACACAAAGGG AT TTTACCA GGGTGG G CATTG GAGTT
 AATAC C
 AGTTGATAATAATACACACA TGGA || ||||| ||||| | |||| |||| ||||
 AAGTATTTGGATTCACGGTG TA AGATGGT TCCATC T GTGGC CTTAG TTATG
 /
 GGTTACGACTACCTCAGACT AG CAGAC-- AGCAT- GG A GT---- AAA
 GGTAGAGAATG

GAM293 GTACGCGTGTTCGATTCATCA 279 TGAGGCTACC 628 -- ----- A-- AT
 AGGTATATAAACCTGGGGAT TCGACATACG GTACGCGT GTCGA TTCATC AGGT A
 GAGGCTACCTCGACATACGT TGTG ||||| |||| ||||| ||||
 GTGC CGTGTGCA CAGCT GAGTAG TCCA T
 TA CCATCG GGG AA

GAM294 TAATTTTTTATAAACTAACA 280 TAACATGTTA 629 TT AAAC T A-- G
 TTGTTAATTGAAAAGGGATA CAGAATATAA TAATTT TAT TAACAT GTTA TT A
 ACATGTTACAGAATATAAAT ATTA ||||| ||| ||||| |||| ||
 TA ATTAAA ATA ATTGTA CAAT GA A
 T- AGAC - AGG A

GAM295 AACACGGCAGAATATCGCCC 281 TGAGATATTC 630 ----- GC----- TACT
 ATATACTTTATTTATGGATT TGAGCGCTAA AACACGG CAGAATATC CCATA T
 TGAATGAGATATTCTGAGCG CCTT ||||| ||||| ||||
 CTAACCTTATCCGTGTT TTGTGCC GTCTTATAG GGTAT /
 TATTCCAATCGCGA AGTAAGTTTA TTAT

GAM296 AGTAGCATACGGATGCTCGA 282 TGTACAAATT 631 GCA ---- - T C ATAT GT GT
 TATT--- GT
 TGTACAAATTGATATGGTCG GATATGGTCG GTA TACGG ATGC TCGA GTA AAATTG G C
 CG CA C
 TCGTATTCAGTCAATGTTAC TCGT ||| |||| ||| |||| ||||| || || ||
 AGTCGGTGGTCCAATTTTAA CAT ATGCC TACG AGCT CAT TTAAAC C G GC GT
 /
 CTTGACGCATAGTCCCGTA AAC CTGA C T T ---- TG TG TGACATT AA
 CAATACT

GAM297 CCCTATTTTCAATCCCCATG 283 CATGGAGTAG 632 AT TCAA CCA - TCA T A C
 TA
 TTTCCTCTTCAGTCTTCTCA ATGATAGAGG CCCT TT TCC TGTTTCC TCT GTCT CTC CAT
 GTC A
 CATCGTCTAATAGACATGGA GGAA |||| || ||| ||||| ||| ||| ||| |||
 GTAGATGATAGAGGGGAACA GGGA AA AGG ACAAGGG AGA TAGA GAG GTA CAG
 /

GAAGGACTATAATCAGGG

CT TATC AAG G TAG T - - AT

GAM298 GAAAAGACGTGGGTACTAAA 284 AAGTTGGCTG 633 - C AA T C CA- A T
GTTGGCTGTCATCTTACCAA TCATCTTACC GAAAAGACGTG GGTATA GT GG TGT TCTT
CCAAT G
TTGCAATTGGAAGAACAACG AATT ||||| ||| || || ||| ||| ||||
ACCTGCACTAATACCACATG CTTTTTGTAC CCAT AT CG CC GCA AGAA GGTTA C
TTTTTTC A A CA T A ACA - A

GAM299 GTCGTTAAAAGCGCTTCTAT 285 AATTATAGAT 634 C A CT TC CAT
ATCTCTCATTAGCTAGAATT ACGCTATTAA GT GTTAA AGCG TCTATA TCT T
ATAGATACGCTATTAATTAT TTAT || |||| ||| ||||| |||
TA TAATT TCGC AGATAT AGA A
T A AT TA TCG

GAM300 TGGTCGTGTAGCGCGATAGA 286 TTAGATATCC 635 C A C AGAGATA T
GATAGTCTAATATTAATATT GTAACACTAC TGGT GTGT GCG GAT GTCTAATA T
AGATATCCGTAACACTACCA CA ||| ||| ||| ||| |||||
ACCA CACA TGC CTA TAGATTAT A
T A - ----- A

GAM301 GACATGGTAAGATTACTGGC 287 TGGTAAGATT 636 T-- G ACTG - TCTAA
TCGTTTTCTAACTCCATGAA ACTGGCTCGT GACA GGTAATT GC TCGTTT C
TGATGCAAAATATTACCCTT TTTC ||| |||| ||| || |||||
TGTC CTGT CCATT TAA CG AGTAAG /
TTC A AA-- T TACCT

GAM302 AAGGGTGAATGCGATACAT 288 AAGAATTTAT 637 GAATG ACAT C --- ACACA
TGATCTATGTAGTTTAAAA ATAAATCATT AAGGGTG CGAT TGAT TATGTAG TTTTAAA
C
CACACGCAAACCTTTGAAGAA CCAT ||||| ||| ||| ||||| |||||
TTTATATAAATCATTCCATC TTCCTAC GCTA ACTA ATATATT GAAGTTT G
GATACATCCTT ATA-- CCTT A TAA CAAAC

GAM303 ACTGTATGCTCCTAGCGGAG 289 TGTATGCTCC 638 A - A AATCCTTCG T
TTAATCCTTCGTTGTTTCTA TAGCGGAGTT ACTGT TGCTC CT GCGGAGTT TTGT T
CAAAGTCTCTCGACTCCGCG AATC |||| |||| || ||||| |||
AGAGAGTAACAGT TGACA ATGAG GA CGCCTCAG AACAC
- A G CTCTCTGA- T

GAM304 ATAATTCAGTAATAATAATT 290 TCAGTAATAA 639 - A ATAATTC T AAA
CAGTAATGTATATAAAAATG TAATTCAGTA ATAATT CAGTA TA AGTAA GTATATAA T
CATTGTATATTTACTCCAAT ATGT ||||| |||| || |||| |||||

ACTACTGTAGTTGT TGTTGA GTCAT AT TCATT TATATGTT /
T C AACC--- - ACG

GAM305 ATAGAGTCTACATTTATATG 291 TCTACATTTA 640 CTACATTT TCT -- AGAT
TTCTCTATCGGTGAGATACA TATGTTCTCT ATAGAGT ATATGT CTATC GGTG A
AATACCTAGATAGTCGCGTA ATCG ||||| ||||| |||| ||||
TCTTCATCCATTCTAT TATCTTA TATGCG GATAG CCAT /
 CCTACTTC CT- AT AAAC

GAM306 ATATCTTCAGTACATCGTTT 292 TACAAATAGC 641 T T G C--- A A
GTAAAGTAATTATTATACAA AGTGTAGTGC ATA CT CA TACAT GTTTGTA AGT A
ATAGCAGTGTAGTGCAGTAT AGTA ||| || ||||| ||||| |||
 TAT GA GT ATGTG TAAACAT TTA T
 - C G ACGA A T

GAM307 ATTGCACGAAGTTCTTCGGC 293 ATTGTCCCAC 642 C C TTTCAT-- G A AA
TTTAATG TC CG
 GGTTCATGGAGTCATTTT GGAAGTGAAT GTTCTT GG GGT GGA TCATTTCTG TG ACA
ATC CA C
 TGATGAAACATTTAATGATC CCTT ||||| || ||| || ||||| || ||| ||| ||
TCCACGCAATTGTCGATATT CGAGAA CC CCA CCT AGTGAAGGC AC TGT TAG
GT A
 GTCCCACGGAAGTGAATCCT A A CTCAACTT A - CC TA----- CT TA
TCAACTCACCACCAAAGAGC
TCCGTTGCAT

GAM308 CCACATCCTTTATTAATAAT 294 TGAGAAAGAC 643 A TT ATAATAA AA TCTAT
AATTTAACAATCTCTATATC CAGTAGTATT CC CATCC TATTA TTT CAATC A
TATGGTTGAGAAAGACCAGT GGAT || ||||| ||||| || |||||
AGTATTGGATGGG GG GTAGG ATGAT AAA GTTGG /
 - TT GACCAG- GA TATCT

GAM309 GAAGGTAGTAATGTTAGTAG 295 TAGTTTATCA 644 GTA TTA A TAT G
ACAATTTTTATCTGTGAAAA TATACCTTT GAAGGTA ATG GTAGAC ATTTT CTGT A
CAGGAAATAGTTTATCATAT ||||| ||| ||||| ||||| |||||
ACCTTT TTTCCAT TAC TATTTG TAAAG GACA A
 A-- --- A --- A

GAM310 GCAATACTTCTGGTCTCGGA 296 TTCTGGTCTC 645 ACTTC A ----- C
TTAGGCGTCGTTACGTATAT GGATTAGGCG GCAAT TGGTCTCGGATT GG CGT G
ATCCACCAATCCGAGACCAT TCGT ||||| ||||| ||||| |||
TGATTGC CGTTA ACCAGAGCCTAA CC GCA T
 GTT-- - ACCTATATAT T

GAM311 GGCCTTTTTTATCGTTATCG 297 CCTTTTTTAT 646 C TT- CG CG - - TCACCTGG

GTTTTCTACACTCACCTGGT CGTTATCGGT GGC TT TTAT TTAT GT TTTC TACAC T
 TTATAAACGTGTGCGAGACA TTTC ||| ||| ||| ||| ||| |||
 CAAATAATAATAATGTAACG TCG AA AATA AATA CA AGAG GTGTG /
 CT C TGT AT AA C C CAAATATT

GAM312 TCATAATATTAGAATATATT 298 TAGAATATAT 647 ATT TATATTTTAAAGGA TTA TAT
 TTAAAGGACTTATCGTTATT TTAAAGGAC TCATAAT AGAA CTTATCG TTA T
 ATATTTTTTTAACTCGGTGA TTAT ||||| ||| ||||| |||
 GGTATCTTCTTAACTTTCTC AGTATTA TCTT GAGTGGC AAT T
 GAATTATGA AGC TCAATTCTTCTATG TC- TTT

GAM313 TTCTGAAAGAGATGAGAAGC 299 TCTATGGGTC 648 GAAAG A AA CCC
 CTGTAGAGAGACCCTGCGCT CATCTATGAG TTCT AGATG G GCCTGTAGAGAGA T
 TTCTCTATGGGTCCATCTAT AA ||| ||||| ||||| |||||
 GAGAA AAGA TCTAC C TGGGTATCTCTTT G
 GTA-- --- CGC

GAM314 TTTCTTTTCACGATGCATCT 300 ATAAGTGGAC 649 TC- GA- ----- GA CGT
 TATTGAATGACGTTTTCTCA ATATAGATGC TTTCTTT AC TGCATCT TATT ATGA T
 TAAGTGGACATATAGATGCA AGAA ||||| || ||||| ||| |||
 GAAGTAATGAAGAAA AAAGAAG TG ACGTAGA GTGA TACT /
 TAA AAG TATACAG A- CTT

GAM315 TTTTATAAACATGAAACCA 301 TGTCTAAATG 650 --- AAACCACT- AAA TAATTA G
 T CTGTCTAAATGTAATTATGA TAATTATGAT TTTTATA AACATG GTCT TG TGATCTT
 ATT A TCTTGATTTATAGATGAAGA CTTG ||||| ||||| ||| || ||||| |||
 TCAGCCTTTAGAGGATTTTA AAAAGTAT TTGTAT TAGG AT ACTAGAA TAG T
 ACCAGTATGTTTAATATGAA AAT GACCAATTT AG- TTCCG- G A
 AA

GAM316 ATGTAGTAATCGTTGTCGTG 302 ATGGTTCTTT 651 C TG GTGTTCC- TCC TTCTCC -
 T TTCT TTCCTGTTTCCTACTTCTCC CCGTACAACA AT GT TC TGTT TAC AATCAT
 ATAGATATT TCT A TACT ||| || ||| ||| ||||| ||||| |||
 AATCATATAGATATTTTCTT TATA AG ACAA ATG TTGGTA TGTTTATAA AGG /
 TCTATCATGGATAATATTTG - GT ATTTGTCAT C- CTTTC A T TACT
 TAATGGTTCTTTCCGTACAA CATACTGTTTAGATGATATT
 GCGCAT

GAM317 GAATGACTCGTCCCTTAATA 303 TGAATCGTCC 652 GA G TAATA AGTAG - TCT
 GGCAGTAGGCTAGTATCTTT CTTAATAGGC GAAT CTC TCCCT GGC GCTA GTA T
 TTTACGTAGTAATCGTCGTA AGTA ||| ||| ||| ||| ||| |||
 GGGAGAGAATTC CTTA GAG AGGGA CTG TGAT CAT /
 A- - TG--- CTAA- G TTT

GAM318 GAGATTGTATCAGTTTCGTA 304 GATTGTATCA 653 -- - T TA TGA G T
 GTCTTGAGTATTGGTATTAC GTTTCGTAGT GAGATTGTA TC AGT TCG GTCT GTATTG TAT A
 TATATAGTATATAGATGTCTG CTTG ||||| || ||| ||| ||||| |||
 ACGCTAGATATACAGTCTC CTCTGACAT AG TCG AGC TAGA TATGAT ATA C
 AT A C TG TA- - T

GAM319 GGCAAATCTTATCATTGGTC 305 TAACATCGAT 654 CTT - --- TG- TTGCTTT
 GGTGTTTGGTCTTGCTTTGT TCCCATATGA GGCAAAT ATCAT TGG TCGGTGTT GTC G
 GACTTTGATAATAACATCGA TGTT ||||| ||||| ||||| |||
 TTCCCATATGATGTTTGT TTGTTTG TAGTA ACC AGCTACAA TAG /
 --- T CTT TAA TTTCAGT

GAM320 ACCTCTTTCTGATGGAGTCG 306 TGATGGAGTC 655 TTTCT- T TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT C GA GGAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA | ||||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT G CT TCTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT T -- GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCCTTCGAT
 GGT

GAM321 ACCTCTTTCTGATGGAGTCG 307 TGATGGAGTC 656 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM322 ACCTCTTTCTGATGGAGTCG 308 TGATGGAGTC 657 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT

GAM323 ACCTCTTTCTGATGGAGTCG 309 TGATGGAGTC 658 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA

TTATCTCTTTCTCTCTTCGA
 TGGT
 GAM324 ACCTCTTTCTGATGGAGTCG 310 TGATGGAGTC 659 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT
 GAM325 ACCTCTTTCTGATGGAGTCG 311 TGATGGAGTC 660 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT
 GAM326 ACCTCTTTCTGATGGAGTCG 312 TGATGGAGTC 661 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT
 GAM327 ACCTCTTTCTGATGGAGTCG 313 TGATGGAGTC 662 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT
 GAM328 ACCTCTTTCTGATGGAGTCG 314 TGATGGAGTC 663 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A
 CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||||
 AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
 GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
 TTATCTCTTTCTCTCTTCGA
 TGGT
 GAM329 ACCTCTTTCTGATGGAGTCG 315 TGATGGAGTC 664 TTTCT TG TC AAG CT TC
 TCTTC T CTCACAA
 TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
 GGT A

CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||| || |||
AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
TTATCTCTTTCTCTCTTCGA
TGGT

GAM330 ACCTCTTTCTGATGGAGTCG 316 TGATGGAGTC 665 TTTCT TG TC AAG CT TC
TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAGT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
CTCTCTTCGATGGTCTCACA TTTA || || ||| ||||| ||||| ||| || |||
AAAATATTAAACCTCTTTCT AG CT TTC TATTTT AAAATG GAG AG CT CCA A
GATGGAGTCGTAAAAAAGTT CTTCT CT TC GAA CT GT TCTTT - AATTATA
TTATCTCTTTCTCTCTTCGA
TGGT

GAM331 ACCTCTTTCTGATGGAGTCG 317 CGTAAAAAAG 666 TTTCT TG TC AAG CT C TTC--
T CTCACAA
TAAAAAAGTTTTATCTTTCT TTTTATCTTT TC GA GAG GTAAAA TTTTAT TTCT TC GA
GGT A
CTCTTCGATGGTCTCACAAA CTCT || || ||| ||||| ||||| ||||| ||| |||
AATATTAAACCTCTTTCTGA AG CT TTC TATTTT AAAATG GAGG AG CT CCA
A
TGGAGTCGTAAAAAAGTTTT CTTCT CT TC GAA CT T TCTTT - AATTATA
ATCTCTTTCTCTCTTCGATG
GT

GAM332 ATTAATTATAAAATTATGTA 318 TAAGTTAGTA 667 TA-- - A-- - T
TATGATTTACTAACTTTAGT ATACATAAAT ATTAAT TAAAATT ATGTAT TGATTTA CTAAC T
TAGATAAGTTAGTAATACAT TTTA ||||| ||||| ||||| ||||| |||||
AAATTTTAGTATATTAAT TAATTA ATTTTAA TACATA ATTGAAT GATTG T
TATG A ATG A A

GAM333 GATGGAGTCGTAAAAAAGTT 319 TGATGGAGTC 668 T TC AAG -- T TCCTTC T
CTCACAA
TTATCTCTTTCTCCTTCGAT GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTCT TC GA GGT
A
GGTCTCACAAAAATATTAATA TTTA || |||| ||||| ||||| ||||| ||| |||
CCTCTTTCTGATGGAGTCGT CT TCTC TATTTT AAAATG GAGG AG CT CCA A
AAAAAAGTTTTATCTCTTTC T -- GAA CT T TCTTT- - AATTATA

GAM334 GATGGAGTCGTAAAAAAGTT 320 TGATGGAGTC 669 T TC AAG -- T TCCTTC T
CTCACAA
TTATCTCTTTCTCCTTCGAT GTAAAAAAGT GA GGAG GTAAAA TTTTAT CTCT TC GA GGT
A
GGTCTCACAAAAATATTAATA TTTA || |||| ||||| ||||| ||||| ||| |||
CCTCTTTCTGATGGAGTCGT CT TCTC TATTTT AAAATG GAGG AG CT CCA A
AAAAAAGTTTTATCTCTTTC T -- GAA CT T TCTTT- - AATTATA

GAM335 GATGGAGTCGTAAAAAAGTT 321 TGATGGAGTC 670 T TC AAG -- T TCCTTC T
CTCACAA

TTATCTCTTTCTCCTTCGAT	GTAAAAAAGT	GA GGAG GTAAAA TTTTAT CTCT TC	GA GGT
A			
GGTCTCACAAAAATATTA	TTTA		
CCTCTTTCTGATGGAGTCGT		CT TCTC TATTTT AAAATG GAGG AG	CT CCA A
AAAAAAGTTTTATCTCTTC		T -- GAA CT T TCTTT- - AATTATA	

GAM336 GATGGAGTCGTAAAAAAGTT 322 TGATGGAGTC 671 T TC AAG CT TC TCTTC T CTCACAA

TTATCTCTTTCTCTCTTCGA	GTAAAAAAGT	GA GGAG GTAAAA TTTTAT CTT TC	GA GGT
A			
TGGTCTCACAAAAATATTA	TTTA		
ACCTCTTTCTGATGGAGTCG		CT TCTC TATTTT AAAATG GAG AG	CT CCA A
TAAAAAAGTTTTATCTCTTT		T -- GAA CT GT TCTTT - AATTATA	
C			

GAM337 GATGGTCTCATAAAAAAGT 323 ATAAAAAAG 672 G TCATAAAA TTTTAC ATTCT-CTCTCTT TG

TTTACAAAAATATTTTTATT	TTTTACAAAA	AT GTC	AAAG	AAAAATATTTTT	CTTT
TGA G					
CTCTTTCTCTCTTTGATGGT	ATAT				
CTCATAAAAAAGTTTTACA		TG TAG TTTC TTTTATAAAAA	GAAA	ACT /	
AAAATATTTTTATTCTCTTT		G TTTCTCTC TCTTA-	CATTTT	AAAAT--	CT
CTCTCTTTGATGGTC					

GAM338 GGAGTCATAAAATATTTTTTA 324 TAAAATATTT 673 TC A T- T TCTCTTC T CTCACAA

TTCTCTTTCTCTCTTCGATG	TTATTCTCTT	GGAG ATAAAAT TTTTAT CTCT TC	GA GGT
A			
GTCTCACAAAAATATTAAC	TCTC		
CTCTTTCTGATGGAGTCGTA		TCTC TATTTTG AAAATG GAGG AG	CT CCA A
AAAAAGTTTTATCTCT		-- A CT T TCTTT-- - AATTATA	

GAM339 TTAAACCTCTTTCTGATGGA 325 TGATGGAGTC 674 CTTTCT TG TC AAG -- T TCCTTC T CTCACAA

GTCGTAAAAAAGTTTTATCT	GTAAAAAAGT	GA GAG GTAAAA TTTTAT CTCT TC	GA
GGT A			
CTTTCTCCTTCGATGGTCTC	TTTA		
ACAAAAATATTAACCTCTT		CT TTC TATTTT AAAATG GAGG AG	CT CCA A
TCTGATGGAGTCGTAAAAAA		TCTTTC CT TC GAA CT T TCTTT- - AATTATA	
GTTTTATCTCTTTCTCCTTT			
CTCACAAAAA			

GAM340 TTTTCTTTGGTACAAAATT 326 TCTTTGGTAC 675 T TT CACAA --- CA A TCACACAAGTTTTTATACAG AAAATTTTAC TTTTCTT GGTACAAAA TCA GTTTT TATA GACAA T

ACAAATTCTTGTCATATAT	ACAA		
TTTAAACATTGACTTTTGT		AAAAAGAA TCATGTTTT AGT	CAAAA ATAT CTGTT T
ACTAAGAAAAA		- C- TA--- TTTT AC C	

GAM341 AGAGATAAACTTTTTTACG 327 TGAGACCATC 676 -- AC ----- A A AAGA A T
 ACTCCATCAGAAAGAGGTTT GAAGGAGACT AGAGATA AACTTTTTT GA CTCC TC GA
 GGTTT ATA T
 AATATTTTTGTGAGACCATC CCAT ||||| ||||| || ||| || ||||| ||
 GAAGGAGACTCCATCAGAAA TTTTAT TTTGGAGAAA CT GAGG AG CT CCAGA
 TGT T
 GAGGTTTAATATTTTT AA GA ACCTCA A - A--- G T

GAM342 ATAAAAATATTTTTGTAAAA 328 AATATTTTTG 677 AAAA A-- GA
 CTTTTTTATGAGACCATCA TAAACTTTT ATAAAAATATTTTTGT CTTTTTT TGA C
 AAGAGAGAAAGAGAATAAAA TTTA ||||| ||||| ||
 ATATTTTTGT TGTTTTATAAAAATA GAAAGAGA ACT /
 AGA- GAA AC

GAM343 ATAAAAATATTTTTGTAAAA 329 AATATTTTTG 678 AAAA A-- GA
 CTTTTTTATGAGACCATCA TAAACTTTT ATAAAAATATTTTTGT CTTTTTT TGA C
 AAGAGAGAAAGAGAATAAAA TTTA ||||| ||||| ||
 ATATTTTTGT TGTTTTATAAAAATA GAAAGAGA ACT /
 AGA- GAA AC

GAM344 ATGGATTTTACTAGATCATT 330 TTATACGATC 679 - TTT - ATTT- ACC
 TATATACCAAAAATATTAT TACGTTTTAT ATG GAT AC TAGATC ATAT A
 ACGATCTACGTTTTATTATA TATA ||| ||| ||||| |||
 T TAT TTA TG ATCTAG TATA A
 A TTT C CATAT AAA

GAM345 CTTTTTTACGACTCCATCAG 331 CATCAGAAAG 680 A CTCCA G G T A G GACCA -
 AAAGA
 AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
 AAGAGAG G
 TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||||| ||| |||||
 AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
 A
 ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
 AATATTTTTGTGAGACCATC
 GAAGAGAG

GAM346 CTTTTTTACGACTCCATCAG 332 CATCAGAAAG 681 A CTCCA G G T A G GACCA -
 AAAGA
 AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
 AAGAGAG G
 TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||||| ||| |||||
 AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
 A
 ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
 AATATTTTTGTGAGACCATC

GAAGAGAG

GAM347 CTTTTTTACGACTCCATCAG 333 CATCAGAAAG 682 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT I III III IIII III III IIII III IIII
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM348 CTTTTTTACGACTCCATCAG 334 CATCAGAAAG 683 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT I III III IIII III III IIII III IIII
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM349 CTTTTTTACGACTCCATCAG 335 CATCAGAAAG 684 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT I III III IIII III III IIII III IIII
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM350 CTTTTTTACGACTCCATCAG 336 CATCAGAAAG 685 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT I III III IIII III III IIII III IIII
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG

GAM351 CTTTTTTACGACTCCATCAG 337 CATCAGAAAG 686 A CTCCA G G T A G GACCA -
AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT I III III IIII III III IIII III IIII
AGAGATAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC

GAAGAGAG

GAM352 CTTTTTTACGACTCCATCAG 338 CATCAGAAAAG 687 A CTCCA G G T A G GACCA -
AAAG

AAAGAGGTTTAATATTTTTG AGGTTTAATA TT CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AAGAGAG A

TGAGACCATCGAAGAGAGAA TTTT || ||| ||| ||||| ||| ||||| ||| |||||
AGATAAACTTTTTTACGAC AA GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTC T

TCCATCAGAAAGAGGTTTAA - ACCAG G A T G G ACCTC A AAAA
TATTTTTGTGAGACCATCGA
AGAGAG

GAM353 GTGTGCCTGAATCGTTCGAT 339 TGAATAGAGT 688 C TTCGAT C C CAA
TAACCCTACTCATCCAATTT TATCGATTCA GTGTG CTGAATCG TAAC CTA TCATC T
CAGATGAATAGAGTTATCGA GACA ||||| ||||| ||||| |||||
TTCAGACACAC CACAC GACTTAGC ATTG GAT AGTAG T
A T----- A A ACT

GAM354 TCAGAAAGAGGTTTAATATT 340 AGAGGTTTAA 689 AAA GTTT-- GAGACCA- GA
TTTGTGAGACCATCGAAGAG TATTTTTGTG TCAG GAG AATATTTTTGT TC A
AGAAAGAGAATAAAAATATT AGAC ||| ||| ||||| |||
TTATGACTCCATTGA AGTT CTC TTATAAAAATA AG /
AC- AGTATT AGAGAAAG AG

GAM355 TGAGACCATCAAAGAGAGAA 341 AGAGAGAAAAG 690 ACCA AAG AGA- AAAA
A-- GA

AGAGAATAAAAAATATTTTTG AGAATAAAAA TCA AGAGAAAG ATAAAAATATTTTTGT
CTTTTTTT TGA C

TAAACTTTTTTTATGAGAC TATT ||| ||||| ||||| ||||| ||||| |||
CATCAAAGAGAGAAAGAGAA AGT TTTTTTC TGTTTTTATAAAAATA GAAAGAGA
ACT /

TAAAAATATTTTTGTAAAC CCAG A-- AAAA AGA- GAA AC
TTTTTTTATGAGACCATCA

GAM356 TTTTATGAGACCATCAAAGA 342 GAAGAGAGAA 691 ACCA AAG AGA- AAAA---
- A

GAGAAAGAGAATAAAAAATAT AGAGAATAAA TCA AGAGAAAG ATAAAAATATTTTTGT
CTTTTTTTG TG G

TTTTGTAAACTTTTTTTGT AATA ||| ||||| ||||| ||||| ||||| |||
GAGACCATCGAAGAGAGAAA AGT TTTTTTC TGTTTTTATAAAAATA
GAGAGAAGC AC A

GAGAATAAAAAATATTTTTGT CCAG A-- AAAA AGAGAAA T C
AAAACTTTTTTTATGAGACC
ATCAAAGAGAG

GAM357 TTTTCTTAGTACAAAAGTC 343 TCAATGTTTT 692 A- G- AT--- AAAA G
AATGTTTTTAAATATATGGA AAAATATATG TTTTCTT GTACAAAA TCA GTTTT
TATATGGACAA A

CAAGAATTTGTCTGTATAAA GACA ||||| ||||| ||| ||| |||||
AACTTGTGTGAAATTTTGTA AAAAGAA CATGTTTT AGT CAAAA ATATGTCTGTT A

CCAAAGAAAAA

AC AA GTGTT ---- T

GAM358 TCACCTTATCAAAGTCGTTT 344 TTGGTTGTGG 693 CCTT A TT CACAT TATA T-
TT

ATATCACATTGTATATAGTT ATCTTCTACA TCA ATCA AGTCGT ATAT TGTA
GTTTATAACC TAACT C
TATAACCTTAACTTTTCGAGG ATAT ||| ||| ||||| ||| ||| ||||| |||||
TTATTGGTTGTGGATCTTCT AGT TAGT TCAGTA TATA ACAT TAGGTGTTGG
ATTGG /
ACAATATCTATGACTCTGAT TCTT C TC ---- CTTC TT AG
TTCTTGA

GAM359 TCGGCCATACGTTTACTTTT 345 TATCATAAAG 694 AC T C- - GT
TGCGTATACATGTCCTGGTG GGTATGCTCA TCGGCCAT GT TACTTTTTG GTATA CAT C
ATATATCATAAAGGGTATGC TGGC ||||| || ||||| ||||| |||
TCATGGCCGA AGCCGGTA CG ATGGGAAAT TATAT GTG C
CT T AC A GT

GAM360 TCGATGATACATGTATTA 346 TGATACATGT 695 A--- TGTA T TCC
ATACTTTCCGAATAAGTCTT ATTAAAATAC TCG TGATACA TAAAA ACTT G
TTAAATATTGTATTAATTAT TTTC ||| ||||| ||||| |||
GA AGT ATTATGT AATTTT TGAA /
ATTA TATA C TAA

GAM361 AAAATCGATTCCGTCCAAGA 347 TCGATTCCGT 696 C CCAAG AAAAACA
TGATAAAAACATTTACCGGC CCAAGATGAT AAAAT GATTCCGT ATGAT T
ATCATAAACACGGAGTTTAT AAAA ||||| ||||| |||||
TTT TTTTA TTGAGGCA TACTA T
T CAAA- CGGCCAT

GAM362 CATGGAGATACTTTATTACT 348 TAATGTCCTG 697 ----- T TAAATA
CCATTAAATAATTTATCATG TTTCATTTGT CATGGAGAT AC TTATTACTCCAT A
GAGTGATAATGTCCTGTTTC TTCC ||||| || ||||| |||||
ATTTGTTTCCATG GTACCTTTG TG AATAGTGAGGTA /
TTTACTTTGTCC T CTATTT

GAM363 AGTATGTTGTACGGAAAGAA 349 TGATTGGAGA 698 -- A GAAAGAACCA-- AAATATTA
TG--- AAGA
CCATTACAAATATTATCCAT AGTAGGAAAC AGTA TGTTGT CG TTAC TCCA
ATAGA A
GATAGAAAGAAAATATCTAT AGGA ||| ||||| || ||| ||| |||||
ATGATTGGAGAAGTAGGAAA TCAT GCAACA GC GATG AGGT TATCT /
CAGGAACACGACAACGATTA TA - ACAAGGACAAAG AAG----- TAGTA ATAA
CT

GENE	TARGET	UTR	SEQUENCE	SEQID	BINDING-SITE
=====					
GAM15	CAPN2	3'	AAAACTTTATGAACTTCACCA	855	A _ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM15	DAAM2	3'	AAAATTTTTCTAAAACTCCATC	3559	CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM15	SELE	3'	AAAACTCTCCTACACTTCCATT	747	_ C AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM15	KIAA0475	3'	AAAACCTTGCATTCCATCA	1570	C AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C _		
GAM15	LOC222671	5'	GCTTCTACGACTCCGCCA	3582	A AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM15	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A _ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM15	LOC257615	5'	GCTTCTACGACTCCGCCA	3749	A AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM16	CAPN2	3'	AAAACTTTATGAACTTCACCA	855	A _ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM16	DAAM2	3'	AAAATTTTTCTAAAACTCCATC	3559	CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM16	SELE	3'	AAAACTCTCCTACACTTCCATT	747	_ C AAAA
	A		TGATGGA GT GTA AGTTTT		

			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM16	KIAA0475	3'	AAAACCTTGCATTCCATCA	1570	C AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM16	LOC222671	5'	GCTTCTACGACTCCGCCA	3582	A AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM16	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A _ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM16	LOC257615	5'	GCTTCTACGACTCCGCCA	3749	A AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM17	CAPN2	3'	AAAACCTTTATGAACCTTCACCA	855	A _ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM17	DAAM2	3'	AAAATTTTTCTAAAACCTCCATC	3559	CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM17	SELE	3'	AAAACCTCTCCTACACTTCCATT	747	_ C AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM17	KIAA0475	3'	AAAACCTTGCATTCCATCA	1570	C AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM17	LOC222671	5'	GCTTCTACGACTCCGCCA	3582	A AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM17	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A _ A A
			TG TGGAGTC GT AA AAGTT		

			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM17	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM18	CAPN2	3'	AAAACCTTTATGAACTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A ____		
GAM18	DAAM2	3'	AAAATTTTTCTAAACTCCATC 3559		CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM18	SELE	3'	AAAACCTCTCCTACACTTCCATT 747		_ C AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM18	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570		C AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM18	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM18	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM18	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM19	CAPN2	3'	AAAACCTTTATGAACTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A ____		
GAM19	DAAM2	3'	AAAATTTTTCTAAACTCCATC 3559		CG A
	A		TGATGGAGT TA AAAAGTTTT		

			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM19	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM19	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM19	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM19	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM19	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM20	CAPN2	3'	AAACTTTATGAAGTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM20	DAAM2	3'	AAAATTTTCTAAAAGTCCATC 3559	CG A	
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM20	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM20	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM20	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		

			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM20	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A	_ A A
			TG TGGAGTC GT AA AAGTT			
			AC ACCTCAG CA TT TTAA			
			C	T C C		
GAM20	LOC257615	5'	GCTTCTACGACTCCGCCA	3749	A	AAA
			TG TGGAGTCGTA AAGT			
			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM21	CAPN2	3'	AAAACCTTTATGAACTTCACCA	855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT			
			AC ACTTCA GTATT TCAAAA			
			C	A _		
GAM21	DAAM2	3'	AAAATTTTTCTAAACTCCATC	3559		CG A
	A		TGATGGAGT TA AAAAGTTTT			
			ACTACCTCA AT TTTTAAAA			
			AA C			
GAM21	SELE	3'	AAAACCTCTCCTACACTTCCATT	747		_ C AAAA
	A		TGATGGA GT GTA AGTTTT			
			ATTACCT CA CAT TCAAAA			
			T _ CCTC			
GAM21	KIAA0475	3'	AAAACCTTGCATTCCATCA	1570		C AAAA
			TGATGGAGT GTAA GTTTT			
			ACTACCTTA CGTT CAAAA			
			_ C__			
GAM21	LOC222671	5'	GCTTCTACGACTCCGCCA	3582	A	AAA
			TG TGGAGTCGTA AAGT			
			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM21	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A	_ A A
			TG TGGAGTC GT AA AAGTT			
			AC ACCTCAG CA TT TTAA			
			C	T C C		
GAM21	LOC257615	5'	GCTTCTACGACTCCGCCA	3749	A	AAA
			TG TGGAGTCGTA AAGT			
			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM22	CAPN2	3'	AAAACCTTTATGAACTTCACCA	855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT			

			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM22	DAAM2	3'	AAAATTTTCTAAACTCCATC 3559	CG	A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM22	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM22	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C _		
GAM22	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM22	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM22	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM23	CAPN2	3'	AAACTTTTATGAAGTTACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM23	DAAM2	3'	AAAATTTTCTAAACTCCATC 3559	CG	A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM23	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM23	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		

			ACTACCTTA CGTT CAAAA		
			— C—		
GAM23	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C—		
GAM23	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	— A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM23	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C—		
GAM24	CAPN2	3'	AAACTTTTATGAACCTTCACCA 855	A	— AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A —		
GAM24	DAAM2	3'	AAAATTTTCTAAACTCCATC 3559		CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM24	SELE	3'	AAACTCTCCTACACTTCCATT 747		— C AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T — CCTC		
GAM24	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			— C—		
GAM24	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C—		
GAM24	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	— A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM24	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		

			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM25	CAPN2	3'	AAAACCTTTATGAACTTCACCA	855	A	_ AAA
			TG TGGAGT CGTAA	AGTTTT		
			AC ACTTCA GTATT	TCAAAA		
			C	A		
GAM25	DAAM2	3'	AAAATTTTTCTAAACTCCATC	3559		CG A
	A		TGATGGAGT TA	AAAAGTTTT		
			ACTACCTCA AT	TTTTTAAAA		
			AA	C		
GAM25	SELE	3'	AAAACCTCTCCTACACTTCCATT	747		_ C AAAA
	A		TGATGGA GT GTA	AGTTTT		
			ATTACCT CA CAT	TCAAAA		
			T	_ CCTC		
GAM25	KIAA0475	3'	AAAACCTTGCATTCCATCA	1570		C AAAA
			TGATGGAGT GTAA	GTTTT		
			ACTACCTTA CGTT	CAAAA		
				C__		
GAM25	LOC222671	5'	GCTTCTACGACTCCGCCA	3582	A	AAA
			TG TGGAGTCGTA	AAGT		
			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM25	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A	_ A A
			TG TGGAGTC GT AA	AAGTT		
			AC ACCTCAG CA TT	TTTAA		
			C	T C C		
GAM25	LOC257615	5'	GCTTCTACGACTCCGCCA	3749	A	AAA
			TG TGGAGTCGTA	AAGT		
			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM26	ITGB7	5'	AGAGAAAGTCTGACTTGCCCCA	783		AAAA_ TTAT
	C		GT AAGTT CTTTCTCT			
			CA TTCAG GAAAGAGA			
			CCCCG	TCT_		
GAM26	RPP30	3'	AGAGAAAGACAACCTGTTCTGCG	1297	A A	TTA
			CGTA AA AGTT	TCTTTCTCT		
			GCGT TT TCAA	AGAAAGAGA		
			C G	C__		
GAM26	FLJ13263	3'	AGAGAAAGATTTTAGCTTTT	2139		TT_
			AAAAGTT ATCTTTCTCT			

			TTTTCGA TAGAAAGAGA		
			TTT		
GAM26	FLJ23074	5'	AGAGAAAGACAAGGGTTT 2133	G A	
			AAA TTTT TCTTTCTCT		
			TTT GGAA AGAAAGAGA		
			G C		
GAM26	GTF2A2	3'	AGAAAAAATATGACTTTTTTTAC 1119	T C_	
			GTAAAAAAGTT TAT TTTCT		
			CATTTTTTCAG ATA AAAGA		
			T AA		
GAM26	IMP-2	3'	AGAGAAAGCAGGCTTTTCTA 1308	A TAT	
			TA AAAAGTTT CTTTCTCT		
			AT TTTTCGGA GAAAGAGA		
			C C_		
GAM26	KIAA0212	3'	AGAAAGGTAAATCTTTTTTAC 1518	A T	
			GTAAAAA G TTTATCTTTCT		
			CATTTTT C AAATGGAAAGA		
			_T		
GAM26	OSBPL2	5'	AGAGAAAGTTTGTAATAATTCCT 1566	AAA	___
	TAC		GTAA AGTTTTAT CTTTCTCT		
			CATT TTAAATG GAAAGAGA		
			CC_ TTT		
GAM26	OSBPL2	5'	AGAGAAAGTTTGTAATAATTCCT 2482	AAA	___
	TAC		GTAA AGTTTTAT CTTTCTCT		
			CATT TTAAATG GAAAGAGA		
			CC_ TTT		
GAM26	RBM9	3'	AGAAAGAATACTTTTTTAT 1489	TTTA	
			GTAAAAAAGT TCTTTCT		
			TATTTTTTCA AGAAAGA		
			TA_		
GAM26	LOC254826	3'	AGAGAAAGTCTTGCTTTTT 3732	TTTAT	
			AAAAAGT CTTTCTCT		
			TTTTTCG GAAAGAGA		
			TTCT_		
GAM27	CAPN2	3'	AAACTTTTATGAACCTCACCA 855	A _ AAA	
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM27	DAAM2	3'	AAAATTTTTCTAAACTCCATC 3559	CG A	
	A		TGATGGAGT TA AAAAGTTTT		

			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM27	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM27	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM27	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM27	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM27	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM28	CAPN2	3'	AAACTTTATGAAGTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM28	DAAM2	3'	AAAATTTTCTAAAAGTCCATC 3559	CG A	
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM28	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM28	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM28	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		

			AC GCCTCAGCAT TTCG		
			C C__		
GAM28	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM28	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM29	CAPN2	3'	AAAACCTTTATGAACTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM29	DAAM2	3'	AAAATTTTTCTAAACTCCATC 3559		CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM29	SELE	3'	AAAACCTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM29	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM29	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM29	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM29	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM30	FGF2	3'	ATATTTTTGTGGCTGCTTTTT 884	T_	
			AAAAAGT TTACAAAAATAT		

			TTTTTCG GGTGTTTTTATA		
			TC		
GAM30	MPHOSPH1	3'	ATATTTTTATAAGGCTTTTTT 1670	C	
			AAAAAAGTTTTTA AAAAATAT		
			TTTTTTCGGAAT TTTTATA		
			A		
GAM30	FLJ11274	3'	ATATCTTTGTAGTAGCTTTTTT 1820	—	A
	TA		TAAAAAAGTT TTACAAA ATAT		
			ATTTTTTTCGA GATGTTT TATA		
			T C		
GAM30	FLJ31101	3'	ATATTTTTGTAAAATGTATTTG 1771	AAAA	
	T		ATAAA GTTTTACAAAAATAT		
			TGTTT TAAAATGTTTTTATA		
			ATG_		
GAM30	GPT2	3'	ATATTTTTGTAACAATTGCTTT 2417	T_____	
	TTT		AAAAAAGT TTACAAAAATAT		
			TTTTTTCG AATGTTTTTATA		
			TTAAC		
GAM30	RMP	3'	TTTGTAAAACTTTTTTTTC 2430	T	
			A AAAAAAAGTTTACAAAA		
			C TTTTTTTCAAAATGTTTT		
			T		
GAM30	RMP	3'	TTTGTAAAACTTTTTTTTC 1059	T	
			A AAAAAAAGTTTACAAAA		
			C TTTTTTTCAAAATGTTTT		
			T		
GAM30	SOX6	3'	ATATTTTTGTCTTACTTTTTTTT 2328	TTT	
			AAAAAAAGT ACAAAAATAT		
			TTTTTTTCA TGTTTTTATA		
			TTC		
GAM30	LOC136288	3'	ATATTTCTGAGGCTTTTTTTGT 3018	CAA	
			ATAAAAAAAGTTTTA AAATAT		
			TGTTTTTTTCGGAGT TTTATA		
			C_		
GAM31	AICDA	3'	AGAAAGAGAACAATATTT 1922	TTTA	
			AAATATT TTCTCTTTCT		
			TTTATAA AAGAGAAAGA		
			C_		
GAM31	AS3	3'	AGAAAGATTTAAAGTATTTTA 1652	TATTC	
			TAAAATATTTT TCTTTCT		

			ATTTTATGAAA	AGAAAGA	
			TTT__		
GAM31	EPM2A	3'	AGAAAGAGAAGTGT	TTT 1234	TTT
			AAAATAT	TTCTCTTCT	
			TTTTGTG	AAGAGAAAGA	

GAM31	HRH1	3'	AGAAAGAGAAAATGAAATATTTT	780	TA
			AAAATATTTT	TTCTCTTCT	
			TTTTATAAAG	AAGAGAAAGA	
			TA		
GAM31	MAPK14	3'	GAGAAAGGGCAAATTATTTTA	818	T TATT
			TAAAATA TTT	CTCTTTCTC	
			ATTTTAT AAA	GGGAAAGAG	
			T C__		
GAM31	MAPK14	3'	GAGAAAGGGCAAATTATTTTA	2465	T TATT
			TAAAATA TTT	CTCTTTCTC	
			ATTTTAT AAA	GGGAAAGAG	
			T C__		
GAM31	MAPK14	3'	GAGAAAGGGCAAATTATTTTA	2466	T TATT
			TAAAATA TTT	CTCTTTCTC	
			ATTTTAT AAA	GGGAAAGAG	
			T C__		
GAM31	NOTCH2	3'	GAGAATTAATAATATTTTA	2058	T
			TAAAATATTTT	ATTCTC	
			ATTTTATAAAA	TAAGAG	
			T		
GAM31	SIM1	3'	GAGAAAGAGAGAGATA	1181	TAT
			TATTTT	TCTCTTCTC	
			ATAGAG	AGAGAAAGAG	

GAM31	C11orf25	3'	AAAGAGAAAAATATTTTA	2193	TAT
			TAAAATATTTT	TCTCTT	
			ATTTTATAAAA	AGAGAAA	

GAM31	DKFZP564D116	3'	GAAAAGCAATAAAAAATATTTTA	2938	_ C
			TAAAATATTTT	TATT CT TTTC	
			ATTTTATAAAAATAA	GA AAAG	
			C _		
GAM31	DSCR6	3'	GAGAAAGAGAAGGTCTATGTCA	1866	A TTTTA
			A ATAT	TTCTCTTCTC	

			A TGTA AAGAGAAAGAG		
			C TCTGG		
GAM31	FLJ10006	3'	GAGAAAGAAGATATTTTA 3152	A	
			TAAAATATTTTT TTCTC		
			ATTTTATAGAAG AAGAG		
			A		
GAM31	HTPAP	3'	GAGAATAAAAAAGATTTTA 2255	A	
			TAAAAT TTTTATTCTC		
			ATTTTA AAAAATAAGAG		
			G		
GAM31	KIAA0979	3'	AGAAAGATTTAAAGTATTTTA 1601	TATTC	
			TAAAATATTTT TCTTCT		
			ATTTTATGAAA AGAAAGA		
			TTT__		
GAM31	KIAA1634	3'	GAGAATAAAACTATTTTA 2657	T	
			TAAAATA TTTTATTCTC		
			ATTTTAT AAAATAAGAG		
			C		
GAM31	PTD012	3'	GAGATTGGGAACAAAAATAT 1465	A TT	
			ATATTTTT TTCTC TCTC		
			TATAAAAA AAGGG AGAG		
			C TT		
GAM31	SAMHD1	3'	AGAAAGAGAAAGAAATAT 2593	A	
			ATATTTTT TTCTCTTCT		
			TATAAAGA AAGAGAAAGA		
			-		
GAM31	LOC196758	3'	GAGAAAGAGCAGGTGAAATATT 3410	TATT_	
	TT		AAAATATTTT CTCTTCTC		
			TTTTATAAAG GAGAAAGAG		
			TGGAC		
GAM31	LOC219790	3'	GAGAATAAAAAATAATTTA 3520	A	
			TAAA TATTTTTATTCTC		
			ATTT ATAAAAATAAGAG		
			A		
GAM32	CAPN2	3'	AAACTTTTATGAACTTCACCA 855	A _ AAA	
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM32	DAAM2	3'	AAAATTTTTCTAAACTCCATC 3559	CG A	
	A		TGATGGAGT TA AAAAGTTTT		

			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM32	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM32	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM32	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM32	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM32	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM33	CAPN2	3'	AAACTTTATGAAGTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM33	DAAM2	3'	AAAATTTTCTAAAAGTCCATC 3559	CG A	
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM33	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM33	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM33	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		

			AC GCCTCAGCAT TTCG		
			C C_		
GAM33	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM33	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C_		
GAM34	ADCY6	3'	TTGTACAATATTTTGTACAAAG 1617	G	TTCAC
	A		TCTTTG TACAAAAT ACAA		
			AGAAAC ATGTTTTA TGTT		
			_ TAACA		
GAM34	ADCY6	3'	TTGTACAATATTTTGTACAAAG 1933	G	TTCAC
	A		TCTTTG TACAAAAT ACAA		
			AGAAAC ATGTTTTA TGTT		
			_ TAACA		
GAM34	APBB2	5'	TGAGCTTTGTACCAAAGA 2946		AT
			TCTTTGGTACAAA TTCA		
			AGAAACCATGTTT GAGT		
			C_		
GAM34	ATP8B2	3'	TGATTTTTATACCAAAGA 2716	C	TT
			TCTTTGGTA AAAA TCA		
			AGAAACCAT TTTT AGT		
			A T_		
GAM34	CEACAM1	3'	TGTGTGAAGTAGCAAAGA 848	G	CAAAAT
			TCTTTG TA TTCACACA		
			AGAAAC AT AAGTGTGT		
			G C_		
GAM34	CHST1	3'	TGTGATATTTCTTTGTGCCAAA 1046		_ T
			TTTGGTACAAA AT TCACA		
			AAACCGTGTTT TA AGTGT		
			CTT T		
GAM34	FBXL7	3'	TGCGTGTTTTCCACCAAAGA 1425	AC	TTT A
			TCTTTGGT AAAA CAC CA		
			AGAAACCA TTTT GTG GT		
			CC _ C		
GAM34	HOXC9	3'	TGCGTGCGAGATTTTGTAC 2592	_	A
			GTACAAAATTT CAC CA		

			CATGTTTTAGA GTG GT		
			C C		
GAM34	IGF1	3'	TGTGGCATTGTACCAA 763	ATT	
			TTTGGTACAAA TCACA		
			AAACCATGTTT GGTGT		
			AC_		
GAM34	ITGAL	3'	TGTGAAATTCTGTCCAAA 907	T A	
			TTTGG ACA AATTTCACA		
			AAACC TGT TTAAAGTGT		
			_ C		
GAM34	LBR	3'	TGTACTGGATTGCACCAAGGA 2522	A AAT C_	
			TCTTTGGT CAA TTCA ACA		
			AGGAACCA GTT AGGT TGT		
			C ____ CA		
GAM34	MIP	3'	TGTGTGAAATCTTTCAAG 1399	TACAAA	
			TTTGG ATTTCACACA		
			GAACT TAAAGTGTGT		
			TTC__		
GAM34	RLN2	3'	TGTTGGTTGTACCAA 1175	AATT C	
			TTTGGTACAA TCA ACA		
			AAACCATGTT GGT TGT		
			____ _		
GAM34	SART2	3'	TGATTTTCATACCAAAGA 1444	CA TT	
			TCTTTGGTA AAA TCA		
			AGAAACCAT TTT AGT		
			AC T_		
GAM34	TPK1	3'	AAATTTTGCTACCAAAGA 1987	_	
			TCTTTGGTA CAAAATT		
			AGAAACCAT GTTTTAAA		
			C		
GAM34	TRIP12	3'	TGTGTGAAATTTAAAAAAGG 1094	GGTACA	
			TCTTT AAATTCACACA		
			GGAAA TTAAAGTGTGT		
			AAA__		
GAM34	BRD3	3'	GTGTGAGATTCGTACCGAAGA 1398	AA	
			TCTTTGGTAC AATTCACAC		
			AGAAGCCATG TTAGAGTGTG		
			C_		
GAM34	FLJ13397	3'	GTGTGAAATTTACTAGCAA 2116	G CA	
			TTTG TA AAATTCACAC		

			AAAC AT TTTAAAGTGTG		
			G CA		
GAM34	FLJ22202	3'	TGTATCATTTTGTACCAA 2103	TTC	
			TTTGGTACAAAAT ACA		
			AAACCATGTTTTA TGT		
			CTA		
GAM34	GROS1	3'	TGTGTAGACAACCAAAGA 1986	ACAAAATT _	
			TCTTTGGT TC ACACA		
			AGAAACCA AG TGTGT		
			AC_____ A		
GAM34	KIAA0981	3'	TGTGTAAAACTGCCAAGGA 2598	CAAAA C	
			TCTTTGGTA TTT ACACA		
			AGGAACCGT AAA TGTGT		
			C_____ A		
GAM34	KIAA1243	3'	TGTGACATGACCAAAGA 2978	A AAATT	
			TCTTTGGT CA TCACA		
			AGAAACCA GT AGTGT		
			_ AC_____		
GAM34	KIAA1462	3'	TTGTGTGAGAGGAACCCAAAGA 3524	TACAAAA	
			TCTTTGG TTTACACAA		
			AGAAACC AGAGTGTGTT		
			CAAGG_____		
GAM34	MGC1136	3'	TTGTGTGAAACCCCTAGCATAG 2041	T G CAAAA	
	A		TCT TG TA TTTACACAA		
			AGA AC AT AAAGTGTGTT		
			T G CCCC_____		
GAM34	MSTP043	3'	TGTCTTTATTTTACCAAAGA 2223	C TTC_	
			TCTTTGGTA AAAAT ACA		
			AGAAACCAT TTTTA TGT		
			_ TTTC		
GAM34	Nup43	3'	TGTGCAAATTTTAGTATCAGA 2075	_ CA	
			TTTGGTAC AAAATTT CACA		
			AGACTATG TTTTAAA GTGT		
			A AC		
GAM34	RPS6KA4	3'	TGTGCAATTACGTCCACCAAAG 1072	_ AA T	
	A		TCTTTGGT AC AATT CACA		
			AGAAACCA TG TTAA GTGT		
			CC CA C		
GAM34	SLC17A6	3'	TGAAACTTGTGCCACAGA 1911	T AA	
			TCT TGGTACAA TTTCA		

			AGA ACCGTGTT AAAGT		
			C C_		
GAM34	TERA	3'	TGTATGAATAGTACCAAAG 1949	AAAAT C	
			CTTTGGTAC TTCA ACA		
			GAAACCATG AAGT TGT		
			AT__ A		
GAM34	VAV3	3'	TTGTGTAGAGTTCTAATACCAA 1273	CAA_ TC	
	AGA		TCTTTGGTA AATT ACACAA		
			AGAAACCAT TTGA TGTGTT		
			AATC GA		
GAM34	LOC120892	3'	TGCAATTTTTTTTACCAAAGA 2987	C__ T	
			TCTTTGGTA AAAATT CA		
			AGAAACCAT TTTTAA GT		
			TTT C		
GAM34	LOC155434	3'	TTGTGTGATTTTCGTACCAA 3376	A TT	
			TTTGGTAC AAA TCACACAA		
			AAACCATG TTT AGTGTGTT		
			C _		
GAM34	LOC169966	3'	ATTTTGCCTTTACCAAAGA 3252	_____	
			TCTTTGGTA CAAAAT		
			AGAAACCAT GTTTTA		
			TTCC		
GAM34	LOC221272	3'	TGTCTGCTCTGTACCAGAGA 3616	AAATTT C	
			TCTTTGGTACA CA ACA		
			AGAGACCATGT GT TGT		
			CTC__ C		
GAM34	LOC221968	3'	TTGTGTGAAATTTTGTGCGAA 3569	GT	
			TTTG ACAAATTTACACAA		
			AAGC TGTTTTAAAGTGTGTT		

GAM34	LOC86651	5'	TTGTGTGAAAGATGTTTCATAC 2830	CA _____	
	CAAGGA		CTTTGGTA AAAT TTCACACAA		
			GGAACCAT TTTG AAGTGTGTT		
			AC TAGA		
GAM34	LOC90322	3'	GAGATTCCATACTAAAGA 2632	CAA	
			TCTTTGGTA AATTTC		
			AGAAATCAT TTAGAG		
			ACC		
GAM35	MYO1E	5'	ATGGAGTCCCCTCTAGGGTT 1168	ATC A A	
			GACC GA GG GACTCCAT		

			TTGG CT CC CTGAGGTA		
			GAT C _		
GAM35	ROCK2	3'	ATGAAGTCTTTTAACAGTCTC 2737	CATCGA	C
			GAGAC AGGAGACT CAT		
			CTCTG TTTTCTGA GTA		
			ACAA_ A		
GAM35	MGC15937	5'	GAGTTTCTTCTTCAAGGTCTCA 2383	ATC	_
			TGAGACC GAAGGAGA CTC		
			ACTCTGG CTTCTTCT GAG		
			AA_ TT		
GAM35	STK16	5'	GAGCTCTTCGGTAGCCTCA 2937	ACC	G A
			TGAG ATCGAAG AG CTC		
			ACTC TGGCTTC TC GAG		
			CGA _ _		
GAM35	LOC148029	5'	GGAGTCTCCATCCTCA 3116	ACCATC	A
			TGAG GA GGAGACTCC		
			ACTC CT CCTCTGAGG		
			_ A		
GAM35	LOC169436	5'	TGGAGTTCAATGAGCTCA 3261	AC C	AGGAG
			TGAG CAT GA ACTCCA		
			ACTC GTA CT TGAGGT		
			GA A _		
GAM35	LOC256267	3'	ATGGAGTCTCCCTCTGTC 3713	CATC	A
			GAC GA GGAGACTCCAT		
			CTG CT CCTCTGAGGTA		
			T_ C		
GAM35	LOC257426	3'	GAGTCCTTCGGTGGCCTCA 2755	A	GA
			TGAG CCATCGAAGGA CTC		
			ACTC GGTGGCTTCCT GAG		
			C _		
GAM35	LOC92466	3'	ATGGAGTCTCCCTCTGTC 2858	CATC	A
			GAC GA GGAGACTCCAT		
			CTG CT CCTCTGAGGTA		
			T_ C		
GAM36	MME	3'	AAAAAAAGTTACAGAAATA 785	AA	
			TATTTTTTGTA ACTTTTTTT		
			ATAAAGACAT TGAAAAAAA		
			_		
GAM36	MME	3'	AAAAAAAGTTACAGAAATA 1377	AA	
			TATTTTTTGTA ACTTTTTTT		

ATAAAGACAT TGAAAAAAAA

GAM36	MME	3'	AAAAAAAGTTACAGAAATA	1378	AA
			TATTTTTTGT ACTTTTTTTT		
			ATAAAGACAT TGAAAAAAAA		
GAM36	MME	3'	AAAAAAAGTTACAGAAATA	1379	AA
			TATTTTTTGT ACTTTTTTTT		
			ATAAAGACAT TGAAAAAAAA		
GAM36	DKFZP434C212	3'	AAAAAGTACACAGAAATATT	2832	AAA
			AATATTTTGT ACTTTTTT		
			TTATAAAGACA TGAAAAA		
			CA_		
GAM36	FLJ11275	3'	TAAATGGGATTATAAAAAATA	1821	A TT
	TT		AATATTTTGTAAA CT TTTTA		
			TTATAAAAATATTT GG AAAAT		
			A GT		
GAM36	GOLPH3	3'	TAAAAAAGTTTACTGCCATA	1981	TTTT
	TT		AATAT GTAAACTTTTTTTA		
			TTATA CATTTTGAAAAAAT		
			CCGT		
GAM36	KIAA0563	5'	TAAAAAAGGAGCAAAAGTAT	1565	AAAA
			ATATTTTGT CTTTTTTA		
			TATGAAAACG GAAAAAAT		
			AG_		
GAM36	TAF2	3'	AGAAAGTTTGACAAAAATA	997	A
			TATTTTGT AAACTTTTT		
			ATAAAAACA TTTGAAAGA		
			G		
GAM36	LOC147071	5'	TAAAAAAGGAGCAAAAGTAT	2965	AAAA
			ATATTTTGT CTTTTTTA		
			TATGAAAACG GAAAAAAT		
			AG_		
GAM36	LOC147639	5'	AAAAGTGCTGCAAAAATATT	3110	AA
			AATATTTTGT ACTTTT		
			TTATAAAAACGT TGAAAA		
			CG		
GAM36	LOC201173	5'	TAAAAAAGGAGCAAAAGTAT	3405	AAAA
			ATATTTTGT CTTTTTTA		

			TATGAAAACG GAAAAAAAT	
			AG__	
GAM36	LOC201220	5'	TAAAAAAGGAGCAAAAGTAT 3406	AAAA
			ATATTTTGT CTTTTTTA	
			TATGAAAACG GAAAAAAAT	
			AG__	
GAM37	MME	3'	AAAAAAGTTACAGAAATA 785	AA
			TATTTTGT ACTTTTTT	
			ATAAAGACAT TGAAAAAA	
			—	
GAM37	MME	3'	AAAAAAGTTACAGAAATA 1377	AA
			TATTTTGT ACTTTTTT	
			ATAAAGACAT TGAAAAAA	
			—	
GAM37	MME	3'	AAAAAAGTTACAGAAATA 1378	AA
			TATTTTGT ACTTTTTT	
			ATAAAGACAT TGAAAAAA	
			—	
GAM37	MME	3'	AAAAAAGTTACAGAAATA 1379	AA
			TATTTTGT ACTTTTTT	
			ATAAAGACAT TGAAAAAA	
			—	
GAM37	DKFZP434C212	3'	AAAAAGTACACAGAAATATT 2832	AAA
			AATATTTTGT ACTTTT	
			TTATAAGACA TGAAAA	
			CA_	
GAM37	FLJ11275	3'	TAAATGGGATTATAAAAATA 1821	A TT
	TT		AATATTTTGTAAA CT TTTTA	
			TTATAAAATATTT GG AAAAT	
			A GT	
GAM37	GOLPH3	3'	TAAAAAAGTTTACTGCCATA 1981	TTTT
	TT		AATAT GTAAACTTTTTTTA	
			TTATA CATTTTGAAAAAAT	
			CCGT	
GAM37	KIAA0563	5'	TAAAAAAGGAGCAAAAGTAT 1565	AAAA
			ATATTTTGT CTTTTTTA	
			TATGAAAACG GAAAAAAAT	
			AG__	
GAM37	TAF2	3'	AGAAAGTTTGACAAAATA 997	A
			TATTTTGT AAACTTTT	

			ATAAAAACA TTTGAAAGA		
			G		
GAM37	LOC147071	5'	TAAAAAAGGAGCAAAAGTAT 2965	AAAA	
			ATATTTTGT CTTTTTTA		
			TATGAAAACG GAAAAAAT		
			AG__		
GAM37	LOC147639	5'	AAAAGTGCTGCAAAATATT 3110	AA	
			AATATTTTGTA ACTTTT		
			TTATAAAAACGT TGAAAA		
			CG		
GAM37	LOC201173	5'	TAAAAAAGGAGCAAAAGTAT 3405	AAAA	
			ATATTTTGT CTTTTTTA		
			TATGAAAACG GAAAAAAT		
			AG__		
GAM37	LOC201220	5'	TAAAAAAGGAGCAAAAGTAT 3406	AAAA	
			ATATTTTGT CTTTTTTA		
			TATGAAAACG GAAAAAAT		
			AG__		
GAM38	MARK1	3'	TATAATAAACATGATTGCTTA 1857	TA	TAC
	A		TTA CGATC GTTTATTATA		
			AAT GTTAG CAAATAATAT		
			TC TA_		
GAM39	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_	TAA
			TCAGAAAG AGGTT TATTTT		
			AGTCTTTT TTCGA ATAAAA		
			A TC_		
GAM39	KERA	3'	AAAATATTGAATGCTTTCT 1349	AG	
			AGAAAG GTTTAATATTTT		
			TCTTTC TAAGTTATAAAA		
			G_		
GAM39	PPP1R12A	3'	AAAATACTACATCTTTCTGG 931	G	TTAA
			TCAGAAAGA GT TATTTT		
			GGTCTTTCT CA ATAAAA		
			A TC__		
GAM39	S100B	3'	AAAATTGAAAACCTCTTTC 1284	AAT	
			GAAAGAGGTTT ATTTT		
			CTTTCTCCAAA TAAAA		
			AGT		
GAM39	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT 2196	A	GTT
			ATCAGAA GAG TAATATTTT		

			TAGTCTT CTT GTTATAAAA	
			_ AC_	
GAM39	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT
			AGAAAGAGG AATATTTT	
			TCTTTCTCC TTGTAAAA	
			T__	
GAM39	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA GTTT
			ATCAG AGAG AATATTTT	
			TAGTC TCTC TTATAAAA	
			CG ATT_	
GAM39	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA
			GAAAGAGGT TATTTT	
			CTTTCTCCA GTAAAA	
			TG__	
GAM39	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A TAA
			TCAG AAGAGGTT TATTTT	
			AGTC TTCTTCGA ATAAAA	
			C C__	
GAM39	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_
			CAGAAAG TTTAATATTTT	
			GTCTTTC GAATTATAAAA	
			AATA	
GAM39	LOC148145	5'	AAAATATTAAACCTGGACCTGA 3296	AAAG
		T	ATCAG AGGTTTAATATTTT	
			TAGTC TCCAAATTATAAAA	
			CAGG	
GAM40	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_ TAA
			TCAGAAAG AGGTT TATTTT	
			AGTCTTTT TTCGA ATAAAA	
			A TC_	
GAM40	KERA	3'	AAAATATTGAATGCTTTCT 1349	AG
			AGAAAG GTTTAATATTTT	
			TCTTTC TAAGTTATAAAA	
			G_	
GAM40	PPP1R12A	3'	AAAATACTACATCTTTCTGG 931	G TTAA
			TCAGAAAGA GT TATTTT	
			GGTCTTTCT CA ATAAAA	
			A TC__	
GAM40	S100B	3'	AAAATTGAAAACCTCTTTC 1284	AAT
			GAAAGAGGTTT ATTTT	

			CTTTCTCCAAA TAAAA		
			AGT		
GAM40	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT 2196	A	GTT
			ATCAGAA GAG TAATATTTT		
			TAGTCTT CTT GTTATAAAA		
			_ AC_		
GAM40	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT	
			AGAAAGAGG AATATTTT		
			TCTTTCTCC TTGTAAAA		
			T__		
GAM40	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA	GTTT
			ATCAG AGAG AATATTTT		
			TAGTC TCTC TTATAAAA		
			CG ATT_		
GAM40	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA	
			GAAAGAGGT TATTTT		
			CTTTCTCCA GTAAAA		
			TG__		
GAM40	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A	TAA
			TCAG AAGAGGTT TATTTT		
			AGTC TTCTTCGA ATAAAA		
			C C__		
GAM40	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_	
			CAGAAAG TTTAATATTTT		
			GTCTTTC GAATTATAAAA		
			AATA		
GAM40	LOC148145	5'	AAAATATTAAACCTGGACCTGA 3296	AAAG	
		T	ATCAG AGGTTTAATATTTT		
			TAGTC TCCAAATTATAAAA		
			CAGG		
GAM41	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_	TAA
			TCAGAAAG AGGTT TATTTT		
			AGTCTTTT TTCGA ATAAAA		
			A TC_		
GAM41	KERA	3'	AAAATATTGAATGCTTTCT 1349	AG	
			AGAAAG GTTTAATATTTT		
			TCTTTC TAAGTTATAAAA		
			G_		
GAM41	PPP1R12A	3'	AAAATACTACATCTTTCTGG 931	G	TTAA
			TCAGAAAGA GT TATTTT		

			GGTCTTTCT CA ATAAAA	
			A TC__	
GAM41	S100B	3'	AAAATTGAAAACCTCTTTC 1284	AAT
			GAAAGAGGTTT ATTTT	
			CTTTCTCCAAA TAAAA	
			AGT	
GAM41	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT 2196	A GTT
			ATCAGAA GAG TAATATTTT	
			TAGTCTT CTT GTTATAAAA	
			_ AC_	
GAM41	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT
			AGAAAGAGG AATATTTT	
			TCTTTCTCC TTGTAAAA	
			T__	
GAM41	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA GTTT
			ATCAG AGAG AATATTTT	
			TAGTC TCTC TTATAAAA	
			CG ATT_	
GAM41	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA
			GAAAGAGGT TATTTT	
			CTTTCTCCA GTAAAA	
			TG__	
GAM41	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A TAA
			TCAG AAGAGGTT TATTTT	
			AGTC TTCTTCGA ATAAAA	
			C C__	
GAM41	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_
			CAGAAAG TTTAATATTTT	
			GTCTTTC GAATTATAAAA	
			AATA	
GAM41	LOC148145	5'	AAAATATTAACCTGGACCTGA 3296	AAAG
		T	ATCAG AGGTTTAATATTTT	
			TAGTC TCCAAATTATAAAA	
			CAGG	
GAM42	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_ TAA
			TCAGAAAG AGGTT TATTTT	
			AGTCTTTT TTCGA ATAAAA	
			A TC_	
GAM42	KERA	3'	AAAATATTGAATGCTTTCT 1349	AG
			AGAAAG GTTTAATATTTT	

			TCTTTC TAAGTTATAAAA	
			G_	
GAM42	PPP1R12A	3'	AAAATACTACATCTTTCTGG 931	G TTAA
			TCAGAAAGA GT TATTTT	
			GGTCTTTCT CA ATAAAA	
			A TC__	
GAM42	S100B	3'	AAAATTGAAAACCTCTTTC 1284	AAT
			GAAAGAGGTTT ATTTT	
			CTTTCTCCAAA TAAAA	
			AGT	
GAM42	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT 2196	A GTT
			ATCAGAA GAG TAATATTTT	
			TAGTCTT CTT GTTATAAAA	
			_ AC_	
GAM42	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT
			AGAAAGAGG AATATTTT	
			TCTTTCTCC TTGTAAAA	
			T__	
GAM42	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA GTTT
			ATCAG AGAG AATATTTT	
			TAGTC TCTC TTATAAAA	
			CG ATT_	
GAM42	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA
			GAAAGAGGT TATTTT	
			CTTTCTCCA GTAAAA	
			TG__	
GAM42	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A TAA
			TCAG AAGAGGTT TATTTT	
			AGTC TTCTTCGA ATAAAA	
			C C__	
GAM42	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_
			CAGAAAG TTTAATATTTT	
			GTCTTTC GAATTATAAAA	
			AATA	
GAM42	LOC148145	5'	AAAATATTAACCTGGACCTGA 3296	AAAG
			T ATCAG AGGTTTAATATTTT	
			TAGTC TCCAAATTATAAAA	
			CAGG	
GAM43	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_ TAA
			TCAGAAAG AGGTT TATTTT	

			AGTCTTTT TTCGA ATAAAA	
			A TC_	
GAM43	KERA	3'	AAAATATTGAATGCTTTCT 1349	AG
			AGAAAG GTTTAATATTTT	
			TCTTTC TAAGTTATAAAA	
			G_	
GAM43	PPP1R12A	3'	AAAATACTACATCTTTCTGG 931	G TTAA
			TCAGAAAGA GT TATTTT	
			GGTCTTTCT CA ATAAAA	
			A TC_	
GAM43	S100B	3'	AAAATTGAAAACCTCTTTC 1284	AAT
			GAAAGAGGTTT ATTTT	
			CTTTCTCCAAA TAAAA	
			AGT	
GAM43	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT 2196	A GTT
			ATCAGAA GAG TAATATTTT	
			TAGTCTT CTT GTTATAAAA	
			_ AC_	
GAM43	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT
			AGAAAGAGG AATATTTT	
			TCTTTCTCC TTGTAAAA	
			T_	
GAM43	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA GTTT
			ATCAG AGAG AATATTTT	
			TAGTC TCTC TTATAAAA	
			CG ATT_	
GAM43	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA
			GAAAGAGGT TATTTT	
			CTTTCTCCA GTAAAA	
			TG_	
GAM43	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A TAA
			TCAG AAGAGGTT TATTTT	
			AGTC TTCTTCGA ATAAAA	
			C C_	
GAM43	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_
			CAGAAAG TTTAATATTTT	
			GTCTTTC GAATTATAAAA	
			AATA	
GAM43	LOC148145	5'	AAAATATTAAACCTGGACCTGA 3296	AAAG
			T ATCAG AGGTTTAATATTTT	

				TAGTC TCCAAATTATAAAA	
				CAGG	
GAM44	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_ TAA	
			TCAGAAAG AGGTT TATTTT		
			AGTCTTTT TTCGA ATAAAA		
			A TC_		
GAM44	KERA	3'	AAAATATTGAATGCTTTCT 1349	AG	
			AGAAAG GTTTAATATTTT		
			TCTTTC TAAGTTATAAAA		
			G_		
GAM44	PPP1R12A	3'	AAAATACTACATCTTTCTGG 931	G TTAA	
			TCAGAAAGA GT TATTTT		
			GGTCTTTCT CA ATAAAA		
			A TC__		
GAM44	S100B	3'	AAAATTGAAAACCTCTTTC 1284	AAT	
			GAAAGAGGTTT ATTTT		
			CTTTCTCCAAA TAAAA		
			AGT		
GAM44	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT 2196	A GTT	
			ATCAGAA GAG TAATATTTT		
			TAGTCTT CTT GTTATAAAA		
			_ AC_		
GAM44	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT	
			AGAAAGAGG AATATTTT		
			TCTTTCTCC TTGTAAAA		
			T_		
GAM44	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA GTTT	
			ATCAG AGAG AATATTTT		
			TAGTC TCTC TTATAAAA		
			CG ATT_		
GAM44	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA	
			GAAAGAGGT TATTTT		
			CTTTCTCCA GTAAAA		
			TG_		
GAM44	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A TAA	
			TCAG AAGAGGTT TATTTT		
			AGTC TTCTTCGA ATAAAA		
			C C_		
GAM44	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_	
			CAGAAAG TTTAATATTTT		

			GTCTTTC GAATTATAAAA	
			AATA	
GAM44	LOC148145	5'	AAAATATTAAACCTGGACCTGA 3296	AAAG
		T	ATCAG AGGTTTAATATTTT	
			TAGTC TCCAAATTATAAAA	
			CAGG	
GAM45	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_ TAA
			TCAGAAAG AGGTT TATTTT	
			AGTCTTTT TTCGA ATAAAA	
			A TC_	
GAM45	KERA	3'	AAAATATTGAATGCTTTCT 1349	AG
			AGAAAG GTTTAATATTTT	
			TCTTTC TAAGTTATAAAA	
			G_	
GAM45	PPP1R12A	3'	AAAATACTACATCTTTCTGG 931	G TTAA
			TCAGAAAGA GT TATTTT	
			GGTCTTTCT CA ATAAAA	
			A TC__	
GAM45	S100B	3'	AAAATTGAAACCTCTTTC 1284	AAT
			GAAAGAGGTTT ATTTT	
			CTTTCTCCAAA TAAAA	
			AGT	
GAM45	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT 2196	A GTT
			ATCAGAA GAG TAATATTTT	
			TAGTCTT CTT GTTATAAAA	
			_ AC_	
GAM45	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT
			AGAAAGAGG AATATTTT	
			TCTTTCTCC TTGTAAAA	
			T_	
GAM45	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA GTTT
			ATCAG AGAG AATATTTT	
			TAGTC TCTC TTATAAAA	
			CG ATT_	
GAM45	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA
			GAAAGAGGT TATTTT	
			CTTTCTCCA GTAAAA	
			TG_	
GAM45	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A TAA
			TCAG AAGAGGTT TATTTT	

			AGTC TTCTTCGA ATAAAA	
			C C__	
GAM45	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_
			CAGAAAG TTTAATATTTT	
			GTCTTTC GAATTATAAAA	
			AATA	
GAM45	LOC148145	5'	AAAATATTAACCTGGACCTGA 3296	AAAG
			T ATCAG AGGTTTAATATTTT	
			TAGTC TCCAAATTATAAAA	
			CAGG	
GAM46	EFG1	3'	TGTCTATCTCAACTCTATT 3661	ATC TC
			AATAGAGTT GAT AGACA	
			TTATCTCAA CTA TCTGT	
			CT_ _	
GAM46	PHYH	3'	TCTGCTATAACTCTTTCA 1281	T CGATT
			TGAA AGAGTTAT CAGA	
			ACTT TCTCAATA GTCT	
			_ TC__	
GAM46	SLC6A3	3'	TGTCTGTTGACCAATCTCTATT 795	TTA__ TT
	CA		TGAATAGAG TCGA CAGACA	
			ACTTATCTC AGTT GTCTGT	
			TAACC _	
GAM46	H2AV	3'	TGCCTGACAATTAGCTCTATT 2447	TCGAT A
	A		TGAATAGAGTTA TCAG CA	
			ACTTATCTCGAT AGTC GT	
			TAAC_ C	
GAM46	HMP19	3'	GTCTGAACCGATATTTCT 3408	T A
			AGAG TATCG TTCAGAC	
			TCTT ATAGC AAGTCTG	
			T C	
GAM46	KIAA1726	3'	TGTCTGAAAGCAACCCTACTC 2786	A A ATCGA
			GA TAG GTT TTCAGACA	
			CT ATC CAA AAGTCTGT	
			C C CGA__	
GAM47	SOX11	3'	GTCTCACTGTTTGATCAAACCTT 992	A ATTTT
	CT		AGAGGTTT AT GTGAGAC	
			TCTTCAA TA CACTCTG	
			C GTTTGT	
GAM47	CAP350	3'	TCTTGTAATAGTTAAACCTC 1554	ATTT TG
			GAGGTTTAAT TTG AGA	

			CTCCAAATTG	AAT TCT	
			AT__	GT	
GAM47	DKFZP564A022	3'	TCTCACAAATATAAAACC	2174	A TT
			GGTTT ATATT TGTGAGA		
			CCAAA TATAA ACACTCT		
			A	__	
GAM47	FLJ11730	3'	CTCACAAAGATAAACATC	2005	G TAA
			GA GTT TATTTTTGTGAG		
			CT CAA ATAGAAACACTC		
			A	__	
GAM47	FLJ20686	5'	CTCACAGTCCTACTGAACCTC	1765	A TTT
			GAGGTTTA TA TTGTGAG		
			CTCCAAGT AT GACACTC		
			C CCT		
GAM47	FRSB	3'	GTCCCAGGGAGATATTAGACCT	1236	G A
	CT		AGAGGTTTAATATTTTT TG GAC		
			TCTCCAGATTATAGAGG AC CTG		
			G C		
GAM47	KIAA1600	3'	ACAAAAAGACTAAACCTCT	2919	ATA
			AGAGGTTTA TTTTTGT		
			TCTCCAAAT AAAACA		
			CAG		
GAM47	LOC124801	3'	GTCTCACATTTGGCCCAAACCT	2996	AATATTTT
	C		GAGGTTT TGTGAGAC		
			CTCCAAA ACACTCTG		
			CCCGGTTT		
GAM47	LOC221035	3'	TCCCAGTATTAAACCT	3593	TTTTG A
			AGGTTTAATAT TG GA		
			TCCAAATTATG AC CT		
			__ C		
GAM47	LOC51611	3'	CGAAAAATTAAACCTCT	1653	AT
			AGAGGTTTAAT TTTTG		
			TCTCCAAATTA AAAGC		
			—		
GAM48	AXUD1	3'	TTTATTCCATTTCTCTCT	2309	GA
			AGAGAGAAA GAATAAA		
			TCTCTCTTT CTTATTT		
			AC		
GAM48	BSN	3'	ATTTTTCTTTGTTTCTCTCT	1024	G T
			AGAGAGAAA AGAA AAAAAT		

			TCTCTCTTT TTTT TTTTTA		
			G C		
GAM48	DPYSL2	3'	AATATTTTCGTGTCTGTCTCTC 822	A	GA TA
	T		AGAGAGA AGA A AAAATATT		
			TCTCTCT TCT T TTTTATAA		
			G G_ GC		
GAM48	EVA1	3'	AATGTGTTTACTCTCTTTCCTT 1250	A	A A
	C		GAG GAAAGAGA TAAA ATATT		
			CTT CTTTCTCT ATTT TGTA		
			C C G		
GAM48	PTMS	3'	TTTGCTCTCTTTTCTCCCT 959	A	A
			AG GAGAAAGAGA TAAA		
			TC CTCTTTCTCT GTTT		
			C C		
GAM48	SELE	3'	TTTTGTGGCTTTCTTTCT 748	AGA	
			AGAGAGAAAG ATAAAA		
			TCTTTCTTTC TGTTTT		
			GG_		
GAM48	SLC7A6	3'	AATATTTTGTACCTTTCTCCT 1076	A	AGA
			AG GAGAAAG ATAAAAATATT		
			TC CTCTTTC TGTTTTTATAA		
			_ CA_		
GAM48	TGFBR2	5'	TTTCTTCTAGTTCTTTCT 1003	AG	T
			AGAGAGAA AGAA AAA		
			TCTTTCTT TCTT TTT		
			GA C		
GAM48	DKFZP586N0721	5'	TTTTATTCCCTTTCCTCT 1627	A	A
			AGAG GAAAG GAATAAAA		
			TCTC CTTTC CTTATTTT		
			_ C		
GAM48	DKFZp761J139	5'	TTTATTCTCTCTGTCTCT 2242	GAA	
			AGAGA AGAGAATAAA		
			TCTCT TCTCTTATTT		
			GTC		
GAM48	FLJ10468	3'	TTTTATTCTCCTTTC 1779	AAA	
			GAGAG GAGAATAAAA		
			CTTTC CTCTTATTTT		
			—		
GAM48	FLJ20485	3'	AATATTTTAAATCTCCTTTC 1874	AAA	A_
	T		AGAGAG GAGA TAAAAATATT		

TCTTTC CTCT ATTTTATAA
 ____ AAA
 GAM48 H2BFQ 3' ATATTACTCTTCTGTC 2523 G AATAA
 GA AGAAAGAG AAATAT
 || ||||| |||||
 CT TCTTCTC TTTATA
 G A____
 GAM48 KIAA0077 3' TTTTATTCTCTCTCCCTTT 2774 A A
 AGAG GA AGAGAATAAAA
 |||| || |||||
 TTTC CT TCTCTTATTTT
 C C
 GAM48 KIAA0295 3' TTTTTTCCCTTTCTCTCT 2807 A T
 AGAGAGAAAG GAA AAA
 ||||| || |||
 TCTCTCTTTC CTT TTT
 C T
 GAM48 KIAA0828 3' AATATTTTGCTTCTTTCTTTC 3195 AATA
 T AGAGAGAAAGAG AAAATATT
 ||||| |||||
 TCTTCTTTCTT TTTTATAA
 CCG_
 GAM48 KIAA1203 3' AATATTTTATTCTTGAGTTAT 2921 GAGAAA
 CT AGA GAGAATAAAAATATT
 || |||||
 TCT TTCTTATTTTATAA
 ATTGAG
 GAM48 OSBPL8 3' TTTTATTATCCTCCTCTCT 1928 AAA G
 AGAGAG GA AATAAAAA
 |||| || |||||
 TCTCTC CT TTATTTT
 CTC A
 GAM48 PAK6 3' AATATTTTATGATTCTTCTGCT 1897 _ A AA
 C GAG AGAA GAG TAAAAATATT
 || ||| || |||||
 CTC TCTT CTT ATTTTATAA
 G _ AG
 GAM48 POLR3F 3' AATATTTTCACTGTTCCCTTCTT 2547 A A ____
 TCT AGAGAGAA G GAATA AAAATATT
 ||||| || |||||
 TCTTCTT C CTTGT TTTTATAA
 _ _ CAC
 GAM48 RNF11 3' TTTATTCTCTTCTTCT 1495 G
 AGA AGAAAGAGAATAAA
 || |||||
 TCT TCTTCTCTTATTT
 _
 GAM48 SLC16A6 5' TTTATTCTCTTCCCTTCT 1143 AGA
 AGAG AAGAGAATAAA
 || |||||

			TCTT TTCTCTTATTT	
			CCC	
GAM48	LOC144321	3'	TTTTATTCCCTTCTCTC 3267	A A
			GAGAGAA G GAATAAAA	
			I	
			CTCTCTT C CTTATTTT	
			_ C	
GAM48	LOC150951	5'	ATATTTTATTTTCTTCCT 3336	A
			AG AAGAGAATAAAAATAT	
			TC TTCTTTTATTTTATA	
			C	
GAM48	LOC199920	5'	AATATTTTATTCTTTGATTCT 3435	AA
		T	GAGAG AGAGAATAAAAATATT	
			TTCTT TTTCTTATTTTATAA	
			AG	
GAM48	LOC256435	3'	AATATTTTAAATGTTGTCTCT 3675	AAGAGAA
		CT	AGAGAGA TAAAAATATT	
			TCTCTCT ATTTTATAA	
			GTTGTAA	
GAM49	ADAMTS5	3'	TATTTTCACAACTACTTTCTCT 1352	_ AATA_
		CT	AGAGAGAAAG AG AAAATA	
			TCTCTCTTTC TC TTTTAT	
			A AACAC	
GAM49	ADAT1	3'	TATTCCCAGCCTTTCTTTCTTC 1404	A_____
			GAAGAGAGAAAG GAATA	
			CTTCTTTCTTTC CTTAT	
			CGACC	
GAM49	ADCY2	3'	TTTTATTTTCCTGTCTTC 2711	G AAA
			GAAGA AG GAGAATAAAA	
			CTTCT TC CTTTTATTTT	
			G ____	
GAM49	AHR	3'	ATTTTGTACTCTCTTC 840	_ A
			GAAGAGAG AA GAGAAT	
			CTTCTCTC TT TTTTAA	
			A G	
GAM49	BSN	3'	ATTTTCTTTTGTTCCTCTCT 1025	G T
			AGAGAGAAA AGAA AAAAAT	
			TCTCTCTTT TTTT TTTTAA	
			G C	
GAM49	BSN	3'	TCTCCCCCTTCTCTCTTC 1026	_____
			GAAGAGAGAAA GAGA	

			CTTCTCTCTTT CTCT		
			CCCC		
GAM49	C7	3'	TATTCCTTATTTCTCTTT 756	_ A	
			GAAGAGAGA AAG GAATA		
			TTTCTCTTT TTC CTTAT		
			A _		
GAM49	CFTR	3'	TATTCCTTTTTCTCTCCTC 753	A _	
			GA GAGAGAAAGAG AATA		
			CT CTCTCTTTTTTC TTAT		
			C C		
GAM49	CHD2	3'	ATATTTTTTCTGATCCCCCACT 813	AA____ GAAT_	
			CTCTCTTC AGA GA AAAAATA T		
			TCT CT TTTTAT A		
			CACCCC AGTCT		
GAM49	CKN1	3'	TATTTTATTCTTTCTTC 703	AG	
			GAAGAGAGAA AGAATA		
			CTTCTTTCTT TTTTAT		
			A_		
GAM49	CTH	5'	TGTTCTTTTCCTCTCTTC 867	A	
			GAAGAGAG AAGAGAATA		
			CTTCTCTC TTTTCTTGT		
			C		
GAM49	EVA1	3'	ATTTTTATTTTTATGTCTCTC 1251	AA_	
			GAGAGA GAGAATAAAAAAT		
			CTCTCT TTTTATTTTTA		
			GTA		
GAM49	FBXL11	3'	TTGTTCCCCCTCTCTCTTT 1426	AAGA	
			GAAGAGAGA GAATAA		
			TTTCTCTCT CTTGTT		
			CCCC		
GAM49	GATA3	3'	TATTTTCCTTCTCTCTC 893	A A	
			GA GAGAGAA GAGAATA		
			CT CTCTCTT CTTTTAT		
			_ C		
GAM49	GDI2	5'	TTTTCCTCTCTTTCTCTT 832	AT	
			GAGAGAAAGAGA AAAA		
			TTCTCTTTCTCT TTTT		
			CC		
GAM49	HD	3'	ATTCTCCCTTCTCTCTTT 899	A_	
			GAAGAGAGAA GAGAAT		

			TTTCTCTCTT CTCTTA		
			CC		
GAM49	HTR2C	3'	TATTTTGGCTCTCCCTCCCTTC 781	A AAA A	
			GAAG GAG GAGA TAAAAATA		
			CTTC CTC CTCT GTTTTAT		
			C C__ C		
GAM49	LGR6	3'	TTCTCTTCCCCTCTCTTC 3302	A__	
			GAAGAGAG AAGAGAA		
			CTTCTCTC TTCTCTT		
			CCC		
GAM49	LRP8	3'	TCTCTTATTTCTCTTTTC 2326	___	
			GAAGAGAGAA AGAGA		
			CTTTTCTCTT TCTCT		
			TAT		
GAM49	LRP8	3'	TCTCTTATTTCTCTTTTC 1139	___	
			GAAGAGAGAA AGAGA		
			CTTTTCTCTT TCTCT		
			TAT		
GAM49	MEF2C	5'	TTTTTTTTCTCTCTCTCTCT 926	_ A T	
	C		GA AGAGAGA AGAGAA AAAAA		
			CT TCTCTCT TCTCTT TTTT		
			C C T		
GAM49	MSR1	3'	TATTTTGGTTTCTCTCT 929	___	
			AGAGAGAAA GAGAATA		
			TCTCTCTT TTTTAT		
			GG		
GAM49	PCDH11X	3'	TATTTTCACATTTTCTCTCT 2299	___	
			AGAGAGAAA GAGAATA		
			TCTCTCTT CTTTAT		
			TACA		
GAM49	PCDH11X	3'	TATTTTCACATTTTCTCTCT 2301	___	
			AGAGAGAAA GAGAATA		
			TCTCTCTT CTTTAT		
			TACA		
GAM49	PCDH11Y	3'	TATTTTCACATTTTCTCTCT 2303	___	
			AGAGAGAAA GAGAATA		
			TCTCTCTT CTTTAT		
			TACA		
GAM49	PCMT1	3'	TATCTTCTGCTCTTTCTTC 1205	A_ GA	
			GAAGAGAGA AGA ATA		

			CTTCTTTCT TCT TAT		
			CG TC		
GAM49	PCNA	3'	TATTTTTTTTCTCTATTC 939 G		
			GAA AGAGAAAGAGAATA		
			CTT TCTCTTTTTTTTAT		
			A		
GAM49	PRELP	3'	ATTCGTTTTCTCTCTCTC 950 _ A		
			GA AGAGAGAAAG GAAT		
			CT TCTCTCTTTT CTTA		
			C G		
GAM49	PTMS	3'	TTTGCTCTCTTTTCTCCCT 958 A A		
			AG GAGAAAGAGA TAAA		
			TC CTCTTTCTCT GTTT		
			C C		
GAM49	SLC4A4	3'	TATTTTTATTCTCTTAAGTCTT 1054 GAGA		
	T		GAAGA AAGAGAATAAAAAATA		
			TTTCT TTCTCTTATTTTAT		
			GAA_		
GAM49	TRPS1	5'	TATTCCTTTCTCTTTCTCTCT 1471 TAA		
			AGAGAGAAAGAGAA AAATA		
			TCTCTCTTTCTCTT TTTAT		
			TCC		
GAM49	ARS2	5'	TTTGTTGCGCTCTCTTC 1650 AAAGA		
			GAAGAGAG GAATAAAA		
			CTTCTCTC CTTGTTTT		
			CG__		
GAM49	BRD4	3'	TATTTTTAATTCTCTCTTC 2368 A_		
			GAAGAGAGAA GAGAATA		
			CTTCTCTCTT TTTTAT		
			AA		
GAM49	CAPN13	3'	TATTTTACCTGCCTCTCTTC 2485 AA _		
			GAAGAGAG AG AGAATA		
			CTTCTCTC TC TTTTAT		
			CG CA		
GAM49	CECR6	3'	TTACCCTCTCCTCTCTTC 2218 AA AA		
			GAAGAGAG AGAG TAA		
			CTTCTCTC TCTC ATT		
			C_ CC		
GAM49	DKFZP434I0714	5'	TTTTTGTTTTTCCCCCTCTTC 3362 AGAAA		
			GAAGAG GAGAATAAAAA		

CTTCTC TTTTGTTTT
 CCCC_
 GAM49 DKFZP564G092 5' TATTCCTCTTTCTTTTC 1639 A A
 GAAGAGAGA AG GAATA
 ||||| || ||||
 CTTTCTTT TC CTTAT
 C _
 GAM49 DKFZp564K142 3' TATCCTCTTAACCTTCTCTTC 2231 A__ A
 GAAGAGAG AAGAG ATA
 ||||| |||| |||
 CTTCTCTT TTCTC TAT
 CCAA C
 GAM49 DKFZp566D234 3' TATTTTTTTTCTCTGTC 2612 AG
 GA AGAGAAAGAGAATA
 || |||||
 CT TCTCTTTTTTTAT
 G_
 GAM49 DKFZP566I1024 3' TTTTAAATCTATTCTCTC 2878 _ GAA
 GAGAGAA AGA TAAAA
 ||||| || ||||
 CTCTCTT TCT ATTTT
 A AAA
 GAM49 EPI64 3' TATTTTGACATCTCTCTCTCTT 3681 A GAATA
 C GAAGAGAGA AGA AAAATA
 ||||| || ||||
 CTTCTCTCT TCT TTTTAT
 C ACAG_
 GAM49 FLJ00012 3' TATTTTTATCTCTATCTCCT 2985 A A A
 AG GAGA AGAGA TAAAAATA
 || |||| |||||
 TC CTCT TCTCT ATTTTTAT
 _ A _
 GAM49 FLJ10460 3' ATTTTTATTCTACCTTTC 1778 AAAG
 GAGAG AGAATAAAAAAT
 |||| |||||
 CTTTC TCTATTTTAA
 CA_
 GAM49 FLJ10687 3' TTTATTCATTTCTCTCCTC 1793 A GA
 GA GAGAGAAA GAATAAA
 || ||||| |||||
 CT CTCTCTTT CTTATTT
 C A_
 GAM49 FLJ10738 3' TATTTTTACTCTCCCTCTTC 1799 AGAAA A
 GAAGAG GAGA TAAAAATA
 |||| |||||
 CTTCTC CTCT ATTTTTAT
 C__ C
 GAM49 FLJ13158 3' TTCTCTCCCTTTCTCTTC 2109 A_
 GAAGAGAGA AGAGAA
 ||||| |||||

CTTCTCTTT TCTCTT
 CCC
 GAM49 FLJ20294 5' TATTCCTGTCTCCTCTTT 1747 _ A A
 GAAGAG AGA AG GAATA
 ||||| ||| || |||||
 TTTCTC TCT TC CTTAT
 C G _
 GAM49 FLJ21657 3' TATTCTACTTCTCTCTTC 1991 AG
 GAAGAGAGAA AGAATA
 ||||| |||||
 CTTCTCTCTT TCTTAT
 CA
 GAM49 GT650 3' TATTTCTGATTCTCCCTCTCTT 2341 AAA AA_
 C GAAGAGAG GAGAAT AAATA
 ||||| ||||| |||||
 CTTCTCTC CTCTTA TTTAT
 C_ GTC
 GAM49 HEY2 3' TATTCTCTTTTTTTTCTC 1420 AG
 GA AGAGAAAGAGAATA
 || ||||| |||||
 CT TTTTTTCTCTTAT
 CT
 GAM49 HIC2 3' ATTTTTTTTCTCTCTCTTTTC 2717 A T
 GAAGAGAGA AGAGAA AAAAAT
 ||||| ||||| |||||
 CTTTTCTCT TCTTTT TTTTA
 C _
 GAM49 HOOK3 3' ATTTTGAGGACTTTTCTCTCT 2249 AATA_
 AGAGAGAAAGAG AAAAT
 ||||| |||||
 TCTCTCTTTTC TTTTA
 AGGAG
 GAM49 IL1RAPL1 5' TATTCTATTTTCCCCTCTCTT 1488 AAA A
 T GAAGAGAG GAGAATAA AATA
 ||||| ||||| |||||
 TTTCTCTC CTTTATT TTAT
 CC_ C
 GAM49 KALI 3' TTTTGTCTTGTCCTCTC 2347 AAA_
 GAGAG GAGAATAAAA
 |||| ||||| |||||
 CTCTC TTCTTGTTTT
 CCTG
 GAM49 KIAA0077 3' TTTTATTCTCTCTCCCTT 2773 A AA
 GAAG GAGA GAGAATAAAA
 ||| ||| ||||| |||||
 TTTC CTCT CTCTTATTTT
 C _
 GAM49 KIAA0089 3' ATTTTtagcCTCTTTTCTCTTC 2873 A AA
 GAAGAGAGAA GAG TAAAAAT
 ||||| ||| |||||

			CTTCTCTTTT CTC ATTTTTA	
			— CG	
GAM49	KIAA0286	3'	TATTTTCACCCTCTTTTC 2814	AAA
			GAAGAGAG GAGAATA	
			CTTTTCTC CTTTAT	
			CCA	
GAM49	KIAA0295	3'	TTTTTCCCTTTCTCTCT 2808	A T
			AGAGAGAAAG GAA AAA	
			TCTCTCTTTC CTT TTT	
			C T	
GAM49	KIAA0342	3'	TATTCTCATTACTTCTCTTT 2890	— A
			GAAGAGA G AA GAGAATA	
			TTTCTCT C TT CTCTTAT	
			T A A	
GAM49	KIAA0564	3'	TATTTTATTTTCTCCCTGCTC 2743	— AA
			GAG AG AGAGAATAAAAATA	
			CTC TC TCTTTATTTTAT	
			G CC	
GAM49	KIAA0630	3'	TATTTTAAAGTCTTCTCT 3465	GAAT—
	CT		AGAGAGAAAGA AAAAATA	
			TCTCTCTTCT TTTTAT	
			GAAAAT	
GAM49	KIAA0662	3'	TGTTCTCTCTCTCTCTT 3215	A
			GAAGAGAGA AGAGAATA	
			TTTCTCTCT TCTCTTGT	
			C	
GAM49	KIAA0830	3'	TTTGCTTCTCTTCTCCT 2866	A —
			AG GAGAAAGAGAA TAAA	
			TC CTCTTCTCTT GTTT	
			— C	
GAM49	KIAA0964	3'	ATTCTTATGTTTTCTCTTTTC 1579	GA A
			GAAGAGAGAAAGA ATAA AAT	
			CTTTTCTCTTTT TATT TTA	
			G_ C	
GAM49	KIAA1076	3'	TATTTTGGCTTCTCTC 2723	AGAAT
			GAGAGAAAG AAAAATA	
			CTCTCTTTC TTTTAT	
			GT—	
GAM49	KIAA1181	3'	ATTCCTCTCCTCTCTC 2817	A —
			GAAGAGAG AAGAG AAT	

			CTTCTCTC TTCTC TTA		
			C C		
GAM49	KIAA1319	3'	TATTTTGTCTTCTTCCTTTC 1925	A	GA
			GAGAG AAGA ATAAAAATA		
			CTTTC TTCT TGTTTTAT		
			C TC		
GAM49	KIAA1522	3'	ATTCTCTGACCTTTCTCTCT 2708	_____	
			AGAGAGAA AGAGAAT		
			TCTCTCTT TCTCTTA		
			TCCAG		
GAM49	KIAA1906	3'	ATTTTATTCTCTGCTT 2971	AA	
			GAG AGAGAATAAAAAAT		
			TTC TCTCTTATTTTTA		
			G_		
GAM49	MAPK6	5'	TATTTTCTTCTCCCTTT 952	A	AG
			GAAG GAGAA AGAATA		
			TTTC CTCTT TTTTAT		
			C CT		
GAM49	MGC13138	3'	TATTTTATTCTTGTGACCCTC 2332	AGAAA_	
			GAG GAGAATAAAAAATA		
			CTC TTCTTATTTTAT		
			CCAGTG		
GAM49	MGC2742	5'	TATTTCTTTTCTCTCTTC 2040	AG	
			GAAGAGAGAAAG AATA		
			CTTCTCTCTTTT TTAT		
			CT		
GAM49	MGC32043	3'	TATTCCTGTTTTCTCTTT 2486	_ A	
			GAAGAGAGAA AG GAATA		
			TTTCTCTTTT TC CTTAT		
			G _		
GAM49	NFAT5	3'	TATTCCTTTTTCTCTTC 2452	A	
			GAAGAGAGAAAG GAATA		
			CTTCTCTTTTTC CTTAT		
			C		
GAM49	OSBPL8	3'	TTTTTATTATCCTCCTCTCTTC 1929	AAA G	
			GAAGAGAG GA AATAAAAA		
			CTTCTCTC CT TTATTTT		
			CTC A		
GAM49	RAB10	3'	TGTTCTGCTTTTCCTCCTC 3337	A AG _	
			GA GAG AAAG AGAATA		

			CT CTC TTTC TCTTGT		
			C CT G		
GAM49	RANBP1	3'	TATTTTCTTTTCCTCTCTTT 969	—	
			GAAGAGAG AAAGAGAATA		
			TTTCTCTC TTTCTTTTAT		
			CT		
GAM49	RASSF2	3'	TATTTTCACAATCCTCTCTTC 1537	AAA—	
			GAAGAGAG GAGAATA		
			CTTCTCTC CTTTAT		
			CTAACA		
GAM49	STK22D	3'	TATTTTCATCAGCTTCTCTCT 2226	AG AATA—	
	CT		AGAGAGAA AG AAAATA		
			TCTCTCTT TC TTTTAT		
			CT GACTAC		
GAM49	SYNJ2	3'	ATTTTATAGGTTTCTCTTC 2606	AGAGAA	
			GAAGAGAGAA TAAAAAT		
			CTTCTCTTTT ATTTTA		
			GG—		
GAM49	TBLR1	3'	TATTCTTTTTTTCCCTTC 2079	A	
			GAAG GAGAAAGAGAATA		
			CTTC CTTTTTTTCTTAT		
			C		
GAM49	TM9SF1	3'	TATTGCTGTTCTCTCCCTTTCT 1296	AA AA	
	TC		GAAGAGAG AGAGAATA AATA		
			CTTCTTTC TCTCTTGT TTAT		
			CC CG		
GAM49	ULK2	3'	TATTCTATCCTCTCCTCTTC 1523	— AAG—	
			GAAGAG AGA AGAATA		
			CTTCTC TCT TCTTAT		
			C CCTA		
GAM49	UNC5D	3'	TTATTCTTTCTTCCTCTTC 2393	A —	
			GAAGAG GAA AGAGAATAA		
			CTTCTC CTT TTTCTTATT		
			— C		
GAM49	LOC121219	5'	TTATTAACCTCTCTCTTT 2988	A —	
			GAAGAGAGAA GAG AATAA		
			TTTCTCTCTT CTC TTATT		
			C AA		
GAM49	LOC128077	3'	ATTTGTTTTCTCTTTCTTTCCT 3006	A TAA	
	C		GA GAGAGAAAGAGAA AAAT		

		CTCTTTCTTTCTCTT TTTA		
		C TTG		
GAM49	LOC143451 3'	TTCTCTCCTTCTCTTC 3058	—	
		GAAGAGAGAA AGAGAA		
		CTTCTCTCTT TCTCTT		
		CC		
GAM49	LOC145125 3'	TTCTCTCCTTCTCTTC 3075	—	
		GAAGAGAGAA AGAGAA		
		CTTCTCTCTT TCTCTT		
		CC		
GAM49	LOC149351 3'	ATTTTTCAGATCTTTCTCTTT 3131		GAAT
		AGAGAGAAAGA AAAAAT		
		TTTCTCTTTCT TTTTAA		
		AGAC		
GAM49	LOC149722 5'	TATTCTTTCTTTCTCTTC 3312		A
		GAAGAGAGA AGAGAATA		
		CTTCTCTTT TTTCTTAT		
		C		
GAM49	LOC149837 5'	TATTCCTGTCTTTCTCTCT 3318	—	
		AGAGAGAAAGA GAATA		
		TCTCTCTTTCT CTTAT		
		GTC		
GAM49	LOC150054 3'	TATTCTGTCTTTCTCCTC 3323	— —	
		GAG AGAAAGA GAATA		
		CTC TCTTTCT CTTAT		
		C GT		
GAM49	LOC150150 5'	TTTTGTGCCTCTCTTTCTTC 3324		AA A_
		GAAGAGAGA GAG ATAAAA		
		CTTCTTTCT CTC TGTTTT		
		— CG		
GAM49	LOC150225 3'	TATTTTGTTTCCCTCTTC 3327		A G
		GAAGAG GAAA AGAATA		
		CTTCTC CTTT TTTTAT		
		C G		
GAM49	LOC152816 3'	TATTTTATCCTCAACCTCTT 3364		AAA A
		GAGAG GAG ATAAAAATA		
		TTCTC CTC TATTTTAT		
		CAA C		
GAM49	LOC155038 3'	ATTGCGTTTCTCTTTCTCCTTC 3198		A TAAA
		GAAG GAGAAAGAGAA AAT		

		CTTC CTCTTTCTCTT TTA	
		— TGCG	
GAM49	LOC158629 3'	TATTTTCTTTCCCTCTC 3394	A A
		GA GAG GAAAGAGAATA	
		CT CTC CTTTCTTTTAT	
		— C	
GAM49	LOC158943 3'	TATTTTCTTTTCCTCTCTT 2572	—
		GAAGAGAG AAAGAGAATA	
		TTTCTCTC TTTCTTTTAT	
		CT	
GAM49	LOC170082 3'	ATTCTTTTCCCTCTCTTTTC 3254	—
		GAAGAGAGA AAGAGAAT	
		CTTTTCTCT TTTCTTA	
		CCCC	
GAM49	LOC199920 5'	TATTTTATTCTTTGATTCTTC 3436	AGAA
		GAAGAG AGAGAATAAAAATA	
		CTTCTT TTTCTTATTTTAT	
		AG—	
GAM49	LOC219667 3'	ATTTTGTATCTCTCTTC 3516	AAGAG
		GAAGAGAGA AATAAAAT	
		CTTCTCTCT TTGTTTTA	
		A—	
GAM49	LOC220279 5'	TATTTTCTTCCCTACCTCTCT 3653	A—
	TC	GAAGAGAG AAGAGAATA	
		CTTCTCTC TTCTTTTAT	
		CATCCCC	
GAM49	LOC221830 3'	TATTTTCTTTTCTTTCTTC 3567	—
		GAAGAGAGAAA GAGAATA	
		CTTCTTTCTTT CTTTAT	
		T	
GAM49	LOC222166 3'	ATTTTACCTTCTCTCTT 3635	AG—
		GAAGAGAGAA AGAAT	
		TTTCTCTCTT TTTA	
		CCA	
GAM49	LOC254440 3'	TTCTCTCCTTCTCTCTC 3729	—
		GAAGAGAGAA AGAGAA	
		CTTCTCTCTT TCTCTT	
		CC	
GAM49	LOC51123 3'	ATTTTATGCTGTTCCCTCTT 2571	A AG A
		AAGAG GAA AG ATAAAAAT	

			TTCTC CTT TC TATTTTTA		
			C G_ G		
GAM49	LOC51596	5'	TATTTTCCAAGTTTCTCTCTC 1651	A	_____
			GA GAGAGAAA GAGAATA		
			CTCTCTCTT CTTTAT		
			_ GAAC		
GAM49	LOC84570	5'	TTTCGTTTTCTCTCTTC 2257	AA	TA
			GAAGAGAGA GAGAA AAA		
			CTTCTCTCT CTTT TTT		
			C_ GC		
GAM49	LOC92710	5'	TATTTTTATGCCTCTGTCTC 2885	A	A_
			GAGA AGAG ATAAAAATA		
			CTCT TCTC TATTTTTAT		
			G CG		
GAM50	FANCF	3'	GTCCCTTTAAAGCATTGA 1997	ATATAT	
			TCAATGTTTTAAA GGAC		
			AGTTACGAAATTT CCTG		
			C_____		
GAM50	GPR65	5'	TCCACCCTTTAAAGCATTGA 2544	A	TATA
			TCAATGTTTT AAA TGGA		
			AGTTACGAAA TTT ACCT		
			A CCC_		
GAM50	LMNB1	3'	TGTCCATACACTTTGTTGCA 1226	TT	ATA
			TGT TAAA TATGGACA		
			ACG GTTT ATACCTGT		
			TT CAC		
GAM50	MEN1	5'	CATAATATTTTAAACATT 3600	-	
			AATGTTTTAAATAT ATG		
			TTACAAAATTTTATA TAC		
			A		
GAM50	PLAG1	3'	TGTCCATATACCAGATTTAAAA 944	A_____	
		TATT	AATGTTTTAAA TATATGGACA		
			TTATAAAATTT ATATACCTGT		
			AGACC		
GAM50	S100A11	3'	TGTCACCTTTTTTAAACATGA 1231	A	TATATG
			TCA TGTTTTAAAA GACA		
			AGT ACAAATTTT CTGT		
			_ TTCA_		
GAM50	SLC9A6	3'	TCCAGTTAGAACATTGA 1290	AATATA	
			TCAATGTTTTAA TGGA		

			AGTTACAAGATT	ACCT	
			G_____		
GAM50	SOD2	3'	TCCATATACTTTGGGGACTTG	766	T TA _
			CAA GTTT AAA TATATGGA		
			GTT CAGG TTT ATATACCT		
			_ GG C		
GAM50	BIRC2	5'	TATATTTTTTAAAACATTGA	2784	T
			TCAATGTTTTTAAAA ATATG		
			AGTTACAAAATTTT TATAT		
GAM50	CXorf1	5'	TGTCCATAGAAAAAATATT	1145	AAAATA
			AATGTTTT TATGGACA		
			TTATAAAA ATACCTGT		
			AAG_____		
GAM50	KIAA0367	3'	TGTCCCACAATGCCTAAAACAT	2787	AAATATAT_
			TGA TCAATGTTTTA GGACA		
			AGTTACAAAAT CCTGT		
			CCGTAACAC		
GAM50	KIAA1321	3'	TCCTTGAGCTTTAAAGCATTGA	2627	ATATAT
			TCAATGTTTTTAAA GGA		
			AGTTACGAAATTT CCT		
			CGAGTT		
GAM50	KIAA1718	3'	TGTATTTTAAAATATTGA	2686	
			TCAATGTTTTTAAAATATA		
			AGTTATAAAATTTTATGT		
GAM50	KIAA1789	5'	TGTCCCTGCCCTAGAAACATTG	2781	AAAATATAT
			A TCAATGTTTT GGACA		
			AGTTACAAAG CCTGT		
			ATCCCGTC_		
GAM50	PRO2964	3'	CAAGTATTTTAAAACACTG	1842	A A
			CA TGTTTTTAAAATAT TG		
			GT ACAAATTTTATG AC		
			C A		
GAM50	SLC17A6	3'	TGTCCATACACAGAAACAT	1912	AAAATA
			ATGTTTT TATGGACA		
			TACAAAG ATACCTGT		
			ACAC_____		
GAM50	TRAF3	5'	CATTTTATTTTAAAACGTTGA	2542	T_
			TCAATGTTTTTAAAATA ATG		

			AGTTGCAAAATTTTAT TAC	
			TT	
GAM50	LOC151361	3'	TGTCTGTGTTTTTAAAAC 3344	T
			GTTTTAAAA ATATGGACA	
			CAAAATTTT TGTGTCTGT	
			—	
GAM50	LOC158714	3'	TCCACACATTTAAAACATTGA 3224	ATATA
			TCAATGTTTTTAAA TGGA	
			AGTTACAAAATTT ACCT	
			ACAC_	
GAM50	LOC219667	3'	TATACCTTAGAACATTGA 3518	AA
			TCAATGTTTTTAA TATA	
			AGTTACAAGATT ATAT	
			CC	
GAM50	LOC91565	3'	TCCATTTTAAAACATT 2749	ATAT
			AATGTTTTTAAA ATGGA	
			TTACAAAATTT TACCT	
			—	
GAM51	C1orf1	5'	TATGCTGACAGAAGAACCA 809	CC A A
			TGGTTCTTT GT CA CATA	
			ACCAAGAAG CA GT GTAT	
			A_ _ C	
GAM51	LRAT	3'	AGTATGCATACATAAAAGCAAC 2556	_ CC_ CAA
	CA		TGGTTCTTT GTA CATACT	
			ACCAA GAAA CAT GTATGA	
			C ATA AC_	
GAM51	MYBL1	3'	AGTATGTTATACAAATGCCA 2679	TCTTCC C
			TGGT GTA AACATACT	
			ACCG CAT TTGTATGA	
			TAAA_ A	
GAM51	KIAA1028	3'	TATGTCTGCATTGAAAAGAACC 3547	C TA_ _
	A		TGGTTCTTT CG CA ACATA	
			ACCAAGAAA GT GT TGTAT	
			A TAC C	
GAM51	MGC2488	3'	TGTAGTGGAAGAAGCAT 2045	G _
			ATG TTCTTTCCG TACA	
			TAC AAGAAAGGT ATGT	
			G G	
GAM52	CX3CR1	3'	ACTGCCTACTGCATCGAGTCA 2891	TCCCTTAA
			TGACTCG TAGGCAGT	

			ACTGAGC	ATCCGTCA	
			TACGTC__		
GAM52	WNT14	3'	CTGCAAGGGACGAGTC	1014	AATAG
			GACTCGTCCCTT	GCAG	
			CTGAGCAGGGAA	CGTC	
GAM52	FLJ20275	3'	TACTGCCTTCATAAGATCAAGT	1745	CGTCC AT_
			CA	TGACT CTTA AGGCAGTA	
			ACTGA	GAAT TCCGTCAT	
			ACTA_	ACT	
GAM52	FLJ22390	5'	TACTGCCTATCAAACG	2002	CCC A
			CGT TT	ATAGGCAGTA	
			GCA	AA TATCCGTCAT	
			__	C	
GAM53	LOC120864	5'	CAAGGTCCAAACTGATATAA	2986	CGTAG
			TTGTATCAGTTT	TCTTG	
			AATATAGTCAAA	GGAAC	
			CCT__		
GAM54	KIAA0626	3'	AACATCAGGGTGCAGAATTGAT	1954	C_ A_
			ATCGATTC	CAT TGATGTT	
			TAGTTAAG	GTG ACTACAA	
			AC	GG	
GAM54	KIAA1239	3'	AACATCATGATTATTGATG	2914	TCCCA
			CATCGAT	TATGATGTT	
			GTAGTTA	GTACTACAA	
			TTA__		
GAM54	LOC201475	5'	AACATCATATATTTTGATGTTA	3428	TTCCC
			TAACATCGA	ATATGATGTT	
			ATTGTAGTT	TATACTACAA	
			TTA__		
GAM55	ARCN1	3'	CCCATTTCCTTCCAGTCA	844	GAAGT CA
			TGATTGGA	AGGAAA GG	
			ACTGACCT	TCCTTT CC	
			__	AC	
GAM55	CTSK	3'	TCCTACTTTGCTTCTCTCCACC	736	AT
			CA	TG TGGAGA AGTAGGA	
			AC	ACCTCT TCATCCT	
			CC	CTTCGTT	
GAM55	HMG20A	3'	TCCTATTTCCCTGCCATCA	1800	T__ A
			TGAT	GG GAAGTAGGA	

			ACTA CC CTTTATCCT		
			CCGT _		
GAM55	PRDM2	3'	TCCTGTTTCCCACCCAG 1415	AGAA A	
			TTGG GT GGAAACAGGA		
			GACC CA CCTTTGTCCT		
			____ C		
GAM55	RNMT	3'	CCTGCCTATCCTCTCCGATCA 1060	A_ AAA	
			TGATTGGAGA GTAGG CAGG		
			ACTAGCCTCT TATCC GTCC		
			CC ____		
GAM55	SCAP1	3'	TCCCACTCCCTACTTCTGCCA 1052	_ AAACA	
			TGG AGAAGTAGG GGA		
			ACC TCTTCATCC CCT		
			G CTCAC		
GAM55	USH3A	5'	CCTATTTTATTTCTCCATCA 2355	T AAC	
			TGAT GGAGAAGTAGGA AGG		
			ACTA CCTCTTTATTT TCC		
			_ A_		
GAM55	VAT1	3'	TCCTGTTTCCCACCTCCTTCTC 1292	TA____	
	C		GGAGAAG GGAAACAGGA		
			CCTCTTC CCTTTGTCCT		
			CTCCAC		
GAM55	AIF1	5'	CCTGCTGAAAACCTCCAGTCA 2297	A_____	
			TGATTGGAG AGTAGG		
			ACTGACCTC TCGTCC		
			CCAAAAG		
GAM55	CPLX1	3'	CCTGTTTCTCCTCCATTCA 1317	T AAGTA	
			TGA TGGAG GGAAACAGG		
			ACT ACCTC TCTTTGTCC		
			T C_		
GAM55	CXYorf1	3'	CCTGTTCCCCACCTCCCGGCTC 3228	_ A A A A	
			GA TTGG GA GT GG AACAGG		
			CT GGCC CT CA CC TTGTCC		
			C _ C C C		
GAM55	FLJ12221	3'	CCCACCCTTGCTCTCCAATTA 2637	A AAACA	
			TGATTGGAGA GTAGG GG		
			ATTAACCTCT CGTTC CC		
			_ CCAC_		
GAM55	FLJ20207	3'	CCTGCCCTGCTTCCCCACCCA 1741	AT A AAA	
			TG TGG GAAGTAGG CAGG		

		AC ACC CTTCGTCC GTCC		
		CC C C__		
GAM55	FLJ22215 3'	CCTGCCCCCTACCCTGTTCTCC 3715	___	AAA
		GGAGAA GTAGG CAGG		
		CCTCTT CATCC GTCC		
		GTCC CCC		
GAM55	FLJ31547 3'	TCCCATAATTTCTCCCGCAATC 2511	___	A__
	A	TGATT GGAGAAGT GGA		
		ACTAA CCTCTTTA CCT		
		CGC ATAC		
GAM55	HSCBCIP1 3'	TCCTACCTATGTCTTCTCCAAT 3449	___	AAAC
		ATTGGAGAAG TAGG AGGA		
		TAACCTCTTC ATCC TCCT		
		TGT A__		
GAM55	KIAA0515 5'	TCCTACCAGAACTCCTCCGATC 2670	A A__	AAAC
	A	TGATTGGAG AGT GG AGGA		
		ACTAGCCTC TCA CC TCCT		
		C AGA A__		
GAM55	KIAA1514 3'	CCTGCTCAACTTCTCCA 1877	A AAA	
		TGGAGAAGT GG CAGG		
		ACCTCTTCA CT GTCC		
		A C__		
GAM55	KIAA1553 3'	TCCTCACTTCTCCATCCA 3544	AT	_
		TG TGGAGAAGT AGGA		
		AC ACCTCTTCA TCCT		
		CT C		
GAM55	KIAA1656 3'	CCCACTTCCTTCCAGTCA 2730	___	A
		TGATTGGA GAAGT GG		
		ACTGACCT CTTCA CC		
		TC C		
GAM55	KIAA1877 3'	CCTACCTTATTTCTCCAGCCA 2741	AT	AAAC
		TG TGGAGAAGTAGG AGG		
		AC ACCTCTTTATTTC TCC		
		CG CA__		
GAM55	MTCH1 3'	CCCGTCTACCCCTCCAGTCA 1493	AA	AAACA
		TGATTGGAG GTAGG GG		
		ACTGACCTC CATCT CC		
		CC GC__		
GAM55	N-PAC 3'	CCGCCCTCACCCCTCCAATC 2902	AA _	AAACA
		GATTGGAG GTAGG GG		

			CTAACCTC CA TCC CC		
			CC C CG__		
GAM55	SEMA4B	5'	CCTGTTTCCCACCTCC	2839	AA A
			GGAG GT GGAAACAGG		
			CCTC CA CCTTTGTCC		
			__ C		
GAM55	SPRY1	3'	CCTGTTTCCCACCTTCTCT	2709	TA_
			GGAGAAG GGAAACAGG		
			TCTCTTC CCTTTGTCC		
			CAC		
GAM55	WS-3	5'	CCTGCCAGGCTCTCCAATC	1312	A A_ AAA
			GATTGGAGA GT GG CAGG		
			CTAACCTCT CG CC GTCC		
			_ GA _		
GAM55	LOC123242	5'	TCTGTACCTTCTCCATCCA	3030	AT TAGGAA
			TG TGGAGAAG ACAGG		
			AC ACCTCTTC TGTCT		
			CT CA__		
GAM55	LOC127702	3'	CCTGCCACAACCTTCTCCAAAC	3024	A A__ AAA
	A		TG TTGGAGAAGT GG CAGG		
			AC AACCTCTTCA CC GTCC		
			A ACA C__		
GAM55	LOC146745	5'	TCCTGCCACCATTCTCCAACC	3099	A A AAA
	A		TG TTGGAGAAGT GG CAGGA		
			AC AACCTCTTTA CC GTCCT		
			C _ ACC		
GAM55	LOC147791	3'	CCCATTCCTAACCTCCAATC	3294	AAG A CA
			GATTGGAG TAGG AA GG		
			CTAACCTC ATCC TT CC		
			CA_ C AC		
GAM55	LOC196892	3'	TCCTGGTGATTCTTCTCCAATC	3417	TAGGAAA
	A		TGATTGGAGAAG CAGGA		
			ACTAACCTCTTC GTCCT		
			TTAGTG_		
GAM55	LOC200093	3'	CCTGTTCCCCACCTCCCGGCTC	2648	_ A A A A
			GA TTGG GA GT GG AACAGG		
			CT GGCC CT CA CC TTGTCC		
			C _ C C C		
GAM55	LOC201243	5'	TCCTGCCACCATTCTCCAACC	3426	A A AAA
	A		TG TTGGAGAAGT GG CAGGA		

			AC AACCTCTTTA CC GTCCT		
			C _ ACC		
GAM55	LOC219404	3'	CCTGCTCCCTACTTCCTGGCA 3606	A TG A	AAA
			TG T G GAAGTAGG CAGG		
			AC G C CTTTCATCC GTCC		
			_GT _ CTC		
GAM55	LOC222066	3'	TCCTGCAAACCCACCTTCTCCAA 3574	TA AAA_	
			TCA TGATTGGAGAAG GG CAGGA		
			ACTAACCTCTTC CC GTCCT		
			CA AAAC		
GAM55	LOC253001	5'	TCTGTACCTTCTCCATCCA 3698	AT	TAGGAA
			TG TGGAGAAG ACAGG		
			AC ACCTCTTC TGTCT		
			CT CA_		
GAM55	LOC91040	3'	CCTGTTCCCCACCTCCCGGCTC 2700	_ A A A A	
			GA TTGG GA GT GG AACAGG		
			CT GGCC CT CA CC TTGTCC		
			C _ C C C		
GAM56	GCNT2	5'	TCTCGGGATGAAACGGAATCGA 831	_____ A	
			TCGATTCCGT CC AGA		
			AGCTAAGGCA GG TCT		
			AAGTAG C		
GAM56	BLP1	3'	TTACCTTGCAGACGGAATGA 2222	G _ A	
			TC ATTCCGTC CAAG TGA		
			AG TAAGGCAG GTTC ATT		
			_ AC C		
GAM56	BLP1	3'	TTACCTTGCAGACGGAATGA 2371	G _ A	
			TC ATTCCGTC CAAG TGA		
			AG TAAGGCAG GTTC ATT		
			_ AC C		
GAM56	LOC143914	5'	TCACTCAAACGGAATCGA 3062	CCA A	
			TCGATTCCGT AG TGA		
			AGCTAAGGCA TC ACT		
			AAC _		
GAM56	LOC253891	5'	CACTGGGACGGAATCGG 3654	A A	
			TCGATTCCGTCC AG TG		
			GGCTAAGGCAGG TC AC		
			G _		
GAM57	ADSS	3'	GAAACAAATGATGAAAACAT 2925	CCTGTT	
			ATGT TCATTTGTTTC		

			TACA AGTAAACAAAG		
			AAAGT_		
GAM57	CASP6	3'	GAAACAAAATCCTCAGGAAATT 2305	G	TTTCA
	A		TAAT TCCTG TTTGTTTC		
			ATTA AGGAC AAACAAAG		
			A TCCTA		
GAM57	CASP6	3'	GAAACAAAATCCTCAGGAAATT 810	G	TTTCA
	A		TAAT TCCTG TTTGTTTC		
			ATTA AGGAC AAACAAAG		
			A TCCTA		
GAM57	CKTSF1B1	3'	AAGTGGATAAACAGAACATT 1445	C	C TG
			AATGT CTGTTT ATT TTT		
			TTACA GACAAA TAG GAA		
			A _ GT		
GAM57	F2R	3'	AAACAATGCAGTACAGGACAT 879	TTCAT_	
			ATGTCCTGT TTGTTT		
			TACAGGACA AACAAA		
			TGACGT		
GAM57	GPRK7	3'	GGAAACAAATGTTTCTGACATT 2476	CTGTTT	
			AATGTC CATTTGTTTCC		
			TTACAG GTAAACAAAGG		
			TCTTT_		
GAM57	NLGN1	3'	AAACAAATGAGATGGAC 1591 T		
			GTCC GTTTCATTTGTTT		
			CAGG TAGAGTAAACAAA		
			—		
GAM57	APC10	5'	GGAAACTGTAACAGGACATT 1574	T TTT	
			AATGTCCTGTT CA GTTTCC		
			TTACAGGACAA GT CAAAGG		
			T _		
GAM57	C20orf139	3'	GGAACAAAAACAGGACATTA 3319	CAT	
			TAATGTCCTGTTT TTGTTTC		
			ATTACAGGACAAA AACAAAGG		
			—		
GAM57	FLJ11186	3'	GAAGCCCGAAACAAGACATTA 1818	C ATTT	
			TAATGTC TGTTTC GTTTC		
			ATTACAG ACAAAG CGAAG		
			A CC_		
GAM57	FLJ22116	5'	GGAATTGCGGAAAACAGGAC 2073	CA _	
			GTCCTGTTT TTTGT TTCC		

CAGGACAAA AGGCG AAGG
 — TT
 GAM57 FLJ32978 3' AAACAAATGAAATCAACA 2487 CCT
 TGT GTTTCATTTGTTT
 ||| |||||
 ACA TAAAGTAAACAAA
 AC_

GAM57 KIAA1164 3' GGAAACAAAACAAAAC 2862 CC CA_
 GT TGTTC TTTGTTTCC
 || |||| |||||
 CA ACAA AAACAAAGG
 AA ACA

GAM57 KIAA1762 3' AAAGAGAGAAACGGACA 2668 T A G
 TGTCC GTTTC TTT TTT
 |||| |||| ||| ||
 ACAGG CAAAG AGA AAA
 — — G

GAM57 KIAA1918 5' GAAAGGAGACAGAACATTA 2969 C ATTTG
 TAATGT CTGTTTC TTTC
 |||| |||| |||
 ATTACA GACAGAG AAAG
 A G____

GAM57 POPX1 3' GGAAACAAACTTCAGGTCA 1583 T TTTCA
 TG CCTG TTTGTTTCC
 || |||| |||||
 AC GGAC AAACAAAGG
 T TTC__

GAM57 PRO0800 3' AAACAAAGAGACAGGAATTA 1852 G A
 TAAT TCCTGTTTC TTTGTTT
 ||| ||||| |||||
 ATTA AGGACAGAG AAACAAA

GAM57 LOC142779 3' GGAGTAACAAAATAGGACATTA 3050 CATT _
 TAATGTCCTGTTT TGTT TCC
 ||||| ||| |||
 ATTACAGGATAAA ACAA AGG
 — TG

GAM57 LOC143274 5' GGAAACAAAACAAAAGGA 3053 G CA
 TCCT TTT TTTGTTTCC
 ||| || |||||
 AGGA AAA AAACAAAGG
 — AC

GAM57 LOC154089 3' AAACAAATACTGAGACAG 3186 _
 CTGTTTCA TTTGTTT
 ||||| |||||
 GACAGAGT AAACAAA
 CAT

GAM57 LOC169679 3' AGCATATGAAGACAGGACAT 3404 _ T
 ATGTCCTGTTT CAT TGTT
 ||||| ||| |||

			TACAGGACAGA GTA ACGA	
			A T	
GAM57	LOC202052	5'	GAAACAAATACCCAGAAGACA 3484	___ TTTC
			TGTC CTG ATTTGTTTC	
			ACAG GAC TAAACAAAG	
			AA CCA_	
GAM57	LOC256021	3'	GAAACGAGAACAATGACATTA 3708	C_ CAT
			TAATGTC TGTTT TTGTTTC	
			ATTACAG ACAAG AGCAAAG	
			TA _	
GAM57	LOC91650	5'	AAACAAAACATCTCAGGACAT 2765	TTTCA_
			ATGTCCTG TTTGTTT	
			TACAGGAC AAACAAA	
			TCTACA	
GAM57	LOC91752	5'	AAGTCAAATAAAACAGGACA 2777	C _
			TGTCCTGTTT ATTTG TTT	
			ACAGGACAAA TAAAC GAA	
			A T	
GAM58	DRD1	3'	ATTAACCTCCGTTTCCAAATACA 774	GCTCCT
			TGTAT AGCGGAGTTAAT	
			ACATA TTGCCTCAATTA	
			AACCT_	
GAM58	KIAA0182	3'	AAGTCCTAGGAGCACACA 2931	A GC G
			TGT TGCTCCTA GGA TT	
			ACA ACGAGGAT CCT AA	
			C _ G	
GAM58	SSH2	3'	AGCCCCAGGAGCATACA 2626	AGC A
			TGTATGCTCCT GG GTT	
			ACATACGAGGA CC CGA	
			C_ _	
GAM58	LOC90918	5'	ATTAAATCCAGGAACATATA 2687	C AGC G
			TGTATG TCCT GGA TTAAT	
			ATATAC AGGA CCT AATTA	
			A _ A	
GAM59	EHHADH	3'	TATGAATCATACATACACTC 877	TCTC_
			GGGTGTAT ATTCATA	
			CTCACATA TAAGTAT	
			CATAC	
GAM59	ADAM9	3'	TATGAATGAAAACAAAACACC 1063	A C_
			GGTGT TT TCATTGATA	

			CCACA AA AGTAAGTAT		
			A CAAA		
GAM59	BCAR3	3'	ATGAATGAAAATACATCT 1036	C	
			GGGTGTATT TCATTCAT		
			TCTACATAA AGTAAGTA		
			A		
GAM59	XAP135	5'	AATGGCCACCTGATGA 1809	TATTC	
			TCATCGGGTG TCATT		
			AGTAGTCCAC GGTA		
			C		
GAM59	XAP135	5'	AATGGCCACCTGATGA 2408	TATTC	
			TCATCGGGTG TCATT		
			AGTAGTCCAC GGTA		
			C		
GAM59	LOC252983	5'	ATGAATAAAAATACATCTACTG 3668	TC	CTC
			CA GGGTGTATT ATTCAT		
			GT TCTACATAA TAAGTA		
			CA AAA		
GAM60	MGC5242	5'	CCTTACAATCCGAGACTA 2042		
			TGGTCTCGGATT AGG		
			ATCAGAGCCTAA TCC		
			CAT		
GAM60	LOC197259	3'	GCCAATCAAGACCAGAA 3422	CG	A
			TTCTGGTCT GATT GGC		
			AAGACCAGA CTAA CCG		
			A _ _		
GAM61	DKFZP564I052	3'	ATGGATGAAGATGATGACCGAT 2759	A _	ATA
			ATCG TCAT ATCT TCATCCAT		
			TAGC AGTA TAGA AGTAGGTA		
			C G _		
GAM61	KIAA0825	3'	ATGGACAATACTATTGGTCGAT 2588	TATCTA	CA
			ATCGATCA TAT TCCAT		
			TAGCTGGT ATA AGGTA		
			TATC_ AC		
GAM61	KIAA0976	3'	ATGATGTATATTATCGAT 1588	C TC	
			ATCGAT ATA TATATCAT		
			TAGCTA TAT ATGTAGTA		
			T _		
GAM61	PLAC3	3'	ATGGAAGGGGAAATATGATAGA 2853	G	CTATA A
	T		ATC ATCATAT TC TCCAT		

			TAG TAGTATA	GG AGGTA		
			A AAGG_ A			
GAM61	LOC147991	5'	ATGTATATAGATATGATC	3115		_
			GATCATATCTATAT CAT			
			CTAGTATAGATATA GTA			
			T			
GAM62	HDAC7A	3'	CTCTGGCAAAGTCTTCAA	1628		CTT
			TTGAAGACT CCAGAG			
			AACTTCTGA GGTCTC			
			AAC			
GAM62	HDAC7A	3'	CTCTGGCAAAGTCTTCAA	1700		CTT
			TTGAAGACT CCAGAG			
			AACTTCTGA GGTCTC			
			AAC			
GAM62	LTBP1	3'	TCTCAAATGAAAAAGTCTTCGA	764		C C _
			TTGAAGACT TT CA GAGA			
			AGCTTCTGA AA GT CTCT			
			A A AAA			
GAM62	PDGFB	3'	CTGGGAGAAGGTCTCCAA	941		A _
			TTG AGAC TCTTCCAG			
			AAC TCTG AGAGGGTC			
			C GA			
GAM62	PRDM4	3'	CTTACAGAAGAGTCTCTAA	1427		A CA_
			TTG AGACTCTTC GAG			
			AAT TCTGAGAAG TTC			
			C ACA			
GAM62	SIRT6	3'	TTCTGGAAAAGTCCTCAA	1695		A C
			TTGA GACT TTCCAGAG			
			AACT CTGA AAGGTCTT			
			C A			
GAM62	XYLB	3'	TCTCTGGAAGAATTTC	1187		A C
			TTG AGA TCTTCCAGAGA			
			AAC TTT AGAAGGTCTCT			
			C A			
GAM62	DKFZP434N093	3'	TGTAAACAGAAGGTCTTCAA	3147		T CAGAG
			TTGAAGAC CTTC ACG			
			AACTTCTG GAAG TGT			
			_ ACAA			
GAM62	DKFZP547E1010	5'	TTTCCAGAAGGGTCTCCAA	2768		A CA
			TTG AGACTCTTC GAGA			

			AAC TCTGGGAAG CTTT			
			C AC			
GAM62	DKFZP547E1010	5'	TTTCCAGAAGGGTCTCCAA	1640	A	CA
			TTG AGACTCTTC GAGA			
			AAC TCTGGGAAG CTTT			
			C AC			
GAM62	FLJ13942	3'	TTGAGATGGAAGAGTCTTTAA	2067		GAGA
			TTGAAGACTCTTCCA CGA			
			AATTTCTGAGAAGGT GTT			
			AGA_			
GAM62	FLJ14596	3'	TCATCTGGGAGTCCCCAA	2282	AA	TT _
			TTG GACTC CCAGA GA			
			AAC CTGAG GGTCT CT			
			CC _ A			
GAM62	HRLP5	3'	TTCTGGAAGAATCTACAA	2364	A	C
			TTG AGA TCTTCCAGAG			
			AAC TCT AGAAGGTCTT			
			A A			
GAM62	KCNS1	3'	CGTTGGAAGAGTCTT	917		GAG
			AAGACTCTTCCA ACG			
			TTCTGAGAAGGT TGC			

GAM62	KIAA0992	5'	TCTCTGGAGTCTTCAA	1662		TCT
			TTGAAGAC TCCAGAGA			
			AACTTCTG AGGTCTCT			

GAM62	KIAA1975	5'	TATCATCTCTGGAAGTTGAGAG	2982	A	_____ C
			CCTCCAA G CTCT TCCAGAGA GAT A			
			C GAGA AGGTCTCT CTA T			
			C GTTGA A			
GAM62	MGC5590	3'	TCTCAGAAAGTCTTCAA	2049	C	CA
			TTGAAGACT TTC GAGA			
			AACTTCTGA AAG CTCT			
			_ A_			
GAM62	SIAT8C	5'	TCTTGAAGAATCTCAA	1648	A	C G
			TTGA GA TCTTCCA AGA			
			AACT CT AGAAGGT TCT			
			_ A _			
GAM62	LOC149706	3'	ATCACCTCTGGAGCCCTTTCA	3313	ACTC	AC
			TGAAG TTCCAGAG GAT			

			ACTTT GAGGTCTC CTA		
			CCC_ CA		
GAM62	LOC160292	3'	CTCTGGAAAGCCTTCAA 3399	A C	
			TTGAAG CT TTCCAGAG		
			AACTTC GA AAGGTCTC		
			C _		
GAM62	LOC203378	3'	GTTTCTAAAGAGTCTTCAA 3491	CC	
			TTGAAGACTCTT AGAGAC		
			AACTTCTGAGAA TCTTTG		
			A_		
GAM62	LOC204200	5'	CTCTGGAAAGGTCTCCAA 3493	A TC	
			TTG AGAC TTCCAGAG		
			AAC TCTG AAGGTCTC		
			C GA		
GAM62	LOC255265	5'	CGTACGGAAAAGTCTTCA 3672	C AGAG	
			TGAAGACT TTCC ACG		
			ACTTCTGA AAGG TGC		
			A CA__		
GAM63	FLJ10737	3'	AGATGTTTTTATTTTATATTAT 1797	TCCCA_	
			TA TAATAATATAAAAT ATCT		
			ATTATTATATTTTA TAGA		
			TTTTTG		
GAM64	COX15	3'	AACAGTCCCAGAATGACCCCA 1104	C AAATC T	
			TGGGGTTA TCT GCT GTT		
			ACCCAGT AGA TGA CAA		
			A CCC__ _		
GAM64	SH2D1A	3'	AACAAGCCTCCTTTTAAAGTAA 920	C TC__	
			CCCTA TGGGGTTACT TAAA GCTTGTT		
			ATCCCAATGA ATTT CGAACA		
			A TCCTC		
GAM64	FLJ12994	3'	ACAAGCAAATGTAAGTCCA 2017	TCTAAATC	
			TGGGGTTAC GCTTGT		
			ACCTCAATG CGAACA		
			TAAA__		
GAM64	FLJ12994	3'	ACAAGCAAATGTAAGTCCA 3081	TCTAAATC	
			TGGGGTTAC GCTTGT		
			ACCTCAATG CGAACA		
			TAAA__		
GAM65	FGFR2	3'	ACCCTGTCATTACGTCAACGC 712	_ _	
			GCGT GGC AATGACAGGGT		

			CGCA CTG T TACTGTCCCA		
			A CA		
GAM65	FGFR2	3'	ACCCTGTCATTACGTCAACGC 2023	—	—
			GCGT GGC AATGACAGGGT		
			CGCA CTG T TACTGTCCCA		
			A CA		
GAM65	FGFR2	3'	ACCCTGTCATTACGTCAACGC 2024	—	—
			GCGT GGC AATGACAGGGT		
			CGCA CTG T TACTGTCCCA		
			A CA		
GAM65	FGFR2	3'	ACCCTGTCATTACGTCAACGC 2026	—	—
			GCGT GGC AATGACAGGGT		
			CGCA CTG T TACTGTCCCA		
			A CA		
GAM65	FGFR2	3'	ACCCTGTCATTACGTCAACGC 2027	—	—
			GCGT GGC AATGACAGGGT		
			CGCA CTG T TACTGTCCCA		
			A CA		
GAM65	FGFR2	3'	ACCCTGTCATTACGTCAACGC 2028	—	—
			GCGT GGC AATGACAGGGT		
			CGCA CTG T TACTGTCCCA		
			A CA		
GAM65	MMP19	5'	ACCAAGGCTGCCACGCTCTAA 2010	T	ATGACAG
			TTAG AGCGTGGCA GGT		
			AATC TCGCACCGT CCA		
			— CGGAA—		
GAM66	ARHGEF12	3'	AATAATGTCATTCTCAATTAA 1619	TA	
			TTAATTG AATGATATTATT		
			AATTAAC T TACTGTAATAA		
			TC		
GAM66	OS4	3'	AATATTTGTATTACTTACAATT 1239	A	TAT
	AA		TTAATTGTAA TGATAT TATT		
			AATTAACATT ATTATG ATAA		
			C TTT		
GAM66	LOC148289	3'	AATAATAACATATACAATTAA 3300	A	A
			TTAATTGTA ATG TATTATT		
			AATTAACAT TAC ATAATAA		
			A A		
GAM66	LOC253160	3'	AATAATAACATATACAATTAA 3714	A	A
			TTAATTGTA ATG TATTATT		

			AATTAACAT TAC ATAATAA		
			A A		
GAM67	GAN	3'	TGAGTGTGGTACATTA ACT 1975	A CA _	
			AG TAA TACCACAC CA		
			TC ATT ATGGTGTG GT		
			A AC A		
GAM67	IDH3A	3'	AAAGAGTGAATGTGGTATATTT 1222	TAAC C_	
	CT		AGA ATACCACA CATTTTTT		
			TCT TATGGTGT GTGAGAAA		
			TTA_ AA		
GAM67	PEX1	3'	AAAAAATGGTGTCTATGAATTT 749	TAA_ CC	
	CT		AGA CATA ACACCATTTTTT		
			TCT GTAT TGTGGTAAAAA		
			TTAA C_		
GAM67	PYGO2	3'	AAAAATTGGGATATGTTATCT 2676	CCACA T	
			AGATAACATA CCA TTTTT		
			TCTATTGTAT GGT AAAAA		
			AG__ T		
GAM67	FLJ21477	3'	TGGCGTGAGATGTTATCT 2142	AC A	
			AGATAACAT CAC CCA		
			TCTATTGTA GTG GGT		
			GA C		
GAM67	NS1-BP	3'	AAAAAATGGTGTTTTATCT 2953	CATACC	
			AGATAA ACACCATTTTTT		
			TCTATT TGTGGTAAAAA		
			T_____		
GAM67	UNC5D	5'	AAAAAAGCTGTAATATGTTATC 2391	CC CCA	
	T		AGATAACATA ACA TTTTTT		
			TCTATTGTAT TGT AAAAAA		
			AA CG_		
GAM67	LOC257451	3'	AAAAATTGGGATATGTTATCT 3678	CCACA T	
			AGATAACATA CCA TTTTT		
			TCTATTGTAT GGT AAAAA		
			AG__ T		
GAM68	CHAC	3'	TGCCCATATGTCCATTTAT 1612	AGAT	
			ATAAGTGGACATAT GCA		
			TATTTACCTGTATA CGT		
			CC__		
GAM68	GGCX	3'	CTGCACCCTGCCACTTGT 778	A TATAGA	
			ATAAGTGG CA TGCAG		

TGTTCACC GT ACGTC
 _ CCC_
 GAM68 ITPKB 3' TCTGCATCTGTCCAC 911 TATA
 GTGGACA GATGCAGA
 ||||| |||||
 CACCTGT CTACGTCT

 GAM68 KCNAB1 3' TCTAATGTTATGTCCACTTA 2584
 TAAGTGGACATA TAGA
 ||||| |||||
 ATTACCTGTAT ATCT
 TGTA
 GAM68 KLRC4 5' CTGTCAAAATATACACCACTTA 1451 ACA GA_ _
 T ATAAGTGG TATA TG CAG
 ||||| ||| |||||
 TATTCACC ATAT AC GTC
 AC_ AAA T
 GAM68 MLF2 3' TCTGCATCTACTGACTTG 1212 _ ACATA
 TAAGT GG TAGATGCAGA
 ||||| || |||||
 GTTCA TC ATCTACGTCT
 G
 GAM68 NR1I2 3' TCTGCATCCATTTGAACAC 1067 GA T A
 GTG CA AT GATGCAGA
 ||| ||| |||||
 CAC GT TA CTACGTCT
 AA T C
 GAM68 NR1I2 3' TCTGCATCCATTTGAACAC 1971 GA T A
 GTG CA AT GATGCAGA
 ||| ||| |||||
 CAC GT TA CTACGTCT
 AA T C
 GAM68 CEP3 3' TTCTACATCAGATGTTGTCACT 1304 _ ATA C
 TAT ATAAGTGG GACAT GATG AGAA
 ||||| ||||| |||||
 TATTCAC TTGTA CTAC TCTT
 TG GA_ A
 GAM68 FHX 3' TCATGGATCATGTCCAC 1825 ATA G _
 GTGGACAT GAT CA GA
 ||||| ||| |||
 CACCTGTA CTA GT CT
 _ G A
 GAM68 FLJ10352 3' TTCTGCATCTACAACTCAACAT 2233 GACATA_
 TTA TAAGTG TAGATGCAGAA
 ||||| |||||
 ATTTAC ATCTACGTCTT
 AACTCAAC
 GAM68 FLJ22127 3' TCGAGTCCATATGTCCAC 2008 A GCA
 GTGGACATAT GAT GA
 ||||| ||| ||

			CACCTGTATA CTG CT		
			C AG_		
GAM68	GDAP1L1	3'	TCTGCATCCATGCCAC 2043	A	ATA
			GTGG CAT GATGCAGA		
			CACC GTA CTACGTCT		
			_ C_		
GAM68	H-L(3)MBT	3'	TCTGCTCTCTACCCACT 2230	ACA	T T
			AGTGG TA AGA GCAGA		
			TCACC AT TCT CGTCT		
			C_ C _		
GAM68	KIAA1340	3'	TCTAAGCTATGCCCATTTAT 2846	A	___
			ATAAGTGG CATA TAGA		
			TATTTACC GTAT ATCT		
			C CGA		
GAM68	KNSL7	3'	TTCTGCATCCATATACACCCT 1905	T AC_	A
			AG GG ATAT GATGCAGAA		
			TC CC TATA CTACGTCTT		
			_ ACA C		
GAM68	P5-1	3'	CTCCATTTATGTACCCAC 1322	AC	C
			GTGG ATATAGATG AG		
			CACC TGTATTTAC TC		
			CA C		
GAM68	PP1044	5'	CTGCATCTTTACCTATATCCAT 1956	C T_	___
	TTA		TAAGTGGA ATA AGATGCAG		
			ATTTACCT TAT TCTACGTC		
			A CCATT		
GAM68	SIRPB1	3'	TGCATGTGTCCACTTA 1272	ATAG	
			TAAGTGGACAT ATGCA		
			ATTCACCTGTG TACGT		

GAM68	LOC148811	3'	CTGCATCTCTCCCCTTA 3126	T	CATAT
			TAAG GGA AGATGCAG		
			ATTC CCT TCTACGTC		
			C C_		
GAM68	LOC149711	3'	TCCATATGTCTATCCACTTA 3315	___	A
			TAAGTGGA CATAT GA		
			ATTCACCT GTATA CT		
			ATCT C		
GAM68	LOC150630	5'	CTGCATCTTCTGCCACT 3332	A	TAT
			AGTGG CA AGATGCAG		

		TCACC GT TCTACGTC		
		_ CT_		
GAM68	LOC150819 5'	CTGCATTTTAGTCCAACT 3333	_	ATAT
		AGT GGAC AGATGCAG		
		TCA CCTG TTTACGTC		
		A AT_		
GAM68	LOC154877 3'	TCTGCATCCATTCCACT 3373	CAT	A
		AGTGGA AT GATGCAGA		
		TCACCT TA CTACGTCT		
		_ C		
GAM68	LOC158327 3'	TTCTGCAGGGACACCACTTAT 3216	ACATATAGA	
		ATAAGTGG TGCAGAA		
		TATTCACC ACGTCTT		
		ACAGGG_		
GAM68	LOC196540 3'	TCTGCATCCATGTACTCC 3467	C_ A	
		GGA ATAT GATGCAGA		
		CCT TGTA CTACGTCT		
		CA C		
GAM68	LOC220394 5'	TCTCAGAATATGTCCAT 3581	AGA	C
		GTGGACATAT TG AGA		
		TACCTGTATA AC TCT		
		AG_ _		
GAM68	LOC254428 3'	CTGTTGACCCATGTCCACCTAT 3677	A	ATAGAT
		ATA GTGGACAT GCAG		
		TAT CACCTGTA TGTC		
		C CCCAGT		
GAM68	LOC92405 3'	TTCTGTTACACATGTCTACTTA 2848	ATAGAT	
		TAAGTGGACAT GCAGAA		
		ATTCATCTGTA TGTCTT		
		CACAT_		
GAM69	DKFZP434G1411 3'	TAGGTTGATACATGTATCA 3554	AA	
		TGATACATGTATTAA TA		
		ACTATGTACATAGTT AT		
		GG		
GAM69	DKFZP564I052 3'	GAAAGTATTCCTATCATGTAT 2760	T TAA	
		ATACATG AT AATACTTTC		
		TATGTAC TA TTATGAAAG		
		_ TCC		
GAM69	KLHL8 3'	AAAGTATTTGTTACATAATCA 2639	AC	TTA
		TGAT ATGTA AAATACTTT		

			ACTA TACAT TTTATGAAA		
			A_ TG_		
GAM69	XLKD1	3'	AAAGTGCCATTAACAAATGTAT 1323	GTA	AA_
	CA		TGATACAT TTAA TACTTT		
			ACTATGTA AATT GTGAAA		
			AAC ACC		
GAM69	LOC51003	3'	GAGGCACTTAATACATGTAT 1658	AATA	
			ATACATGTATTAA CTT		
			TATGTACATAATT GAG		
			CACG		
GAM70	NEU3	3'	ATGATTTGTTCCATTTTAA 1319	TA	
			TAAAAAT AACAAATCGT		
			ATTTTAA TTGTTTAGTA		
			CC		
GAM70	CHPT1	3'	AACATTTGTTTAATTTTAA 1906	C	
			TAAAAATTAAACAAAT GTT		
			ATTTTAAATTTGTTTA CAA		
			-		
GAM70	LOC143310	3'	AATTTGTGATTTGTTTAATTT 3057	TT_	
			AAATTAAACAAATCG ATT		
			TTTAATTTGTTTAGT TAA		
			GTT		
GAM70	LOC152578	5'	TAATAACAAATGTTTAATTTTT 3361	AATC	
	A		TAAAAATTAAACA GTTATTA		
			ATTTTAAATTTGT CAATAAT		
			AAA_		
GAM71	HNF3A	3'	ACAGCATAATAAAATCC 2543	C GTT	
			GGATT TGT TATGCTGT		
			CCTAA ATA ATACGACA		
			A _		
GAM71	MUC12	3'	AGCTGCAAACACAGAGCCCA 3643	AT TA T	
			TGG TCTGTGTT TGC GTT		
			ACC AGACACAA ACG CGA		
			CG _ T		
GAM71	OGN	3'	ACAGCATTACAAAATCC 2307	C TTT	
			GGATT TGTG ATGCTGT		
			CCTAA ACAT TACGACA		
			A _		
GAM71	OGN	3'	ACAGCATTACAAAATCC 1467	C TTT	
			GGATT TGTG ATGCTGT		

			CCTAA ACAT TACGACA		
			A _		
GAM71	OGN	3'	ACAGCATTACAAAATCC 2059	C	TTT
			GGATT TGTG ATGCTGT		
			CCTAA ACAT TACGACA		
			A _		
GAM71	PTPRA	3'	AGATAAACACAAAATCCAT 962	C	G
			ATGGATT TGTGTTTAT CT		
			TACCTAA ACACAAATA GA		
			A _		
GAM71	PTPRA	3'	AGATAAACACAAAATCCAT 2389	C	G
			ATGGATT TGTGTTTAT CT		
			TACCTAA ACACAAATA GA		
			A _		
GAM71	PTPRA	3'	AGATAAACACAAAATCCAT 2390	C	G
			ATGGATT TGTGTTTAT CT		
			TACCTAA ACACAAATA GA		
			A _		
GAM71	TIRAP	3'	AGCTAGAAACAGAAAACCCAT 2344	A_	G T
			ATGG TTCTGT TTTA GCT		
			TACC AAGACA AGAT CGA		
			CAA A _		
GAM71	ATF3	3'	AGCGTTAACACAAAATCCAT 1080	C	T
			ATGGATT TGTGTT ATGCT		
			TACCTAA ACACAA TGCGA		
			A T		
GAM71	FLJ22457	3'	AACATCTTCAACACAGAACACA 2106	GA	TATGC
			TG TTCTGTGTT TGTT		
			AC AAGACACAA ACAA		
			AC CTTCT		
GAM71	LIPG	3'	AGCCTAAACACAAAATTCAT 1266	C	T
			ATGGATT TGTGTTTA GCT		
			TACTTAA ACACAAAT CGA		
			A C		
GAM71	MGC4643	3'	AACAGCATAAACAGCTGGACC 2271	A T_	
			GG TTC G TGTTTATGCTGTT		
			CC AGG C ACAAATACGACAA		
			_ TG		
GAM71	LOC143888	3'	AGTCTAAACACAAAATTCAT 3064	C	T
			ATGGATT TGTGTTTA GCT		

			TACTTAA ACACAAAT TGA		
			A C		
GAM71	LOC149619	5'	AACATCTTCAACACAGAACACA 3311	GA	TATGC
			TG TTCTGTGTT TGTT		
			AC AAGACACAA ACAA		
			AC CTTCT		
GAM71	LOC91464	5'	AACAGCATAAAGGACCCCA 2740	AT	GTG
			TGG TCT TTTATGCTGTT		
			ACC AGG AAATACGACAA		
			CC _		
GAM72	CLDN1	3'	ATATTAATTAGTTTATATTA 1940	_	
			TAATATAAACTAAT AATAT		
			ATTATATTTGATTA TTATA		
			A		
GAM72	KIAA1706	3'	ACAGTGTTTCATAGTTTATATTA 3577		ATAAT
			TAATATAAACTA ATATTGT		
			ATTATATTTGAT TGTGACA		
			ACT_		
GAM73	B3GALT5	3'	GTGCTGAAATCCACGCCAGA 2317	A	A_ T
			TCT GCGTGGAT CAG CAC		
			AGA CGCACCTA GTC GTG		
			C AA _		
GAM73	B3GALT5	3'	GTGCTGAAATCCACGCCAGA 1268	A	A_ T
			TCT GCGTGGAT CAG CAC		
			AGA CGCACCTA GTC GTG		
			C AA _		
GAM73	B3GALT5	3'	GTGCTGAAATCCACGCCAGA 2318	A	A_ T
			TCT GCGTGGAT CAG CAC		
			AGA CGCACCTA GTC GTG		
			C AA _		
GAM73	B3GALT5	3'	GTGCTGAAATCCACGCCAGA 2319	A	A_ T
			TCT GCGTGGAT CAG CAC		
			AGA CGCACCTA GTC GTG		
			C AA _		
GAM73	B3GALT5	3'	GTGCTGAAATCCACGCCAGA 2321	A	A_ T
			TCT GCGTGGAT CAG CAC		
			AGA CGCACCTA GTC GTG		
			C AA _		
GAM73	MEF2A	3'	GTGACTGTAGTTACTTAAGA 1229	C C	A
			TCT TAG GTGG TACAGTCAC		

			AGA ATT CATT ATGTCAGTG	
			— — G	
GAM73	ORC2L	3'	GTGAGAAGCCAGGCTAGAGA 1278	G ATACAG
			TCTCTAGC TGG TCAC	
			AGAGATCG ACC AGTG	
			G GAAG__	
GAM73	PART1	3'	CGGTGACTATATGAGAATGGA 1699	GCGTGG C
			TCTA ATA AGTCACCG	
			AGGT TAT TCAGTGGC	
			AAGAG_ A	
GAM73	SLC10A1	3'	GTGACTGTAAACTCTATG 989	—
			CGTGGA TACAGTCAC	
			GTATCT ATGTCAGTG	
			CAA	
GAM73	FUSIP1	3'	GTGACTGTAATATACTAGAG 1314	CG GA
			CTCTAG TG TACAGTCAC	
			GAGATC AT ATGTCAGTG	
			AT A_	
GAM73	RAI17	3'	GTGACTGTGGAGCCTGAGA 3515	T C GGA
			TCTC AG GT TACAGTCAC	
			AGAG TC CG GTGTCAGTG	
			— — AG_	
GAM73	LOC115811	5'	GGTAACTGTGGCTAGGGA 2442	GTGGA C
			TCTCTAGC TACAGT ACC	
			AGGGATCG GTGTCA TGG	
			— — — — A	
GAM73	LOC256946	3'	GTGACTGTAATATACTAGAG 3657	CG GA
			CTCTAG TG TACAGTCAC	
			GAGATC AT ATGTCAGTG	
			AT A_	
GAM74	PEX3	3'	AATATAGATATTTTATATAC 1044	—
			GTATGTA TATCTATATT	
			CATATAT ATAGATATAA	
			TTT	
GAM74	PKD2L2	3'	TTAATATGAGACATACTG 1497	ATATC
			CAGTATGT TATATTAA	
			GTCATACA GTATAATT	
			GA__	
GAM74	BA108L7.2	3'	ATGCATATACATACATGATA 2179	_ C
			TATCA GTATGTATAT TAT	

			ATAGT CATACATATA GTA		
			A C		
GAM74	IDI1	3'	TTAATGTATTATATACACTGAT 2776	A	TC
		A	TATCAGT TGTATA TATATTAA		
			ATAGTCA ATATAT ATGTAATT		
			C T_		
GAM74	PRO0899	5'	AGTGTTTTACACATACTGAT 1846	A	TCT
			ATCAGTATGT TA ATATT		
			TAGTCATACA AT TGTGA		
			C TT_		
GAM74	SEC14L1	3'	TGGTAATACAATACTGATA 980	_	AT
			TATCAGTAT GTAT CTA		
			ATAGTCATA CATA GGT		
			A AT		
GAM74	LOC130074	3'	TTAACATAGAATGTTTACTGAT 3045	TG A	A
		A	TATCAGTA TAT TCTAT TTAA		
			ATAGTCAT GTA AGATA AATT		
			TT _ C		
GAM74	LOC222159	5'	AGACCATGCATACTGATA 3633	A_	
			TATCAGTATGTAT TCT		
			ATAGTCATACGTA AGA		
			CC		
GAM75	RNF28	3'	AAGGAACTTTTGTATAATA 2263	A	
			TATTATACAAAA TTTTTT		
			ATAATATGTTTT AAGGAA		
			C		
GAM75	SWAP70	3'	GAAATAAAAAATTATTTGTATAA 2916	AAT	
		T	ATTATACAAA TTTTATTTT		
			TAATATGTTT AAAAATAAAG		
			ATT		
GAM75	bA430M15.1	3'	AAAAATTTTTGTATAATG 3072		
			TATTATACAAAAATTTTT		
			GTAATATGTTTTTAAAAA		
GAM76	PSG1	3'	TTTGATTCGGATGTTATA 1337	GT	
			TATAACATC AATCAAA		
			ATATTGTAG TTAGTTT		
			GC		
GAM76	RALB	3'	TTTTGAACTACAGATGTTGTA 968	_	A_
			TATAACATC GTA TCAAAA		

			ATGTTGTAG CAT AGTTTT	
			A CA	
GAM76	CEACAM8	3'	TTTGATTGGGATGTTATA 859	G
			TATAACATC TAATCAAA	
			ATATTGTAG GTTAGTTT	
			G	
GAM76	LAT1-3TM	3'	TTTTGGTGGCTCGATGTTA 2183	TA__
			TAACATCG ATCAAAA	
			ATTGTAGC TGGTTTT	
			TCGG	
GAM76	LAT1-3TM	5'	TTTTGGTGGCTCGATGTTA 2827	TA__
			TAACATCG ATCAAAA	
			ATTGTAGC TGGTTTT	
			TCGG	
GAM76	MCFP	5'	TTTTGGCTACTGATGTTA 1863	_ AT
			TAACATC GTA CAAAA	
			ATTGTAG CAT GTTTT	
			T CG	
GAM76	MGC26651	3'	TTTTGATGTGAAAGATGTTATA 2489	GTA__
			TATAACATC ATCAAAA	
			ATATTGTAG TAGTTTT	
			AAAGTG	
GAM76	LOC197423	5'	TTTTGGTGGCTCGATGTTA 3090	TA__
			TAACATCG ATCAAAA	
			ATTGTAGC TGGTTTT	
			TCGG	
GAM76	LOC220565	5'	TTTTGGTGGCTCGATGTTA 3495	TA__
			TAACATCG ATCAAAA	
			ATTGTAGC TGGTTTT	
			TCGG	
GAM77	FLJ13215	3'	GAATATTCTACCTAAATAT 2126	G A
			ATA TTAG TAGAATATTC	
			TAT AATC ATCTTATAAG	
			A C	
GAM77	PTP4A1	3'	CTAATGAATTGAGCACATCTAA 1027	AGAAT__
	T		GTTAGAT ATTCATTAG	
			TAATCTA TAAGTAATC	
			CACGAGT	
GAM77	SDFR1	3'	TGGTAATATTCTATGCAACTAT 1430	AG C
			ATAGTT ATAGAATATT ATTA	

			TATCAA TATCTTATAA TGGT		
			CG _		
GAM77	SDFR1	3'	TGGTAATATTCTATGCAACTAT 1718	AG	C
			ATAGTT ATAGAATATT ATTA		
			TATCAA TATCTTATAA TGGT		
			CG _		
GAM77	LOC221133	3'	CTAATGAAGAGAATATTTAAC 3608	GAATA	
			GTTAGATA TTCATTAG		
			CAATTTAT AAGTAATC		
			AAGAG		
GAM78	DJ667H12.2	3'	TTATGCCATGAACATGCCA 1884	CGATAA	
			TGGTATGTTCA GTATAA		
			ACCGTACAAGT CGTATT		
			AC_		
GAM78	KIAA1799	3'	TTATACTTAGAACTTACCA 3003	T	ACGA
			TGGTA GTTC TAAGTATAA		
			ACCAT CAAG ATTCATATT		
			T _		
GAM78	PPP1R3B	3'	TTTATGTAAACATACCA 2071	C	G
			TGGTATGTT AC ATAAG		
			ACCATACAA TG TATTT		
			A _		
GAM78	LOC144840	3'	ATTTCTCGTGAACACCCA 3071	TA	T
			TGG TGTTACACGA AAGT		
			ACC ACAAGTGCT TTTA		
			C_ C		
GAM78	LOC158674	3'	ATTTCCCGTGAACACCCA 3222	TA	AT
			TGG TGTTACAG AAGT		
			ACC ACAAGTGC TTTA		
			C_ CC		
GAM78	LOC245757	3'	ATTTCCCGTGAACACCCA 3496	TA	AT
			TGG TGTTACAG AAGT		
			ACC ACAAGTGC TTTA		
			C_ CC		
GAM78	LOC81034	3'	ATTTATCGTAAACATCCA 2164	T	C
			TGG ATGTT ACGATAAGT		
			ACC TACAA TGCTATTTA		
			_ A		
GAM79	DTNB	3'	CTAATATCCAGAATCTACAAAG 2316	TA	A G
	A		TCTTT AGA TT TGGATATTAG		

			AGAAA TCT AA ACCTATAATC	
			CA _ G	
GAM79	SP100	3'	AGTAAATACAATTTTAAAA 993	GA
			TTTTAAGAATTGTG TATT	
			AAAATTTTAAACAT ATGA	
			AA	
GAM79	KIAA1229	3'	AATATCCAGAATCTACAAAGA 2620	TA A G
			TCTTT AGA TT TGGATATT	
			AGAAA TCT AA ACCTATAA	
			CA _ G	
GAM79	LOC144776	3'	AATATTCAATATTCTTAAAGA 3070	T TG
			TCTTT AAGAAT TGGATATT	
			AGAAA TTCTTA ACTTATAA	
			_ TA	
GAM79	LOC199775	5'	CTAATTCTTCAATTCTTAA 3432	T T
			TTAAGAATTG GGA ATTAG	
			AATTCTTAAC TCT TAATC	
			T _	
GAM79	LOC222236	3'	GTCTACAATTCCCAAAGA 3651	AA
			TCTTTT GAATTGTGGAT	
			AGAAAA CTTAACATCTG	
			CC	
GAM80	CHRNA1	3'	TTATTATTGATGATAAGA 701	C _
			TCT ATCATCAG AATAA	
			AGA TAGTAGTT TTATT	
			A A	
GAM80	TNFSF9	3'	ATTTATTCTGAGCCTGAG 1062	TCA
			CTCA TCAGAATAAAT	
			GAGT AGTCTTATTTA	
			CCG	
GAM80	AKT3	3'	ATTTATTTTTTAGTGATGAGAA 1214	C__
			TTCTCATCAT AGAATAAAT	
			AAGAGTAGTG TTTTATTTA	
			ATT	
GAM80	FLJ10103	3'	TTGTTTACTGATGAGAA 1773	TCA
			TTCTCATCA GAATAA	
			AAGAGTAGT TTTGTT	
			CA_	
GAM80	FLJ22582	3'	TTTTGTAAATGATGAGAA 2132	__
			TTCTCATCAT CAGAA	

			AAGAGTAGTA GTTTT		
			AAT		
GAM80	KIAA1371	3'	ATTCTAGAAATGGTGAGAA 3454	—	—
			TTCTCATCA TC AGAAT		
			AAGAGTGGT AG TCTTA		
			AA A		
GAM80	MACF1	3'	ATTATTCTGAACGGGAGAA 2308	ATCA	
			TTCTC TCAGAATAAAT		
			AAGAG AGTCTTATTTA		
			GGCA		
GAM80	MACF1	3'	ATTATTCTGAACGGGAGAA 1403	ATCA	
			TTCTC TCAGAATAAAT		
			AAGAG AGTCTTATTTA		
			GGCA		
GAM80	MGC16824	3'	TTATTCTGACAATGAAGA 1910	—	CA
			TCT CAT TCAGAATAA		
			AGA GTA AGTCTTATT		
			A AC		
GAM80	NR2C1	3'	ATTATTCTTGGTGAAGA 1006	A	—
			TC TCATCA GAATAAAT		
			AG AGTGGT CTTATTTA		
			A T		
GAM80	P450RAI-2	3'	ATTATTCACTGATAGAGAA 1887	—	TCA
			TTCTC ATCA GAATAAAT		
			AAGAG TAGT CTTATTTA		
			A CA_		
GAM80	LOC152715	5'	ATTTGGCTGATGATGGAA 3174	T	AA
			TTC CATCATCAG TAAAT		
			AAG GTAGTAGTC GTTTA		
			— G_		
GAM80	LOC222166	3'	ATTCTGTGGGCTGATGAGAA 3634	T	_____
			TTCTCATCA CAGAAT		
			AAGAGTAGT GTCTTA		
			CGGGT		
GAM80	LOC257042	3'	ATTCTGAGTGATGATGAA 3719	—	—
			TTC TCATCA TCAGAAT		
			AAG AGTAGT AGTCTTA		
			T G		
GAM81	CORO2B	5'	TTCTGTTGCCCAAGCTGG 2694	—	GAG TAAA
			CC GCT TGG CAACAGAA		

			GG CGA ACC GTTGTCTT		
			T ____ C____		
GAM81	EFNB2	3'	GTTCTGTTACCCAGGGCTCTGC 1084	T ____	AACA
			GC GAGT GGTA ACAGAAC		
			CG CTCG CCAT TGTCTTG		
			T GGAC ____		
GAM81	GCGR	5'	TCTGCTGCTCTGCCACTCAGC 714	AA_ A	
			GCTGAGTGGTA CA CAGA		
			CGACTCACCGT GT GTCT		
			CTC C		
GAM81	HMOX1	3'	GTTCTGTTGTTTTTATAGCAGG 901	G AGTGGT	
	G		CC CTG AAACAACAGAAC		
			GG GAC TTTGTTGTCTTG		
			_ GATATT		
GAM81	HS3ST2	3'	GTTCTGTTGCTATGAACACAGC 1267	A GGTA	AAA
			GCTG GT CAACAGAAC		
			CGAC CA GTTGTCTTG		
			A AGTATC		
GAM81	PIM2	3'	CTGTTGTTACCCCAAGG 2550	GC AGT A	
			CC TG GGTA CAACAG		
			GG AC CCATT GTTGTC		
			A_ C_ _		
GAM81	PIP5K1B	5'	TCTGTTGCTACTAAGC 1034	G TAA	
			GCT AGTGG CAACAGA		
			CGA TCATC GTTGTCT		
			A ____		
GAM81	RBM3	3'	TTCTGTTGTGTCTCATACAG 2887	A TAA	
			CTG GTGG ACAACAGAA		
			GAC TACT TGTTGTCTT		
			A CTG		
GAM81	SMAC	3'	CTGTCTCCCCACTCAGTGG 1889	TAAACA	
			CCGCTGAGTGG ACAG		
			GGTGA CTACC TGTC		
			CCTC__		
GAM81	SMAC	3'	CTGTCTCCCCACTCAGTGG 2459	TAAACA	
			CCGCTGAGTGG ACAG		
			GGTGA CTACC TGTC		
			CCTC__		
GAM81	SMAC	3'	CTGTCTCCCCACTCAGTGG 2460	TAAACA	
			CCGCTGAGTGG ACAG		

GGTGACTCACC TGTC
CCTC__

GAM81 SOST 3' TTCTGCCCACCACTCACGG 2148 C AAACAA
CCG TGAGTGGT CAGAA
||| ||||| |||||
GGC ACTCACCA GTCTT
_ CCC__

GAM81 ZNF10 5' TCTGCTGTCACTCAAGG 1626 GC GTAA A
CC TGAGTG ACA CAGA
|| ||||| ||| |||||
GG ACTCAC TGT GTCT
A_ _ C

GAM81 ABCA10 5' TTCTGTTAGTTACTCA 2373 GTAA _
TGAGTG AC AACAGAA
||||| || |||||
ACTCAT TG TTGTCTT
_ A

GAM81 H2AFJ 3' GTTCTGCTATTTACTCTGTGG 1807 T TAAACAA
CCGC GAGTGG CAGAAC
||||| |||||
GGTG CTCATT GTCTTG
T TATC__

GAM81 HSH2 3' GTTCTGTTGTCTAAAAGC 2289 GAG TAA
GCT TGG ACAACAGAAC
||| ||| |||||
CGA ATC TGTTGTCTTG
AA_ _

GAM81 KIAA1024 3' TTCTGTTGTTCCACCATTAAGGG 2841 G G A
G CC CT AGTGGT AACAACAGAA
|| || ||||| |||||
GG GA TTACCA TTGTTGTCTT
G A C

GAM81 KIAA1399 3' GTTCTGCTATTTCCAATCAGTC 2881 C G T CAA
A C GCTGA TGG AAA CAGAAC
| ||||| ||| |||||
A TGA CT ACC TTT GTCTTG
C A _ ATC

GAM81 MIC2L1 3' TCTGTTGTCAGAGGCTCACGG 2205 C GGTA
CCG TGAGT ACAACAGA
||| ||||| |||||
GGC ACTCG TGTTGTCT
_ GAGAC

GAM81 RASGRF2 3' TTCTGTTAGAACTCAGGG 2590 G GGTAAC
CC CTGAGT AACAGAA
|| ||||| |||||
GG GACTCA TTGTCTT
_ AGA__

GAM81 TJP2 3' CTGTTACTTGCTTCAGTGG 2534 GT AC
CCGCTGA GGTAAC AACAG
||||| ||||| |||||

			GGTGA	CT	TCGTT	TTGTC		
			__		CA			
GAM81	LOC202020	3'	TTCTGTTGCCTAAGGCAGC	3459	AG_	TAAA		
			GCTG	TGG	CAACAGAA			
			CGAC	ATC	GTTGTCTT			
			GGA	C__				
GAM81	LOC220766	5'	TCTGGATTTCACCACTCAGAGG	3499	G	AAACAA		
			CC	CTGAGTGGT	CAGA			
			GG	GA	CTCACCA	GTCT		
			A	CTTTAG				
GAM81	LOC256277	3'	CTGTTGTTTCAGCAGTG	3664	AG	TAA		
			CGCTG	TGG	ACAACAG			
			GTGAC	ACT	TGTTGTC			
			G_	__				
GAM81	LOC256337	3'	CTGTTGTTTCAGCAGTG	3663	AG	TAA		
			CGCTG	TGG	ACAACAG			
			GTGAC	ACT	TGTTGTC			
			G_	__				
GAM82	PTCRA	3'	ATGACTGAGAACATTAAA	2433	ATC			
			TTTAAT	CTCAGTCAT				
			AAATTA	GAGTCAGTA				
			CAA					
GAM82	PUNC	3'	ATGACTTGGA	ACTGAACTAAC	3469	ATA	TC	
			GTTAGTTTA	TCC	AGTCAT			
			CAATCAAGT	AGG	TCAGTA			
			CA_	T_				
GAM82	KIAA0940	3'	ACTGATATATTATAAACTAAC	1586	__	CC		
			GTTAGTTTA	ATAT	TCAGT			
			CAATCAAAT	TATA	AGTCA			
			AT	T_				
GAM82	RGS18	3'	ATGACTGAGAAATAAGATCCAC	2398	TA	AA	C	
			GT	GTTT	TAT	CTCAGTCAT		
			CA	TAGA	ATA	GAGTCAGTA		
			CC	__	A			
GAM83	ATP12A	3'	CCCTGCAGTGCAGACATCGTCA	846	A	A	C	TT
	A		TTGATGAT	TCT	CAT	GT	GG	
			AACTGCTA	AGA	GTG	CG	CC	
			C	C	A	TC		
GAM83	CRYGS	3'	CCAAATAGGCATCATCAA	1722	AT	ACATC		
			TTGATGAT	CT	GTTTGG			

AACTACTA GA TAAACC
 CG _____
 GAM83 LPIN2 3' TCCAAAGTTAATTGTAAACATC 1514 ATC TCG____
 ATCAG TTGATGAT TACA TTTGGA
 ||||| ||| |||||
 GACTACTA ATGT AAACCT
 CAA TAATTG
 GAM83 KIAA1786 3' TCCATGCTGTAGATACCA 2738 A TC T
 TG TATCTACA GT TGGA
 || ||||| || |||||
 AC ATAGATGT CG ACCT
 C _ T
 GAM83 LOC222008 3' CCAAGTTAGATGTCATCAA 3629 CATCG
 TTGATGATATCTA TTTGG
 ||||| |||||
 AACTACTGTAGAT GAACC
 T____
 GAM83 LOC90639 5' TCTGAACACAGATATCATCAG 2663 ACATC TG
 TTGATGATATCT GTT GA
 ||||| ||| ||
 GACTACTATAGA CAA CT
 CA__ GT
 GAM84 AP1B1 3' GTCAGGATTGAAAGCTG 803 C ATA
 TAGCTTTCA TC TGAC
 ||||| || |||||
 GTCGAAAGT AG ACTG
 T G__
 GAM84 IQGAP1 3' GTCATTTAGAAGTGGAAGCTA 2840 _ AT_
 TAGCTTTCACT C ATGAC
 ||||| | |||||
 ATCGAAGGTGA G TACTG
 A ATT
 GAM84 PDE6A 3' GTCATAGGATTTGAAAGCTG 744 C_ A
 TAGCTTTCA TC TATGAC
 ||||| || |||||
 GTCGAAAGT AG ATACTG
 TT G
 GAM84 PTEN 3' CATATAAATGTGGAGGCTA 728 TC__
 TAGCTTTCACT ATATG
 ||||| |||||
 ATCGGAGGTG TATAC
 TAAA
 GAM84 SH3GL2 3' TCATGTGGAGTGAAAGGC 985 _ _
 GC TTTCACCTC ATATGA
 || ||||| |||||
 CG AAAGTGAG TGTACT
 G G
 GAM84 C1orf16 3' CATGGGAAGTGAAAGCTG 1567 _ A
 TAGCTTTCACT C TATG
 ||||| | |||||

			GTCGAAAGTGA G GTAC		
			A G		
GAM84	DKFZp547A023	3'	GTCATATAAATGAGTGAAA	2956	_____
			TTTCACTCA TATGAC		
			AAAGTGAGT ATACTG		
			AAAT		
GAM84	FLJ11850	5'	GTCATATGTGGCAGCT	2001	T TC
			AGCT TCAC ATATGAC		
			TCGA GGTG TATACTG		
			C _		
GAM84	FLJ12888	3'	GTCATATTTTTGAAAGTTA	2115	CTC
			TAGCTTTCA ATATGAC		
			ATTGAAAGT TATACTG		
			TTT		
GAM84	FLJ21596	3'	GTCATTGCATGGTGAAAGC	2092	T _
			GCTTTCAC CAT ATGAC		
			CGAAAGTG GTA TACTG		
			_ CGT		
GAM84	KIAA1878	3'	GTCACAGATTTTGAAAGCTA	3539	C_ ATA
			TAGCTTTCA TC TGAC		
			ATCGAAAGT AG ACTG		
			TTT AC_		
GAM84	NXPH3	3'	GTCATGGGAGGAAGCTA	2728	A TA
			TAGCTTTC CTCA TGAC		
			ATCGAAGG GGGT ACTG		
			A _		
GAM84	SS18L1	3'	GTCATATGAATGTTGAGC	2719	T_ C
			GCTT CA TCATATGAC		
			CGAG GT AGTATACTG		
			TT A		
GAM84	SYT13	3'	CAGATGCAGAGAAAGCTA	3605	A _ A
			TAGCTTTC CT CAT TG		
			ATCGAAAG GA GTA AC		
			A C G		
GAM84	LOC134301	3'	GTCATATGTTAAAGAGCTA	3016	CACT
			TAGCTTT CATATGAC		
			ATCGAGA GTATACTG		
			AATT		
GAM84	LOC151438	3'	GTCATTTCTGATGAAAGCTG	3346	C T_
			TAGCTTTCA TCA ATGAC		

			GTCGAAAGT AGT TACTG		
			_ CTT		
GAM84	LOC158696	3'	TCATATGAAGAAAGCTA 3223	AC	
			TAGCTTTC TCATATGA		
			ATCGAAAG AGTATACT		
			A_		
GAM84	LOC221975	3'	GTCATATGACAGGGCTG 3570	CAC	
			TAGCTTT TCATATGAC		
			GTCGGGA AGTATACTG		
			C_		
GAM84	LOC84549	3'	GTCAAGTGGAAAGCTA 2256	ACT A	
			TAGCTTTC CAT TGAC		
			ATCGAAAG GTG ACTG		
			_ A		
GAM84	LOC90459	3'	TCATATAGGGTGAAAAGC 2644	- -	
			GCTTT CACTC ATATGA		
			CGAAA GTGGG TATACT		
			A A		
GAM84	LOC90529	3'	GTCTACTGGGCGAAAGCTA 2652	A TAT	
			TAGCTTTC CTCA GAC		
			ATCGAAAG GGGT CTG		
			C CAT		
GAM85	F2RL3	3'	TGGTGAAATCCTATCTCT 1074	AG ATGTAA	
			AGA TAGGATT CATCA		
			TCT ATCCTAA GTGGT		
			CT A_____		
GAM85	RAP1B	3'	ATGTTACAACACTACTTT 1642	GATTA	
			GAAGTAG TGTAACAT		
			TTTCATC ACATTGTA		
			A_____		
GAM85	SLC6A12	3'	TTGCCATCCTGCTTCT 988	TAT	
			AGAAGTAGGAT GTAA		
			TCTTCGTCCTA CGTT		
			C_		
GAM85	ALDH5A1	3'	TGCAAATCCTACCCCTG 799	AA A	
			CAG GTAGGATT TGTA		
			GTC CATCCTAA ACGT		
			CC _		
GAM85	C20orf112	3'	TGATGTTAGAATCCCAC 2379	A ATG	
			GT GGATT TAACATCA		

			CA CCTAA ATTGTAGT		
			C G__		
GAM85	DICER1	3'	GATGCCACATAGTCTTGC	2152	AA
			GTAGGATTATGT CATC		
			CGTTCTGATACA GTAG		
			CC		
GAM85	DKFZP566G1424	5'	TGATGTTAGAATCCAC	3320	A ATG
			GT GGATT TAACATCA		
			CA CCTAA ATTGTAGT		
			C G__		
GAM85	FLJ10858	3'	ATGTTTGGTCCTCCTCTG	1805	A T TGT
			CAGA G AGGATTA AACAT		
			GTCT C TCCTGGT TTGTA		
			_ C _		
GAM85	FLJ13265	3'	TGATGTTACTTGCCACCTACTT	2100	ATTAT_
	C		GAAGTAGG GTAACATCA		
			CTTCATCC CATTGTAGT		
			ACCGTT		
GAM85	FLJ22282	3'	TGATGTGGAAACCTACTTCTG	2089	A ATGTA
			CAGAAGTAGG TT ACATCA		
			GTCTTCATCC AA TGTAGT		
			A GG__		
GAM85	GBTS1	3'	GATGTTGCCTCCTCTCCTG	2516	A T TTAT
			CAG AG AGGA GTAACATC		
			GTC TC TCCT CGTTGTAG		
			C _ C__		
GAM85	KIAA0193	3'	TGATGTCCTAGTCCTACCACT	1545	AA TGTA
			AG GTAGGATTA ACATCA		
			TC CATCCTGAT TGTAGT		
			AC CC__		
GAM85	KIAA1030	3'	TGATGCCCTGTCCTCACCTCTG	3597	A _ TATGTAA
			CAGA GT AGGAT CATCA		
			GTCT CA TCCTG GTAGT		
			C C TCCC__		
GAM85	OR7C1	3'	ATGTTTCATGCATCCATACTTC	1719	_ _ T
	TG		CAGAAGTA GGAT TATG AACAT		
			GTCTTCAT CCTA GTAC TTGTA		
			A C T		
GAM85	PRO2214	3'	TATGTAAATCCTACTTTTG	1834	_
			CAGAAGTAGGATT ATGTA		

			GTTTTTCATCCTAA TGTAT		
			A		
GAM85	SMCR5	3'	ACATGGGGAGATCCTACCTCT 2502	A	_____
			AGA GTAGGATT ATGT		
			TCT CATCCTAG TACA		
			C AGGGG		
GAM85	SSH1	3'	ACATTAAGTCCTACCTCTG 1869	A	___
			CAGA GTAGGATT ATGT		
			GTCT CATCCTGA TACA		
			C AT		
GAM85	TERA	3'	TGGATCATCTCTACTTCTG 1948		_ T G
			CAGAAGTAG GAT AT TA		
			GTCTTCATC CTA TA GT		
			T C G		
GAM85	WBSCR23	5'	ATATAGTGAGACCCTATTTCT 2131		_____
			AGAAGTAGG ATTATGT		
			TCTTTATCC TGATATA		
			CAGAG		
GAM85	LOC134637	3'	ATGTTACATGCACCTTC 3017	AGT	AT
			GA AGG TATGTAACAT		
			CT TCC GTACATTGTA		
			___ AC		
GAM85	LOC146745	5'	GATGCCGAGGACATCTTACTCC 3098	A	TATGTAA_
	TG		CAG AGTAGGAT CATC		
			GTC TCATTCTA GTAG		
			C CAGGAGCC		
GAM85	LOC153416	3'	ATGTTACAACACTACTTT 2573		GATTA
			GAAGTAG TGTAACAT		
			TTTCATC ACATTGTA		
			A_____		
GAM85	LOC157867	5'	TGATTCAACAATCTTACTCCTG 3383	A	TA AAC
			CAG AGTAGGAT TGT ATCA		
			GTC TCATTCTA ACA TAGT		
			C _ ACT		
GAM85	LOC201243	5'	GATGCCGAGGACATCTTACTCC 3425	A	TATGTAA_
	TG		CAG AGTAGGAT CATC		
			GTC TCATTCTA GTAG		
			C CAGGAGCC		
GAM86	OSR1	3'	CGTTAGTAAACTTACTTCATA 1188	AG_	CT
			TATGAAGTAA TAT ACG		

			ATACTTCATT ATG TGC		
			CAA AT		
GAM86	PACE4	5'	CGCAGGCCCTTTACTTCA 2435	TA	A
			TGAAGTAAAG TCT CG		
			ACTTCATTTC GGA GC		
			CC C		
GAM86	KIAA1462	3'	CGTATGATTTTATTTTATA 3522	ATC	
			TATGAAGTAAAGT TACG		
			ATACTTTATTTTA ATGC		
			GT_		
GAM86	LOC145945	3'	TCATAGATACAATACTTTA 3280	AA	C
			TGAAGTA GTATCTA GA		
			ATTTTCAT CATAGAT CT		
			AA A		
GAM86	LOC219401	5'	TCGTGGGCCCGCACTTCATA 3580	AAAGTA	
			TATGAAGT TCTACGA		
			ATACTTCA GGGTGCT		
			CGCCC_		
GAM87	ABCA1	3'	TGGTGGCAGTAACATGCAAC 1219	T	CA
			GTT GCATGTTAC CTATCA		
			CAA CGTACAATG GGTGGT		
			_ AC		
GAM87	CD2AP	3'	ATAATGGTAATAGGAAAAC 1408	GCA	C
			GTTT TGTTACCA TAT		
			CAAA ATAATGGT ATA		
			AGG A		
GAM87	HHIP	5'	TGACACTGGCACAACCTGCAAAC 1989	T	A__ CTA
	GG		CCGTTTGCA GTT CCA TCA		
			GGCAAACGT CAA GGT AGT		
			_ CAC CAC		
GAM87	AKAP7	3'	TGATAGTGTCTGCACAAC 1159	_	TGTTAC
			GTT TGCA CACTATCA		
			CAA ACGT GTGATAGT		
			C CT____		
GAM87	AKAP7	3'	TGATAGTGTCTGCACAAC 1683	_	TGTTAC
			GTT TGCA CACTATCA		
			CAA ACGT GTGATAGT		
			C CT____		
GAM87	AKAP7	3'	TGATAGTGTCTGCACAAC 2446	_	TGTTAC
			GTT TGCA CACTATCA		

			CAA ACGT	GTGATAGT		
			C	CT____		
GAM87	ARHGAP5	3'	TTGATAATGTTGTGCAAAGG	3077	G	TTAC C
			CC TTTGCATG	CA TATCAA		
			GG AAACGTGT	GT ATAGTT		
			_	T__ A		
GAM87	C22orf19	3'	TGACAGTGCAAGTGC	1048	GTTAC	A
			GTTTGCAT	CACT TCA		
			CAAACGTG	GTGA AGT		
			AC__	C		
GAM87	DKFZp566D234	3'	GACAGTGGTAAGTAAA	2611	ATG	A
			TTTGC	TTACCACT TC		
			AAATG	AATGGTGA AG		
			__	C		
GAM87	FLJ11160	3'	TGACAGCGAGATGCAAGC	1815	G	ACCA A
			GTTTGCAT TT	CT TCA		
			CGAACGTA AG	GA AGT		
			G C__	C		
GAM87	FLJ13089	5'	TTGACAATGGTAATAATAAAAT	2899	GCA	CTA
			GG	CCGTTT TGTTACCA TCAA		
			GGTAAA	ATAATGGT AGTT		
			ATA	AAC		
GAM87	FLJ14297	3'	ATAGTTTAAACATGCAAC	2107	T	ACC
			GTT GCATGTT	ACTAT		
			CAA CGTACAA	TGATA		
			_	ATT		
GAM87	HSPC065	3'	TGACAGTGGTAGAATAAAGG	1483	G	CATG A
			CC TTTG	TTACCACT TCA		
			GG AAAT	GATGGTGA AGT		
			_	AA__ C		
GAM87	LOC150737	3'	TGATAGTGGCATTATCAAATG	3149	C	TTA_
			G	CCGTTTG ATG CCACTATCA		
			GGTAAAC TAT	GGTGATAGT		
			_	TTAC		
GAM87	LOC152185	3'	ATAATGGTAATGCAAATCA	2498	C	GT C
			C GTTTGCAT	TACCA TAT		
			A TAAACGTA	ATGGT ATA		
			C	_ A		
GAM88	DAAM2	3'	ACCAACTGGGGAAGTGTG	3560	_	C
			TACAGTTCCTT	GTT GT		

			GTGTCAAGGGG CAA CA		
			T C		
GAM88	FN14	3'	TGACTAAGGAAGTGCAGC 1703	A	TTC
			GCT CAGTTCCTTG GTCG		
			CGA GTCAAGGAAT CAGT		
			C ____		
GAM88	TM4SF2	3'	TGTTTTAAAAAGGAAGTGCAGC 1131	A	GTTTCGTC
			GCT CAGTTCCTT GACA		
			CGA GTCAAGGAA TTGT		
			C AAATT__		
GAM88	WNT3	3'	GTCAGACAGCAAGGAAGTGT 2159	C	_
			ACAGTTCCTTGTT GTC GAC		
			TGTCAAGGAACGA CAG CTG		
			_ A		
GAM88	GLTP	3'	GCCAACGAGGAACACAGC 1686	ACA	C
			GCT GTTCCTTGTT GT		
			CGA CAAGGAGCAA CG		
			CA_ C		
GAM88	PRO0149	5'	GTCCCAAAAACTGTAGT 1473	CC	TTCGTC
			GCTACAGTT TTG GAC		
			TGATGTCAA AAC CTG		
			AA C_____		
GAM89	LAMP2	3'	AGTACTAAAATTAATGCA 1455	T	
			TGCATTAATTTT GTATT		
			ACGTAATTAAAA CATGA		
			T		
GAM89	DKFZp762K2015	3'	AGAATCCATGCTAAAAATTAA 2949	_	T
			TTAATTTT GTAT GATTCT		
			AATTAAAA CGTA CTAAGA		
			T C		
GAM89	FLJ10921	5'	AGAATCAATACTACAAGTGC 1808	TTAATTTT	
			TGCA GTATTGATTCT		
			ACGT CATAACTAAGA		
			CAACAT__		
GAM89	LOC91752	3'	AATCAATACAATATATGC 2778	TAATTT	
			GCAT TTGTATTGATT		
			CGTA AACATAACTAA		
			TAT__		
GAM90	GLP1R	3'	AGACACATGGCTATCCTAGAG 896	C	A
			TTTTG GATAGCCATGT TCT		

			GAGAT CTATCGGTACA AGA	
			C C	
GAM90	FLJ10891	3'	TACAGCCATTGCAAAACA 1806	A CA
			TGTTTTGCGAT GC TGTA	
			ACAAAACGTTA CG ACAT	
			C _	
GAM90	KIAA0781	3'	CAAGGCCATCACAAAGCA 2793	C A A
			TGTTTTG GAT GCC TG	
			ACGAAAC CTA CGG AC	
			A C A	
GAM90	KIAA1077	3'	CATGGCCACCGCAGAACA 2963	ATA
			TGTTTTGCG GCCATG	
			ACAAGACGC CGGTAC	
			CAC	
GAM90	PELI2	3'	ATACATGGGACTTCACAAACA 1950	T C TAG_
			TGTTT G GA CCATGTAT	
			ACAAA C CT GGTACATA	
			_A TCAG	
GAM91	GPRK6	3'	GAGGAGCCACTGCCAAACT 898	CTA AGA
			AGTTTGGCAG GC TTC	
			TCAAACCGTC CG GAG	
			AC_ AG_	
GAM91	WWP1	5'	GTTTCTAGTGCCAAACTTA 3164	G C
			TAAGTTTGGCA CTAG AGAT	
			ATTCAAACCGT GATC TTTG	
			- -	
GAM91	LOC144559	5'	TGAATCTGCCAGCACCATAACT 3067	_ CA A
	T		AAGTT TGG GCT GCAGATTCA	
			TTCAA ACC CGA CGTCTAAGT	
			T A_ C	
GAM91	LOC200163	3'	TGCTAATGCCAAACTTA 3440	GC
			TAAGTTTGGCA TAGCA	
			ATTCAAACCGT ATCGT	
			A_	
GAM91	LOC219918	5'	TGAATCTGCCAGCACCAGAACT 3531	_ CA A
	T		AAGT TTGG GCT GCAGATTCA	
			TTCA GACC CGA CGTCTAAGT	
			A A_ C	
GAM91	LOC220071	5'	TGAATCTGCCAGCAGCAGAACT 3603	G A A
	T		AAGTTT GC GCT GCAGATTCA	

			TTCAAG CG CGA CGTCTAAGT		
			A A C		
GAM91	LOC255515	3'	TGAATCTGCCAACACCAGAACT 3689	_	CAGCTA
		T	AAGT TTGG GCAGATTCA		
			TTCA GACC CGTCTAAGT		
			A ACAAC_		
GAM92	BCL11B	3'	ACAAATATCATAAAAGGA 2020	CC G	
			TCCT TA GATATTTGT		
			AGGA AT CTATAAACA		
			AA A		
GAM92	M17S2	5'	GATACCTACAACCTCCTAGGAAG 2213	C	TAT A_
		A	TC TCCTAGGA TTGTA TATC		
			AG AGGATCCT AACAT ATAG		
			A C_ CC		
GAM92	CRFG	3'	ATATTACAAATATTTTGAG 2775	CT	
			CTC AGGATATTTGTAATAT		
			GAG TTTTATAAACATTATA		
			—		
GAM92	FLJ23360	5'	ATATTGCATCCCTAGAGA 2030	_	ATATT
			TC CTAGG TGTAATAT		
			AG GATCC ACGTTATA		
			A CT_		
GAM92	KIAA0349	3'	ATATCACAGAGCCTGGGAG 3561	ATA A	
			CTCCTAGG TTTGT ATAT		
			GAGGGTCC AGACA TATA		
			G_ C		
GAM92	PRO2325	5'	GATATTAACAGTCATCCTAG 1836	AT _	
			CTAGGAT TTGT AATATC		
			GATCCTA GACA TTATAG		
			CT A		
GAM92	SCYA16	3'	ATATTTTCTCAATCTTAGGAGG 1130	ATTTGT	
		A	TCCTCCTAGGAT AATAT		
			AGGAGGATTCTA TTATA		
			ACTCTT		
GAM93	DJ-1	3'	CGTTAGGAATCCATTCTCA 1375	ACTAAA	
			TGAGAAT ATTCCTAACG		
			ACTCTTA TAAGGATTGC		
			CC_		
GAM93	FLJ10535	3'	TAGGAATTTTATTCCCA 1787	A CT	
			TG GAATA AAAATTCCTA		

			AC CTTAT TTTTAAGGAT		
			C _		
GAM93	FLJ10539	3'	AGGATTTTAGTATCCTCA 1788	A	T
			TGAG ATACTAAAAT CCT		
			ACTC TATGATTTTA GGA		
			C _		
GAM93	PIB5PA	3'	TTAGGAATTAAATTCTC 2739	ACTAA	
			GAGAAT AATTCCTAA		
			CTCTTA TTAAGGATT		
			AA _		
GAM93	LOC149351	3'	AGGAGTTTAGTATCCTTA 3130	A	A
			TGAG ATACTAAA TTCCT		
			ATTC TATGATTT GAGGA		
			C _		
GAM93	LOC157858	5'	AGGGGAGTGTTCTCA 3384	AAAA	
			TGAGAATACT TTCCT		
			ACTCTTGTGA GGGGA		

GAM94	DLG5	5'	TGATACAGCACAATAACT 3265	CCAC	C
			AGTTA GTGCTGTA CA		
			TCAAT CACGACAT GT		
			AA _ A		
GAM94	DVL3	3'	CAATAAATGGTAGCTATTA 1112	CG	C
			TAATAGTTACCA TG TG		
			ATTATCGATGGT AT AC		
			AA A		
GAM94	ENPP3	3'	GTACACACAGTGACTATTA 1173	CAC	C
			TAATAGTTAC GTG TGTAC		
			ATTATCAGTG CAC ACATG		
			A _ _		
GAM94	FANCF	3'	TGGTACAACCCAGGGGTAAACT 1998	_	ACGTGC_
	ATTA		TAATAGTT ACC TGTACCA		
			ATTATCAA TGG ACATGGT		
			A GGACCCA		
GAM94	PCDH11X	3'	ACAGCACACAAGTGGCTATTG 2298	CAC_	
			TAATAGTTAC GTGCTGT		
			GTTATCGGTG CACGACA		
			AACA		
GAM94	PCDH11X	3'	ACAGCACACAAGTGGCTATTG 2300	CAC_	
			TAATAGTTAC GTGCTGT		

			GTTATCGGTG CACGACA	
			AACA	
GAM94	PCDH11Y	3'	ACAGCACACAAGTGGCTATTG 2302	CAC_
			TAATAGTTAC GTGCTGT	
			GTTATCGGTG CACGACA	
			AACA	
GAM94	FLJ10539	3'	TACAGTATGACAACTATT 1789	ACCA
			AATAGTT CGTGCTGTA	
			TTATCAA GTATGACAT	
			CA_	
GAM94	FLJ10898	3'	TAGTCATTCGTGGTAACTA 2528	T_
			TAGTTACCACG GCTG	
			ATCAATGGTGC TGAT	
			TTAC	
GAM94	KIAA0680	3'	TGGTACAGTATAGTACCATTA 1530	A T CAC
			TAAT GT AC GTGCTGTACCA	
			ATTA CA TG TATGACATGGT	
			C _ A_	
GAM94	KIAA1804	3'	GCAGTACAGTACTATTA 2868	T CAC
			TAATAGT AC GTGCTGT	
			ATTATCA TG CATGACG	
			_ A_	
GAM94	MO25	3'	TAGTAGTATGTA ACTATTA 1677	C_ G
			TAATAGTTAC AC TGCTG	
			ATTATCAATG TG ATGAT	
			TA _	
GAM94	RAB33B	3'	ACAGCTGTAGTAACTAT 2190	C T
			ATAGTTAC ACG GCTGT	
			TATCAATG TGT CGACA	
			A _	
GAM94	RoXaN	3'	TGGTACAGCACACATGTGAGC 2128	AC C_
			GTT CA GTGCTGTACCA	
			CGA GT CACGACATGGT	
			GT ACA	
GAM95	KIF13A	3'	ACCGCAACA ACTTG GTAGGA 1979	ATAG AT
			TCC TAC AGTTGTTGCGGT	
			AGG ATG TCAACAACGCCA	
			_ GT	
GAM95	LOXL3	3'	ACTCATCAGACCATGCACTATG 2264	A A GT_ C
	GA		TCCATAGT CAT GTT TG GGT	

AGGTATCA GTA CAG AC TCA
 C C ACT _
 GAM95 DKFZp547l014 5' CAGCTAACAATGTACTACAGA 1901 CA A _
 TC TAGTACAT GTT GTTG
 || ||||| || ||||
 AG ATCATGTA CAA CGAC
 AC A T
 GAM95 Spir-1 3' ACCATGAACTCGTACTATG 2699 AT GTTGC
 CATAGTAC AGTT GGT
 ||||| ||| |||
 GTATCATG TCAA CCA
 C_ GTA_
 GAM96 GCLC 3' AATTGTACAATACTTGCATTCC 833 CT__ C
 GGA AGTAT GTACAATT
 || |||| |||||
 CCT TCATA CATGTAA
 TACGT A
 GAM96 FLJ21324 5' AATTGTTGCCTAGTCCTGC 3513 TAT T
 GTAGGACTAG CG ACAATT
 ||||| || |||||
 CGTCCTGATC GT TGTAA
 C_ _
 GAM96 KIAA0193 3' AATTGTGATGTCCTAGTCCTAC 1543 T CG
 GTAGGACTAG AT TACAATT
 ||||| || |||||
 CATCCTGATC TG GTGTAA
 C TA
 GAM96 LOC91097 3' AATTGTTGCCTAGTCCTGC 2705 TAT T
 GTAGGACTAG CG ACAATT
 ||||| || |||||
 CGTCCTGATC GT TGTAA
 C_ _
 GAM97 ADAMTS5 3' TTCAATAGATACCACGAA 1353 GG A
 TTTGTGGTATT AT GAA
 ||||| || |||
 AAGCACCATAG TA CTT
 A_ A
 GAM97 BCRP2 3' TTCTATCCAACATTCAA 2633 T A
 TTG GGT TTGGATAGAA
 ||| || |||||
 AAC TTA AACCTATCTT
 _ C
 GAM97 IL13RA1 3' TCTACTAAAACTACAAA 835 A A
 TTTGTGGT TTGG TAGA
 ||||| ||| |||
 AAACATCA AATC ATCT
 A _
 GAM97 IL1A 3' TCTACCCATATTACAGA 2634 T A
 TTTGTGGTAT GG TAGA
 ||||| || |||

			AGACATTATA CC ATCT	
			C _	
GAM97	ISL1	3'	TCTATTTTGCCACAAG 906	TT
			TTTGTGGTA GGATAGA	
			GAACACCGT TTTATCT	
			—	
GAM97	MITF	3'	TTCTATTTTACAACACTACAAA 721	ATT_
			TTTGTGGT GGATAGAA	
			AAACATCA TTTATCTT	
			ACAT	
GAM97	NCF2	3'	TTCTGTGTCATACCACAA 742	T _
			TTGTGGTAT GG ATAGAA	
			AACACCATA CT TGTCTT	
			_ G	
GAM97	NEDD4L	3'	TTCTACTCAACTACAAA 1618	AT GA
			TTTGTGGT TG TAGAA	
			AAACATCA AC ATCTT	
			_ TC	
GAM97	NR3C1	3'	TTCTATCCTACAACAAG 717	G TT
			TTTGT GTA GGATAGAA	
			GAACA CAT CCTATCTT	
			A _	
GAM97	PDK4	3'	TTCTATTTTCCCCACAAA 3733	TATT
			TTTGTGG GGATAGAA	
			AAACACC TTTATCTT	
			CCT_	
GAM97	PSEN1	3'	TTCTACTTTGCCACAGA 1393	TT A
			TTTGTGGTA GG TAGAA	
			AGACACCGT TC ATCTT	
			T_ _	
GAM97	RAG1	3'	TTCTTTCCACCACAAA 746	ATT T
			TTTGTGGT GGA AGAA	
			AAACACCA CCT TCTT	
			_ T	
GAM97	SYNGR1	3'	TTCTGTGCCCACCACAAG 1148	ATT _
			TTTGTGGT GG ATAGAA	
			GAACACCA CC TGTCTT	
			C_ G	
GAM97	TOX	5'	TTCTTAAACAAACCACAAA 1534	A GAT_
			TTTGTGGT TTG AGAA	

			AAACACCA AAC TCTT		
			_ AAAT		
GAM97	TRPC6	3'	TTCTATCCTTCTACCCAAA 1135	T	TT_
			TTTG GGTA GGATAGAA		
			AAAC CCAT CCTATCTT		
			_ CTT		
GAM97	AF9Q34	3'	TTCTACACACTCAGCCACAAA 2258	AT_	GA
			TTTGTGGT TG TAGAA		
			AAACACCG AC ATCTT		
			ACTC AC		
GAM97	C1QR1	3'	TTCCATCCTCATCACAAG 1402	ATT	A
			TTTGTGGT GGAT GAA		
			GAACACTA CCTA CTT		
			CT_ C		
GAM97	FLJ10193	3'	TCTGACAGATACCACGAA 1775	GGA	
			TTTGTGGTATT TAGA		
			AAGCACCATAG GTCT		
			ACA		
GAM97	FLJ10989	3'	CTATTTACTGATCACAAA 1810	AT_	
			TTTGTGGT TGGATAG		
			AAACACTA ATTTATC		
			GTC		
GAM97	FLJ20700	3'	TTCTACCAAAACTACAAA 1767	A	A
			TTTGTGGT TTGG TAGAA		
			AAACATCA AACC ATCTT		
			A _		
GAM97	FLJ31101	3'	TTCTATCTAGCACAA 1772	GTA	
			TTGTG TTGGATAGAA		
			AACAC GATCTATCTT		
			—		
GAM97	KIAA0252	3'	TCTACTAAAACACTACAAA 2638	A	A
			TTTGTGGT TTGG TAGA		
			AAACATCA AATC ATCT		
			A _		
GAM97	KIAA0416	3'	TCATTTCAAACCACAAA 1638	A	TA
			TTTGTGGT TTGGA GA		
			AAACACCA AACTT CT		
			_ TA		
GAM97	KIAA0445	5'	TCTACTAAAACACTACAAA 1519	A	A
			TTTGTGGT TTGG TAGA		

			AAACATCA AATC ATCT		
			A _		
GAM97	KIAA0493	5'	TTCTACTTCCACCACAAG 2683	ATT	__
			TTTGTGGT GGA TAGAA		
			GAACACCA CCT ATCTT		
			__ TC		
GAM97	KIAA0753	3'	TCTATTTTCATACCACAAA 1553	TG	
			TTTGTGGTAT GATAGA		
			AAACACCATA TTATCT		
			CT		
GAM97	KIAA0781	3'	TTCTGCCCCACCACAAA 2794	ATT	A
			TTTGTGGT GG TAGAA		
			AAACACCA CC GTCTT		
			CC_ _		
GAM97	KIAA0825	3'	TTCTATCTAACACATAA 2589	GTA	
			TTGTG TTGGATAGAA		
			AATAC AATCTATCTT		
			AC_		
GAM97	KIAA0831	3'	TTCTATCCGGTAGTCACAAA 1590		_
			TTTGTGG TATTGGATAGAA		
			AAACACT ATGGCCTATCTT		
			G		
GAM97	KIAA1172	3'	TTCTATTTAAAAATAGCCACAA 2897	A	_____
	A		TTTGTGGT TTGGATAGAA		
			AAACACCG AATTTATCTT		
			ATAAA		
GAM97	KR18	3'	TTCTATCCAATTTGTGAA 2325	TG T	
			TTTG G ATTGGATAGAA		
			AAGT T TAACCTATCTT		
			GT_		
GAM97	MAPK13	3'	TCTAACGAATTACCACAAA 953		__ GA
			TTTGTGGTA TTG TAGA		
			AAACACCAT AGC ATCT		
			TA A_		
GAM97	MGC11386	3'	TCTACTAAAACTACAAA 2296	A	A
			TTTGTGGT TTGG TAGA		
			AAACATCA AATC ATCT		
			A _		
GAM97	PRO0641	3'	TCTGCCAATAACCACAAA 1477		_ A
			TTTGTGGT ATTGG TAGA		

			AAACACCA TAACC GTCT	
			A _	
GAM97	PRO0902	3'	TCTACCTTTGCCACAAG 2358	TT A
			TTTGTGGTA GG TAGA	
			GAACACCGT CC ATCT	
			TT _	
GAM97	SMAP-5	3'	TCTACTAAAACTACAAA 2168	A A
			TTTGTGGT TTGG TAGA	
			AAACATCA AATC ATCT	
			A _	
GAM97	SPRY4	3'	TCTACTAAAACTACAAA 2177	A A
			TTTGTGGT TTGG TAGA	
			AAACATCA AATC ATCT	
			_ _	
GAM97	USP24	3'	TCTACGATGCTACAAA 3512	GA
			TTTGTGGTATTG TAGA	
			AAACATCGTAGC ATCT	
			_	
GAM97	ZNF304	3'	TTCATTGTATACCACAA 1921	TG A
			TTGTGGTAT GAT GAA	
			AACACCATA TTA CTT	
			TG _	
GAM97	LOC121344	3'	TCTACCTCAGTTTGCCACAAA 2990	TT___ A
			TTTGTGGTA GG TAGA	
			AAACACCGT CC ATCT	
			TTGACT _	
GAM97	LOC144266	5'	TTCTGTCCCACCAGAAA 3065	G ATT
			TTT TGGT GGATAGAA	
			AAA ACCA CCTGTCTT	
			G C_	
GAM97	LOC145241	3'	CTTACGTCAGTACCACAAA 2640	AT__
			TTTGTGGTATTGG AG	
			AAACACCATGACT TC	
			GCAT	
GAM97	LOC148545	5'	TCTACCTCTTCTGCCACAAA 3120	TT _
			TTTGTGGTA GGA TAGA	
			AAACACCGT TCT ATCT	
			CT CC	
GAM97	LOC149073	5'	TTCTGATGACAAACCACAAA 3305	A GA__
			TTTGTGGT TTG TAGAA	

		AAACACCA AAC GTCTT	
		_ AGTA	
GAM97	LOC149448 3'	CTGTAACAAAATACCACAAA 3309	GG__
		TTTGTGGTATT ATAG	
		AAACACCATAA TGTC	
		AACAA	
GAM97	LOC149579 5'	TCTACTAAAACTACAAA 2907	A A
		TTTGTGGT TTGG TAGA	
		AAACATCA AATC ATCT	
		A _	
GAM97	LOC152641 5'	TTCTAGGGAAACCACAAA 3173	A GGA
		TTTGTGGT TT TAGAA	
		AAACACCA AG ATCTT	
		A GG_	
GAM97	LOC169966 3'	TTCTATCATCATCTACTACAAA 3253	TTG__
		TTTGTGGTA GATAGAA	
		AAACATCAT CTATCTT	
		CTACTA	
GAM97	LOC222234 3'	TCTGTAACAAATTACCACAAA 3647	_ G_
		TTTGTGGTA TTG ATAGA	
		AAACACCAT AAC TGTCT	
		TA AA	
GAM97	LOC254058 3'	TTCTAACCACCACAAG 3735	ATT A
		TTTGTGGT GG TAGAA	
		GAACACCA CC ATCTT	
		_ A	
GAM97	LOC51110 3'	TTCTGGTATACCACAAA 1657	TGGA
		TTTGTGGTAT TAGAA	
		AAACACCATA GTCTT	
		TG_	
GAM97	LOC51292 3'	TCTATCTGCACACACAAA 1698	_ ATT
		TTTGTG GT GGATAGA	
		AAACAC CA TCTATCT	
		A CG_	
GAM97	LOC92573 5'	TTCTGGCCACCACAGA 2870	ATT A
		TTTGTGGT GG TAGAA	
		AGACACCA CC GTCTT	
		_ G	
GAM98	AVP 5'	AGCTCCTAGGCCAGGGCCTGTC 752	A AGA_
		GACAG CC CCTAGGAGCT	

			CTGTC GG GGATCCTCGA			
			C GACC			
GAM98	HTRA3	3'	CTGCAGGTCTGGGCTGCCA 3457	A A	A_	
			TG CAG CCAGACCT GG			
			AC GTC GGTCTGGA TC			
			C G CG			
GAM98	LGALS3BP	3'	AGCCCCTGGTCAGTCTG 2851	CA T A		
			CAGAC GACC AGG GCT			
			GTCTG CTGG TCC CGA			
			A_ _ C			
GAM98	MAD2L1	3'	TAGCTCCTTTTGACCTTCA 921	C AC	CCT	
			TGA AG CAGA AGGAGCTA			
			ACT TC GTTT TCCTCGAT			
			_ CA _			
GAM98	PYGM	5'	TAGCTCCCTGAGCTGCCA 1230	A AC	ACCTA	
			TG CAG CAG GGAGCTA			
			AC GTC GTC CCTCGAT			
			C GA _			
GAM98	SLC35A3	3'	TTCTGGGTCTGATCTGTCA 1418	C		
			TGACAGA CAGACCTAGGA			
			ACTGTCT GTCTGGGTCTT			
			A			
GAM98	ATPAF1	3'	ATAGCTCCCAAATGATGAGTTT 2583	_ GACCTA_		
			GTCA TGACAGAC CA GGAGCTAT			
			ACTGTTTG GT CCTCGATA			
			A AGTAAAC			
GAM98	C7orf13	3'	CTTAAGTCTGGTCCCTCA 2265	CA C		
			TGA GACCAGAC TAGG			
			ACT CTGGTCTG ATTC			
			CC A			
GAM98	CBLC	3'	CTGCCAAGCCTGGTCTGTCA 1407	AC A _		
			TGACAGACCAG CT GG AG			
			ACTGTCTGGTC GA CC TC			
			C_ A G			
GAM98	FLJ10241	3'	AGCTCCTGTCACCCTGTCA 1776	ACCA CT		
			TGACAG GAC AGGAGCT			
			ACTGTC CTG TCCTCGA			
			CCA_ _			
GAM98	FLJ20651	3'	CCAAGCTTGGTCTGTCA 1761	AC A		
			TGACAGACCAG CT GG			

			ACTGTCTGGTT GA CC	
			C_ A	
GAM98	KIAA1203	3'	CTTCAGATCCTGTCTGTCA 2922	CA C A
			TGACAGAC GA CT GGAG	
			ACTGTCTG CT GA CTTC	
			TC A _	
GAM98	PL6	3'	AGCTCCTGGGCGGCCCTCA 1348	CAGA AGA
			TGA CC CCTAGGAGCT	
			ACT GG GGGTCCTCGA	
			CCC_ CC_	
GAM98	SRCRB4D	3'	AGCTCCTACCTTGGGCCCTCA 2386	CAGA ACC
			TGA CCAG TAGGAGCT	
			ACT GGTT ATCCTCGA	
			CCCG CC_	
GAM98	SYNPO2	3'	AGCAGCTCTGGTCTGTCA 2928	C AGGA
			TGACAGACCAGA CT GCT	
			ACTGTCTGGTCT GA CGA	
			C _	
GAM98	LOC145858	5'	CCTAGGTCTGGCCTTCA 3085	C A
			TGA AG CCAGACCTAGG	
			ACT TC GGTCTGGATCC	
			_ C	
GAM98	LOC151162	5'	AGCTCCTAGAGGCTGCTCA 3338	_ A AGAC
			TGA CAG CC CTAGGAGCT	
			ACT GTC GG GATCCTCGA	
			C _ A_	
GAM98	LOC196410	5'	AGCTCAGAGCTGGTCTGCCA 3411	A AC AG
			TG CAGACCAG CT GAGCT	
			AC GTCTGGTC GA CTCGA	
			C _ GA	
GAM98	LOC203339	5'	AGCTCCTAGGAATTCTCTCA 3489	C CCAGA
			TGA AGA CCTAGGAGCT	
			ACT TCT GGATCCTCGA	
			C TAA_	
GAM98	LOC203377	5'	AGCTCCTAGAGGCTGCTCA 3490	_ A AGAC
			TGA CAG CC CTAGGAGCT	
			ACT GTC GG GATCCTCGA	
			C _ A_	
GAM99	SEL1L	3'	CAAGAAAATTTAAACGATCCC 1179	AA TT
	AA		TTG ATTGTTTT ATTTCTTG	

			AAC TAGCAAAA TAAAAGAAC		
			CC TT		
GAM99	DKFZP564O1863	3'	AAAGTAAATACAATTTCAA 2826	TT	
			TTGAAATTGT TTTATTTT		
			AACTTTAACA AAATGAAA		
			T_		
GAM99	LOC129446	3'	CAAGAAAAATGAGAACATTTTC 3042	T TA	
	AA		TTGAAA TGTTTTT TTTTCTTG		
			AACTTT ACAAGAG AAAAGAAC		
			T TA		
GAM100	CYP19	3'	AAAAAGCAGAGGCCAAGAGTTT 705	ATGAT_ C	
	G		CAAA GCCTCTGC TTTT		
			GTTT CGGAGACG AAAA		
			GAGAAC A		
GAM100	CYP19	3'	AAAAAGCAGAGGCCAAGAGTTT 2185	ATGAT_ C	
	G		CAAA GCCTCTGC TTTT		
			GTTT CGGAGACG AAAA		
			GAGAAC A		
GAM100	F8	3'	AAAGGCAAATCATTTGGA 707	A GCCTC	
			TCCAAA TGAT TGCCTTT		
			AGGTTT ACTA ACGGAAA		
			_ A_		
GAM100	MSR1	3'	AAAAGGCAAAACCTTACCTTGG 2453	AA TGCCTC	
	A		TCCAA TGA TGCCTTTT		
			AGGTT ATT ACGGAAAA		
			CC CCAA_		
GAM100	MSR1	3'	AAAAGGCAAAACCTTACCTTGG 2454	AA TGCCTC	
	A		TCCAA TGA TGCCTTTT		
			AGGTT ATT ACGGAAAA		
			CC CCAA_		
GAM100	PCDHB16	3'	AAAAGGCAAAGGTATTAT 1931	C	
			ATGATGCCT TGCCTTTT		
			TATTATGGA ACGGAAAA		
			A		
GAM100	QPCT	3'	AAAAGTCAAGGCATCATTT 1428	C C	
			AAATGATGCCT TG CTTTT		
			TTTACTACGGA AC GAAAA		
			_ T		
GAM100	TWIST	3'	AAAGGAAAGGCATCACTATGGA 750	AAA CTG	
			TCCA TGATGCCT CCTTT		

			AGGT ACTACGGA GGAAA		
			ATC AA_		
GAM100	ATP9A	3'	AAAGGCAGAGGCATCTTTTCGGA 2617	A T	
			TCC AAA GATGCCTCTGCCTTT		
			AGG TTT CTACGGAGACGGAAA		
			C _		
GAM100	CALN1	3'	CAGAAATATCATCTTGGA 2207	A CC	
			TCCAA ATGATG TCTG		
			AGGTT TACTAT AGAC		
			C AA		
GAM100	FLJ23277	3'	AAAAGGCAGAAATCCATTCA 2238	_ CC__	
			TGA TG TCTGCCTTTT		
			ACT AC AGACGGAAAA		
			T CTAA		
GAM100	KIAA0992	3'	AAAAGGCAGAAACATACCTTTG 1661	ATG CC	
			CAAA ATG TCTGCCTTTT		
			GTTT TAC AGACGGAAAA		
			CCA AA		
GAM100	KIAA1045	3'	AAAAGGCAGAACAGTTTTG 2906	GA CC	
			CAAAAT TG TCTGCCTTTT		
			GTTTTG AC AGACGGAAAA		
			_ A_		
GAM100	KIAA1056	3'	AAAGGCAGAGAGGCCAGGA 1575	AAAA AT _	
			TCC TG GCCTCT GCCTTT		
			AGG AC CGGAGA CGGAAA		
			_ _ GA		
GAM100	KIAA1323	3'	AGGGGAGAGGCACATTTT 2646	A G	
			AAAATG TGCCTCT CCTT		
			TTTTAC ACGGAGA GGGA		
			_ G		
GAM100	LMOD1	3'	AGGTGAAAGGCATCTTTCTG 1409	A T CT_	
			CA AA GATGCCT GCCT		
			GT TT CTACGGA TGGA		
			C T AAG		
GAM100	RNF32	3'	AAAAAGTTTACCATCATTTTGG 2172	CCTCT C	
	A		TCCAAAATGATG GC TTTT		
			AGGTTTTACTAC TG AAAA		
			CATT_ A		
GAM100	SS-56	3'	AAAAAGCAGAGGCCAGTCA 2535	_ C	
			TGAT GCCTCTGC TTTT		

		ACTG CGGAGACG AAAA		
		ACC A		
GAM100	LOC122792 3'	AAAAGTGCCTTGCATCATTT 2518		CTCT _
		AAATGATGC GC CTTTT		
		TTTACTACG CG GAAAA		
		TTC_ T		
GAM100	LOC146512 3'	GCAGTGCAAACATCATTTTGGA 3094		CCT____
		TCCAAAATGATG CTGC		
		AGGTTTTACTAC GACG		
		AAACGT		
GAM100	LOC201633 3'	CAGAGGCATCTTCTGGA 3483	A T	
		TCCA AA GATGCCTCTG		
		AGGT TT CTACGGAGAC		
		C _		
GAM100	LOC202126 3'	AAAAAGCAAGTATCATTTGGA 3486	A CTC C	
		TCCAAA TGATGC TGC TTTT		
		AGGTTT ACTATG ACG AAAA		
		_ A_ A		
GAM100	LOC221755 3'	CAGAGGCGCCATCTTGGA 3563	A A	
		TCCAA ATG TGCCTCTG		
		AGGTT TAC GCGGAGAC		
		C C		
GAM100	LOC257334 3'	GCAGAGGCACCATCTTGG 3734	A A	
		CCAA ATG TGCCTCTGC		
		GGTT TAC ACGGAGACG		
		C C		
GAM101	ANGPT1 3'	ACTGAAACATGCTTACCAGATT 804		CATCTC_
	CA	TGAATC TATGTTTCAGT		
		ACTTAG GTACAAAGTCA		
		ACCATTC		
GAM101	GPR61 5'	ACTGAAATTCAGAAGATTCAC 3123		CATC AT
		GTGAATC TCT GTTTCAGT		
		CACTTAG AGA TAAAGTCA		
		A_ CT		
GAM101	PPP1R12B 3'	ACTGAAACCCGGAACAGATTC 2228		CATC AT
		GAATC TCT GTTTCAGT		
		CTTAG AGG CAAAGTCA		
		ACA_ CC		
GAM101	TRIM9 3'	ACTTCTATATAGAGATAGACTT 1610	A C	TTC
	AC	GTGA TC ATCTCTATGT AGT		

			CATT AG TAGAGATATA TCA	
			C A TCT	
GAM101	YWHAE	3'	ACTGAAACACAGCATGGAATTA 1329	A CT A
			TGA TCCAT CT TGTTTCAGT	
			ATT AGGTA GA ACAAAGTCA	
			A C_ C	
GAM101	AKAP9	3'	ACTGAAATAAAAAATGACTTCAC 1242	TC CTCTA
			GTGAA CAT TGTTTCAGT	
			CACTT GTA ATAAAGTCA	
			CA AAA_	
GAM101	LOC166824	3'	ACTGAAACATAATCAATGGATT 3259	CTC_
	CA		TGAATCCAT TATGTTTCAGT	
			ACTTAGGTA ATACAAAGTCA	
			ACTA	
GAM101	LOC254835	3'	TGAAGCAAGAGACAGACCCAC 3722	AA CA A
			GTG TC TCTCT TGTTTCA	
			CAC AG AGAGA ACGAAGT	
			CC AC _	
GAM102	PNPASE	3'	CTGAGGCAGAAGAATCACTTC 2900	GATG G
			GAAGTGATTCTTT GT TCAG	
			CTTCACTAAGAAG CG AGTC	
			A_ G	
GAM102	SEC24D	3'	CAGTATCAATAAATCACTTC 1559	CT G
			GAAGTGATT TTGATG TG	
			CTTCACTAA AACTAT AC	
			AT G	
GAM102	LOC131000	3'	CTGACCTTGAAATAAATCACTT 3037	CT GAT T
	C		GAAGTGATT TT GG GTCAG	
			CTTCACTAA AA TC CAGTC	
			AT AGT _	
GAM102	LOC151658	5'	GAAGTCTCAAAGCATCACTTC 3349	T T TG
			GAAGTGAT CTTTGA GG TC	
			CTTCACTA GAAACT CT AG	
			C _ GA	
GAM102	LOC257428	3'	GCACTTTCAAAGAATCATCC 3649	A T
			A GTGATTCTTTGA GGTGT	
			C TACTAAGAAACT TCACG	
			C T	
GAM103	CARD15	3'	GTAAATAATCAGAGGGGAATAA 1983	GGA TC
	A		TTTGTT T CTGATTATTAC	

			AAATAA G GACTAATAAATG	
			GG_ GA	
GAM103	CLCN4	3'	AAATAACAGAAAACCCAGCAAA 861	ATTC_ A
			TTTGTTGG CTG TTATTT	
			AAACGACC GAC AATAAA	
			CAAAA _	
GAM103	FGF2	3'	TAAATAATTTTATAATTCAACA 885	CCT_
	AA		TTTGTTGGATT GATTATTTA	
			AAACAACCTTAA TTAATAAAT	
			TATT	
GAM103	ZNF135	3'	TGGTGAGAAACCCAACAAA 1022	A C G
			TTTGTTGG TT CT ATTA	
			AAACAACC AA GA TGGT	
			C A G	
GAM103	SEC15B	3'	AATTAAAAATCCAACAAA 2757	CC
			TTTGTTGGATT TGATT	
			AAACAACCTAA ATTAA	
			AA	
GAM103	ZNF334	3'	AAGTAATAAATTCCAACAAA 1780	TTCCTG
			TTTGTTGGA ATTATTT	
			AAACAACCT TAATGAA	
			TAAA__	
GAM103	LOC158954	3'	TGGTGAGAAATCCAACAAA 2567	C G
			TTTGTTGGATT CT ATTA	
			AAACAACCTAA GA TGGT	
			A G	
GAM103	LOC219686	3'	GTAATTGGAAAAAATCCAATAA 3500	C__ TG
	A		TTTGTTGGATT C ATTAT	
			AAATAACCTAA G TAATG	
			AAAA GT	
GAM103	LOC221510	3'	AAATAATCAAAACCCAACA 3508	A CC
			TGTTGG TT TGATTATTT	
			ACAACC AA ACTAATAAA	
			C A_	
GAM104	PLN	3'	TAATAGCCTACTATTGACC 947	C _
			GG CAATAGTAG CTATTA	
			CC GTTATCATC GATAAT	
			A C	
GAM104	PRRG1	3'	GTAATAGCTCTATCAGCC 789	CA T
			GGC ATAG AGCTATTAC	

CCG TATC TCGATAATG
 AC _
 GAM104 LOC149320 3' GCGGCAGCTACTACTGCC 2892 CAA ATTA
 GGC TAGTAGCT CCGT
 ||| ||||| |||
 CCG ATCATCGA GGCG
 TC_ C__
 GAM104 LOC163782 5' ACGGATGCCACTATTGGGC 3234 G A TATTA
 G CCAATAGT GC CCGT
 | ||||| || |||
 C GGTTATCA CG GGCA
 G C TA__
 GAM105 FLJ12668 3' ACTTGAGCAAATAATTGGGATG 2123 CCAA AG
 A TTATCCCAATTA CT AAGT
 ||||| || |||
 AGTAGGGTTAAT GA TTCA
 AAAC G_
 GAM105 KIAA0016 3' ACTTTTAAGGTAAGTGGGATGA 1542 A AAC
 TTATCCCA TTACC TAGAAGT
 ||||| ||| |||||
 AGTAGGGT AATGG ATTTCA
 C A__
 GAM105 ZAK 3' ACTTCCAGTTTTTGATTGGGA 1708 ACC_ A
 TCCCAATT AACT GAAGT
 ||||| ||| |||||
 AGGGTTAG TTGA CTTCA
 GTTT C
 GAM105 LOC58489 3' TGGTTGGTAATGGAATAA 2952 C A
 TTAT CCA TTACCAACTA
 ||| ||| |||||
 AATA GGT AATGGTTGGT
 A _
 GAM106 IL1R1 3' AGAACATCCTCCAATTCC 782 CG A
 GGAATTGGAGG ATG TCT
 ||||| ||| |||
 CCTTAACCTCC TAC AGA
 _ A
 GAM106 SUFU 3' ATCAGTTCGCCTCCATTCC 1668 T _
 GGAAT GGAGGCGA TGAT
 ||||| ||||| |||
 CCTTA CCTCCGCT ACTA
 _ TG
 GAM106 CGRP-RCP 5' AAGATCATCGCACCCCC 1503 AATT AG
 GG GG GCGATGATCTT
 || || |||||
 CC CC CGCTACTAGAA
 _ CA
 GAM106 LOC152348 5' ATCAGTCACCACCAATTCC 3358 A C _
 GGAATTGG GG GA TGAT
 ||||| || |||

			CCTTAACC CC CT ACTA		
			A A G		
GAM106	LOC158219 3'	ATCATTGCCCCCAACTCC	3214	A A	
		GGA TTGG GGCGATGAT			
		CCT AACC CCGTTACTA			
		C C			
GAM106	LOC255177 3'	AGAATCACCTCTAATCC	3711	A C GA	
		GGA TTGGAGG GAT TCT			
		CCT AATCTCC CTA AGA			
		— A —			
GAM106	LOC90522 3'	AGGCACCGCCTCCATCC	2651	AT A A	
		GGA TGGAGGCG TG TCT			
		CCT ACCTCCGC AC GGA			
		— C —			
GAM107	CEACAM4 3'	CTCTGAGTCCTGAGGAG	860	CC TCGT	
		CTCC TAG ACTCAGAG			
		GAGG GTC TGAGTCTC			
		A_ C_			
GAM107	MGC11115 3'	CTCTGAGGCCAGGGGAGC	2244	AGTC A	
		GCTCCCT GT CTCAGAG			
		CGAGGGGA CG GAGTCTC			
		CC_ _			
GAM107	PRO2714 5'	CTCTAAGCAACAAGGGGAGCG	1837	A C ACTC	
		CGCTCCCCT GT GT AGAG			
		GCGAGGGGA CA CG TCTC			
		A A AA_			
GAM107	LOC147057 3'	CTCTGAGTATTGGGAAGAGAGG	3288	G_ C_ GTC	
	C	GC CTC CCTA GTACTCAGAG			
		CG GAG GGGT TATGAGTCTC			
		GA AA _			
GAM107	LOC147976 3'	CTCTGGTGTGACTAAGGAAAG	3114	CC _ T	
		CT CCT AGTCGTAC CAGAG			
		GA GGA TCAGTGTG GTCTC			
		AA A _			
GAM107	LOC57100 3'	CTCTGAGTACCCTGGCGGGAGG	1917	G _ TC	
	C	GC CTCCC CTAG GTACTCAGAG			
		CG GAGGG GGTC CATGAGTCTC			
		_ C _			
GAM108	E2F3 3'	ACAAACCTCGAAACGAACAGTT	875	TCA A A	
	AA	TTAGCTGTTT TC AG TTTGT			

			AATTGACAAG AG TC AAACA		
			CAA C C		
GAM108	SCML1	3'	ACAGAGAACCAAAACAGCTAA 1328		CATCAAGA
			TTAGCTGTTTT TTTGT		
			AATCGACAAAA AGACA		
			CCAAG__		
GAM108	KIAA1468	3'	ACAAATCCTACAGTCAATAGCT 3541		TTCATCAA
	AA		TTAGCTGTT GATTTGT		
			AATCGATAA CTAAACA		
			CTGACATC		
GAM108	MGC16025	3'	ACAAATCTCCAAGAAAACAGCT 2295		ATCA
			AGCTGTTTTT AGATTTGT		
			TCGACAAAAG TCTAAACA		
			AACC		
GAM108	LOC148545	3'	CTTGATAAAAACAATA 3119	C C	
			TTAG TGTTTT ATCAAG		
			AATC AAAAA TAGTTC		
			A A		
GAM108	LOC163669	5'	ACAAATCTTGACGAACAC 3233	T A	
			GT TTC TCAAGATTTGT		
			CA AAG AGTTCTAAACA		
			C C		
GAM108	LOC51652	3'	ACAAATAAGGAAAACAGCT 1660		ATCAAG
			AGCTGTTTTT ATTTGT		
			TCGACAAAAG TAAACA		
			GAA__		
GAM109	CXCL13	3'	GTTATTCAGTTATAAGTAATA 1299		T
			TATTATTTATAACTGA GTAAC		
			ATAATGAATATTGACT TATTG		
			-		
GAM109	RASGRP1	3'	ATCAGTGGCTTAAATAATA 1241		TA__
			TATTATTTA ACTGAT		
			ATAATAAAT TGAATA		
			TCGG		
GAM109	HTGN29	3'	GGGTCATTATCACTTAAATAAT 1899		TAAC TA_
	A		TATTATTTA TGATG ACCC		
			ATAATAAAT ACTAT TGGG		
			TC__ TAC		
GAM109	KIAA1430	3'	GGACCACATCAGTTGCAA 3179	A	AA_
			TTT TAACTGATGT CC		

		AAA GTTGA	CTACA	GG	
		C	CCA		
GAM109	KIAA1764	5'	GCTTCAGTTATAA	ATAGTA	2850 T
			TATTATTTATAA	CTGA	GT
			ATGATAA	ATTTGACT	CG
			T		
GAM109	ZAK	3'	TATCAGTTTCAA	ATAATA	2428 AT
			TATTATTT	AACTGATG	
			ATAATAAA	TTGACTAT	
			CT		
GAM109	LOC151571	5'	GGTTATATACATCATAA	ATGA	3348 AACTG
			TTATTTAT	ATGTAACC	
			AGTAAATA	TATATTGG	
			CTACA		
GAM109	LOC196989	3'	GGGCACATAGAGCTATAA	ATAA	3470 A G_ AA
			TTATTTATA	CT ATGT	CC
			AATAAATAT	GA TACA	GG
			C GA	CG	
GAM109	LOC221431	3'	TATATCAGGTCATAA	ATAATA	3553 AA_
			TATTATTTAT	CTGATGTA	
			ATAATAAATA	GACTATAT	
			CTG		
GAM110	COL12A1	3'	AACCTCCTTGTTT	TAGACAC	1102 CTAGT
			GTGTCTAA	GGAGGTT	
			CACAGATT	CCTCCAA	
			TTGTT		
GAM110	COL12A1	3'	AACCTCCTTGTTT	TAGACAC	2380 CTAGT
			GTGTCTAA	GGAGGTT	
			CACAGATT	CCTCCAA	
			TTGTT		
GAM110	FLJ25473	5'	AACCTCCGAAAGCTCAGC	CACAC	2496 _ AA_ AG
			GTGT	CT CT TGGAGGTT	
			CACA	GA GA GCCTCCAA	
			C CTC	AA	
GAM111	ANK1	5'	CAGCCCCAGCTGCTCCTC	CCTC	699 A TC C A
			GAGGAGGA	TA GT GG GCTG	
			CTCCTCCT	GT CG CC CGAC	
			C _	A C	
GAM111	ANK1	5'	CAGCCCCAGCTGCTCCTC	CCTC	1918 A TC C A
			GAGGAGGA	TA GT GG GCTG	

			CTCCTCCT GT CG CC CGAC	
			C _ A C	
GAM111	CDH5	3'	CAGCCCAGCACCCCTTCCTCG 857	AATATC C A
			CGAGGAGG GT GG GCTG	
			GCTCCTTC CG CC CGAC	
			CCCA_ A _	
GAM111	DSP	5'	CAGCTCCGACGCAGCTCCTC 1110	GAATAT
			GAGGAG CGTCGGAGCTG	
			CTCCTC GCAGCCTCGAC	
			GAC_	
GAM111	GDF5	3'	AGCCCACCATTTCTCCTC 755	ATC C A
			GAGGAGGAAT GT GG GCT	
			CTCCTCTTTA CA CC CGA	
			C_ _ _	
GAM111	OGDH	3'	CAGCTCTGGCCACAATCCTCC 3510	ATATC
			GGAGGA GTCGGAGCTG	
			CCTCCT CGGTCTCGAC	
			AACAC	
GAM111	RFX2	3'	CAGCCCCGCGCGGCGCCTCCTC 765	AATATC A
	G		CGAGGAGG GTCGG GCTG	
			GCTCCTCC CGGCC CGAC	
			GCGGC_ C	
GAM111	SET7	5'	CAGCCCCGACTGCTCCTCCTC 2153	A TC A
			GAGGAGGA TA GTCGG GCTG	
			CTCCTCCT GT CAGCC CGAC	
			C _ C	
GAM111	C17orf31	3'	CAGCTCCCCCTTCACCCCTCCT 1723	AATATCGTC
	TG		CGAGGAGG GGAGCTG	
			GTTCTCCTC CCTCGAC	
			CCACTTCCC	
GAM111	caspr5	5'	CAGCTCCGAAGAATCCCCCG 2396	A A ATA G
			CG GG GGA TC TCGGAGCTG	
			GC CC CCT AG AGCCTCGAC	
			_ _ A_ A	
GAM111	caspr5	5'	CAGCTCCGAAGAATCCCCCG 2462	A A ATA G
			CG GG GGA TC TCGGAGCTG	
			GC CC CCT AG AGCCTCGAC	
			_ _ A_ A	
GAM111	CECR2	5'	AGCCCCGCCCCCTCCTCG 2192	AATATC T A
			CGAGGAGG G CGG GCT	

		GCTCCTCC	C GCC CGA		
		CC_____C			
GAM111	DKFZP434P0111 3'	CAGCCCCGGCCCATTCCTCC	2790	ATC	A
		GGAGGAAT	GTCCG GCTG		
		CCTCCTTA	CGGCC CGAC		
		CC_	C		
GAM111	FLJ10634 3'	CAGCTCCAGCCATCCACCCCTC	1791	A AAT	C C
		GAGG GG	AT GT GGAGCTG		
		CTCC CC	TA CG CCTCGAC		
		_ ACC	C A		
GAM111	FLJ32334 3'	CTCCAAAACGCTATTCCTTC	2483	T	C__
		GGAGGAATA	CGT GGAG		
		CTTCCTTAT	GCA CCTC		
		C	AAA		
GAM111	FLJ32894 3'	CTCTGGTTTCCTCCTC	2491	TATCG	
		GAGGAGGAA	TCGGAG		
		CTCCTCCTT	GGTCTC		
		T__			
GAM111	KIAA0711 5'	AGTTGGACACACCCCTCCTCG	1572	AATATC	G G
		CGAGGAGG	GTC GA CT		
		GCTCCTCC	CAG TT GA		
		CCACA_	G _		
GAM111	KIAA1649 3'	CAGCTGGAAGACATTCCTCC	2245	A G	GG
		GGAGGAAT	TC TC AGCTG		
		CCTCCTTA	AG AG TCGAC		
		C A G_			
GAM111	KIAA1649 3'	CAGCTGGAAGACATTCCTCC	2770	A G	GG
		GGAGGAAT	TC TC AGCTG		
		CCTCCTTA	AG AG TCGAC		
		C A G_			
GAM111	MGC30052 3'	AGTACATCATTCCTCCTC	2500	ATC	CGGA
		GAGGAGGAAT	GT GCT		
		CTCCTCCTTA	CA TGA		
		CTA	_____		
GAM111	MGC4737 3'	CAGCCCCATCTCCTCCTCCTC	2206	ATATC	C A
		GAGGAGGA	GT GG GCTG		
		CTCCTCCT	TA CC CGAC		
		CCTC_	C _		
GAM111	LOC115110 5'	AGCCCCGGTTCCTCCCG	2923	A	ATCGT A
		CG GGAGGAAT	CGG GCT		

	GC CCTCCTTG GCC CGA	
	C _ _ _ C	
GAM111 LOC123242 5'	CAGCTCCACCATATTTCTCC 3029	C C
	GGAGGAATAT GT GGAGCTG	
	CCTCTTTATA CA CCTCGAC	
	C _	
GAM111 LOC146237 3'	CAGCTCTCACATTCCTTC 3282	ATC C
	GGAGGAAT GT GGAGCTG	
	CTTCCTTA CA TCTCGAC	
	_ _ C	
GAM111 LOC147160 5'	CAGCCCCACTCACTCCTTCTC 3291	ATATC C A
	GAGGAGGA GT GG GCTG	
	CTCTTCCT CA CC CGAC	
	CACT_ C _	
GAM111 LOC149670 5'	CAGCCCTGCCACTCCTTCCTC 3138	_ ATATC C A
	GAGGA GGA GT GG GCTG	
	CTCCT CCT CG CC CGAC	
	T CAC_ T _	
GAM111 LOC155072 3'	CAGCTCCGACCACACCATCCTC 3374	_ AATATC
	GAGGA GG GTCGGAGCTG	
	CTCCT CC CAGCCTCGAC	
	A ACAC_	
GAM111 LOC158828 3'	CAGCCCCGGAGCCATTCCTCC 3227	ATCG A
	GGAGGAAT TCGG GCTG	
	CCTCCTTA GGCC CGAC	
	CCGA C	
GAM111 LOC202868 3'	CAGCTCCGACCACACCATCCTC 3487	_ AATATC
	GAGGA GG GTCGGAGCTG	
	CTCCT CC CAGCCTCGAC	
	A ACAC_	
GAM111 LOC253001 5'	CAGCTCCACCATATTTCTCC 3697	C C
	GGAGGAATAT GT GGAGCTG	
	CCTCTTTATA CA CCTCGAC	
	C _	
GAM111 LOC253841 5'	CAGCCCCAGCTGCTCCTCCTC 3704	A TC C A
	GAGGAGGA TA GT GG GCTG	
	CTCCTCCT GT CG CC CGAC	
	C _ A C	
GAM111 LOC51177 5'	CAGCTCCGACGCCCTCCCG 1676	A AATAT
	CG GGAGG CGTCGGAGCTG	

			GC CCTCC GCAGCCTCGAC		
			— C—		
GAM111	LOC91408	3'	CAGCTTTTGGTAATATTCTTCC 2735	CG	—
		TC	GAGGAGGAATAT TCGGA GCTG		
			CTCCTTCTTATA GGTTT CGAC		
			AT T		
GAM112	KIAA1265	3'	CCATATGAATTTTGGTATA 2896	A	—
			TATACCAGAATT ATGG		
			ATATGGTTTTAA TACC		
			GTA		
GAM112	MGC2731	3'	CCACTGATTGGCTGGTGTA 2050	—	A
			TATACCAG AATTA TGG		
			ATGTGGTC TTAGT ACC		
			GG C		
GAM113	C3AR1	3'	ACTGTCAAAGAATCAATCCA 1081	A	GA—
			TG ATTGATTCTT GGT		
			AC TAACTAAGAA TCA		
			C ACTG		
GAM113	GABARAPL3	3'	TATACCTCTCACTCATTCA 2260	T	TTCTT
			TGAAT GA GAGGTATA		
			ACTTA CT CTCCATAT		
			— CACT—		
GAM113	GOLGA2LY	5'	CTCAGTGAAAACATCAATTCA 2684	—	—
			TGAATTGAT TC TTGAG		
			ACTTAACTA AG GACTC		
			CAAA T		
GAM113	PEG10	3'	TACCTCAAGTATCAATTCA 1607	T	
			TGAATTGAT CTTGAGGTA		
			ACTTAACTA GAACTCCAT		
			T		
GAM113	RNF13	3'	TGTAACTCAAGCATCAATTCA 1376	T	G
			TGAATTGAT CTTGAG TATA		
			ACTTAACTA GAACTC ATGT		
			C A		
GAM113	LOC143692	5'	GCCTATCAGAAGTCAATTCA 3060	CT	—
			TGAATTGATT TGA GGT		
			ACTTAACTGA ACT CCG		
			AG AT		
GAM113	LOC151201	5'	GTTTATACCATTGGATTCAATT 3342	T	TGA
		CA	TGAATTGA TCT GGTATAAAC		

		ACTTAACT AGG CCATATTTG		
		T TTA		
GAM113	LOC257431 5'	CTCAGTGAAAACATCAATTCA 3231	_____	—
		TGAATTGAT TC TTGAG		
		ACTTAACTA AG GACTC		
		CAAA T		
GAM113	LOC93259 5'	ATACCCAGGTCAATTC 2927	TT	A
		GAATTGA CTTG GGTAT		
		CTTAACT GGAC CCATA		
		— —		
GAM114	SAMHD1 3'	CATCAAATCCTGCCCCCGT 2594	AA	T
		ACGGG CAGGGTTTG TG		
		TGCCC GTCCTAAAC AC		
		CC T		
GAM114	LOC150864 5'	AATCAACAGGCTCCCG 3150	ACAGG	
		CGGGA GTTTGTTGATT		
		GCCCT CGGACAACTAA		
		—		
GAM114	LOC257358 3'	AATCAACACCCTTGCCCC 3731	AA	TT
		GGG CAGGG TGTTGATT		
		CCC GTTCC ACAACTAA		
		C_ C_		
GAM114	LOC90288 3'	AATCTTGCTCTGTTCCC 2621	TTGTT	
		GGGAACAGGGT GATT		
		CCCTTGTCTCG CTAA		
		TT_		
GAM115	GAD1 3'	GGCTTAGTAATAGATCACGGCA 777	A A	A T
		TGC CGT ATCTATTAT GA GCC		
		ACG GCA TAGATAATG TT CGG		
		_ C A _		
GAM115	KLHL2 3'	TATAATAAATTATGTGCA 1371	C	
		TGCACGTAAT TATTATA		
		ACGTGTATTA ATAATAT		
		A		
GAM115	KIAA0276 3'	CACTGTAATGTTACATGCA 2904	C CT	A
		TGCA GTAAT ATTATAG TG		
		ACGT CATTG TAATGTC AC		
		A _ _		
GAM115	LOC130814 3'	GGCACCTATAATAAATGAC 3012	A C	A
		GT AT TATTATAG TGCC		

			CA TA ATAATATC ACGG	
			G A C	
GAM116	TGFR2	3'	AATGCCTGTATATAAATATGAA 1002	TAG C_
			TTCATATTTAT ATAC GCATT	
			AAGTATAAATA TATG CGTAA	
			___ TC	
GAM116	KIAA1223	3'	AATGAGTCTATTAATAAATATG 2908	ATACCG
	AA		TTCATATTTATTAG CATT	
			AAGTATAAATAATT GTAA	
			ATCTGA	
GAM116	PRO2859	5'	CGGTATGTAAATATGAA 1840	TAG
			TTCATATTTAT ATACCG	
			AAGTATAAATG TATGGC	

GAM116	PSIP2	3'	ATGCTTATACAATAAATATGAA 2324	AG CC
			TTCATATTTATT ATA GCAT	
			AAGTATAAATAA TAT CGTA	
			CA T_	
GAM116	LOC152185	3'	AATGCAAATCAAATAAATATGA 2497	A ACC
			TCATATTTATT GAT GCATT	
			AGTATAAATAA CTA CGTAA	
			A AA_	
GAM116	LOC89953	3'	ATGCTACTCTAATAAATAT 2437	TACC
			ATATTTATTAGA GCAT	
			TATAAATAATCT CGTA	
			CAT_	
GAM116	LOC90509	5'	GTGTTTAATAAATATGAA 2649	
			TTCATATTTATTAGATAC	
			AAGTATAAATAATTTGTG	

GAM117	BPNT1	3'	CAATGAGAGATTATA 2702	TCC
			TATGA TCTCTCATTG	
			ATATT AGAGAGTAAC	

GAM117	FLJ21709	3'	CAATGAGGGTGTGATG 2235	CCT
			TATGAT CTCTCATTG	
			GTAAGT GGGAGTAAC	
			T_	
GAM117	MGC13007	5'	CAATGAGAAAGGAGAGTA 2246	GA C
			TAT TCCT TCTCATTG	

			ATG AGGA AGAGTAAC		
			AG A		
GAM117	MGC14407	5'	CAATGGGGGAGACATA 2294	ATC	
			TATG CTCTCTCATTG		
			ATAC GAGGGGGTAAC		
			A__		
GAM117	LOC151201	3'	CAATGGGGCGGTCATA 3341	T T T	
			TATGA CC CTC CATTG		
			ATACT GG GGG GTAAC		
			_ C _		
GAM117	LOC197131	3'	CAATGAGTGGATCATG 3419	TCT	
			TATGATCC CTCATTG		
			GTACTAGG GAGTAAC		
			T__		
GAM117	LOC219942	3'	CAACAAGCGGGGGGTCATA 3598	_ CA	
			TATGATCCTCT CT TTG		
			ATACTGGGGGG GA AAC		
			C AC		
GAM118	B3GAT1	5'	CAGTTGGGCCGGA CTCTCC 1855	ACTA	
			GGAGAGTT GGCCCAACTG		
			CCTCTCAG CCGGGTTGAC		
			G__		
GAM118	B3GAT1	5'	CAGTTGGGCCGGA CTCTCC 2362	ACTA	
			GGAGAGTT GGCCCAACTG		
			CCTCTCAG CCGGGTTGAC		
			G__		
GAM118	GALNT7	3'	AGTTGAGAACTCTCCTG 2365	A AGGCC	
			TAGGAGAGTT CT CAACT		
			GTCCTCTCAA GA GTTGA		
			A ____		
GAM118	ZNF76	3'	CAGCTGGGCGCCCACTCTCCT 1019	TACTAG A	
			AGGAGAGT GCCCA CTG		
			TCCTCTCA CGGGT GAC		
			CCCG__ C		
GAM118	DKFZp434M0331	5'	CAGTTGAGCCTCATGGCTCTCC 1727	CT C	
			GGAGAGTTA AGGC CAACTG		
			CCTCTCGGT TCCG GTTGAC		
			AC A		
GAM118	FLJ20666	5'	CAGTCACCTGATGACTCTCC 1763	C CCCA	
			GGAGAGTTA TAGG ACTG		

			CCTCTCAGT GTCC TGAC		
			A AC__		
GAM118	FYCO1	3'	CAGTCAGGCCCCAGGTTCTTCC 2064	G TTA A_ CA	
			GGA AG CT GGCC ACTG		
			CCT TC GA CCGG TGAC		
			_ TTG CC AC		
GAM118	ILF3	5'	CAGTTGAACCCAGCAGCCCGCC 1121	AGA A A CC	
			GG GTT CT GG CAACTG		
			CC CGA GA CC GTTGAC		
			GCC C C AA		
GAM118	KIAA0193	3'	CAGTTGGGCCTAATCCTGCCTC 1544	A TAC__	
			GAG GT TAGGCCCACTG		
			CTC CG ATCCGGGTTGAC		
			_ TCCTA		
GAM118	KIAA1163	3'	CAGCTGGACCTAGCTGATTCTC 3121	_ C A	
			GAGAGTTA CTAGG CCA CTG		
			CTCTTAGT GATCC GGT GAC		
			C A C		
GAM118	KIAA1247	3'	GGCTCCCTAGCAACTCCCTA 2609	A A C__	
			TAGG GAGTT CTAGG CC		
			ATCC CTCAA GATCC GG		
			_ C CTC		
GAM118	KIAA1870	5'	CAGCTGGGCCTGCAGTTCCTCC 2293	A TT _ A	
	C		GG GAG ACT AGGCCCA CTG		
			CC CTC TGA TCCGGGT GAC		
			_ CT CG C		
GAM118	LOC146517	3'	CAGTTAAACCTAGATCCCTCCC 3095	A TTA_ CCC	
	T		AGG GAG CTAGG AACTG		
			TCC CTC GATCC TTGAC		
			_ CCTA AAA		
GAM118	LOC162083	5'	CAGCTGGGCTCCATAGACCCTC 3242	A ACTA_ A	
	C		GGAG GTT GGCCCA CTG		
			CCTC CAG TCGGGT GAC		
			C ATACC C		
GAM118	LOC220477	5'	CAGTTGGGCCCTGTACCATCCC 3041	A GT_ TA	
			GG GA TAC GGCCCAACTG		
			CC CT ATG CCGGGTTGAC		
			_ ACC TC		
GAM118	LOC222237	3'	AGCTGGGCCTAGTCAACT 3650	_ A	
			AGTT ACTAGGCCCA CT		

			TCAA TGATCCGGGT GA		
			C C		
GAM118	LOC255096	5'	TGGGCCAGCAGATTCTCC 3745	A_	A
			GGAGAGTT CT GGCCCA		
			CCTCTTAG GA CCGGGT		
			AC _		
GAM118	LOC92340	3'	CAGCCAGGCCCTCTTCTCCTG 2837	TTACTA	CAA
			TAGGAGAG GGCC CTG		
			GTCCTCTT CCGG GAC		
			CTC__ ACC		
GAM119	ARG1	3'	TAAC TTGGCAAAGACTTA 700	__	
			TAAGTCTT CCAAGTTG		
			ATTCAGAA GGTTC AAT		
			AAC		
GAM119	BACH2	3'	TGATGCTGCAGTGGAAAAC 1964	C	AGT
			GT TTCCA TGGCATCA		
			CA AAGGT GTCGTAGT		
			A GAC		
GAM119	CDR1	3'	TGATTTACTGGAAGACTTG 1083	A	TGGC
			TAAGTCTTCCA GT ATCA		
			G TTCAGAAGGT CA TAGT		
			_ TT__		
GAM119	CNTN3	3'	GCATTATTTGGAAGACTTA 2758	TG_	
			TAAGTCTTCCAAGT GC		
			ATTCAGAAGGTTTA CG		
			TTA		
GAM119	ESRRG	3'	GATGTCTGAAGAACTTA 2748	C	CAAG
			TAAGT TTC TTGGCATC		
			ATTCA AAG AGCTGTAG		
			_ A__		
GAM119	FSTL1	3'	GATGCCAGAGAGAACTTA 1357	CT	CAAG
			TAAGT TC TTGGCATC		
			ATTCA AG GACCGTAG		
			AG A__		
GAM119	GABRB2	3'	TGATGTAGGACTTGGAAAAC 1967	C	G_
			GT TTCCAAGTT GCATCA		
			CA AAGGTT CAG TG TAGT		
			A GA		
GAM119	GABRB2	3'	TGATGTAGGACTTGGAAAAC 776	C	G_
			GT TTCCAAGTT GCATCA		

			CA AAGGTTTCAG TGTAGT	
			A GA	
GAM119	MCP	3'	ATGCCAACTCTTAAGATT 925	CCA
			AGTCTT AGTTGGCAT	
			TTAGAA TCAACCGTA	
			TTC	
GAM119	NRIP1	3'	ATGCCAACAAAGCTTA 2548	T CCAA
			TAAG CTT GTTGGCAT	
			ATTC GAA CAACCGTA	
			- A -	
GAM119	OPHN1	3'	GATGCAAACATTGGAAGATT 936	- G
			AGTCTTCCAA GTT GCATC	
			TTAGAAGGTT CAA CGTAG	
			A A	
GAM119	PTPRO	3'	GAAGCACCGGGAAGACTTA 964	AA TG A
			TAAGTCTTCC GT GC TC	
			ATTCAGAAGG CA CG AG	
			GC - A	
GAM119	PTPRO	3'	GAAGCACCGGGAAGACTTA 2155	AA TG A
			TAAGTCTTCC GT GC TC	
			ATTCAGAAGG CA CG AG	
			GC - A	
GAM119	PTPRO	3'	GAAGCACCGGGAAGACTTA 2156	AA TG A
			TAAGTCTTCC GT GC TC	
			ATTCAGAAGG CA CG AG	
			GC - A	
GAM119	PTPRO	3'	GAAGCACCGGGAAGACTTA 2157	AA TG A
			TAAGTCTTCC GT GC TC	
			ATTCAGAAGG CA CG AG	
			GC - A	
GAM119	PTPRO	3'	GAAGCACCGGGAAGACTTA 2158	AA TG A
			TAAGTCTTCC GT GC TC	
			ATTCAGAAGG CA CG AG	
			GC - A	
GAM119	RAD50	5'	TGATGTCAATGGAGAACTTA 2419	CT AG
			TAAGT TCCA TTGGCATCA	
			ATTCA AGGT AACTGTAGT	
			AG -	
GAM119	RORB	3'	GTGTTTCATGAAGACTTA 1338	CAA TG
			TAAGTCTTC GT GCAT	

		ATTCAGAAG TA TGTG		
		___ CT		
GAM119	SORD	3' TAACTTCATGAAGACTTA 990	C__	
		TAAGTCTTC AAGTTG		
		ATTCAGAAG TTCAAT		
		TAC		
GAM119	SULT1C1	3' ATGCCACCCTTTTGAAGC 797	T T__	
		G CTTCCAAG TGGCAT		
		C GAAGGTTT ACCGTA		
		_ TCCC		
GAM119	WRB	3' GTTCTTTGAAGACTTA 1137	C TT	
		TAAGTCTTC AAG GGC		
		ATTCAGAAG TTC TTG		
		T _		
GAM119	ANKRD5	5' TGATCGCCCGGAAGACT 1978	AAGTT _	
		AGTCTTCC GGC ATCA		
		TCAGAAGG CCG TAGT		
		C__ C		
GAM119	C7orf10	3' TGATACCACTAAGAAGAAGATT 2084	CA__ T C	
	TA	TAAGTCTTC AGT GG ATCA		
		ATTTAGAAG TCA CC TAGT		
		AAGAA _ A		
GAM119	DKFZP727M111	5' TGATGCCAACTCAGAC 1633	TCCA	
		GTCT AGTTGGCATCA		
		CAGA TCAACCGTAGT		
		C__		
GAM119	FLJ13262	3' TGATGCCAACTCCCCGCACTT 2113	CTTCCA_	
		AAGT AGTTGGCATCA		
		TTCA TCAACCGTAGT		
		CGCCCCC		
GAM119	FLJ20425	5' TGACGGCTTTTGAACAAGACTT 1755	C_ TT A_	
	A	TAAGTCTT CAAG GGC TCA		
		ATTCAGAA GTTT TCG AGT		
		CA T_ GC		
GAM119	KIAA0953	3' TGGAAACTAGAAGACTTA 2763	CA GG	
		TAAGTCTTC AGTT CA		
		ATTCAGAAG TCAA GT		
		A_ AG		
GAM119	KIAA1450	3' TGATGCTTCATTGAAGACTTA 2732	C GTT	
		TAAGTCTTC AA GGCATCA		

		ATTCAGAAG TT TCGTAGT	
		_ ACT	
GAM119	NEUROD6 5'	TGAAAAGATTTGGAAGAC 2000	GGCA
		GTCTTCCAAGTT TCA	
		CAGAAGGTTTAG AGT	
		AAA_	
GAM119	PRO0255 3'	GTTTCTTGAAAGACTTA 1475	C TT
		TAAGTCTT CAAG GGC	
		ATTCAGAA GTTC TTG	
		A T_	
GAM119	UBE3B 5'	TGATGCCGAGGAAAGACT 3069	_ AAG
		AGTCTT CC TTGGCATCA	
		TCAGAA GG AGCCGTAGT	
		A _	
GAM119	ZIM2 3'	ATGTCAGTAGGAGACTTA 1623	CAAG
		TAAGTCTTC TTGGCAT	
		ATTCAGAGG GACTGTA	
		AT_	
GAM119	LOC112868 3'	TGTAGACATGAAGACTTA 2962	CAA G
		TAAGTCTTC GTT GCA	
		ATTCAGAAG CAG TGT	
		TA_ A	
GAM119	LOC116166 3'	TAAC TTCATGAAGACTTA 2545	C_
		TAAGTCTTC AAGTTG	
		ATTCAGAAG TTCAAT	
		TAC	
GAM119	LOC123855 3'	TGAGCACGCTTGGAATAC 3033	C TG A
		GT TTCCAAGT GC TCA	
		CA AAGGTTTCG CG AGT	
		T CA _	
GAM119	LOC146818 5'	GATGCCGAAGAAGGCT 3100	CAAG
		AGTCTTC TTGGCATC	
		TCGGAAG AGCCGTAG	
		A_	
GAM119	LOC152190 5'	TGACAACTGGAAGACTT 2864	A G
		AAGTCTTCCA GTTG CA	
		TTCAGAAGGT CAAC GT	
		_ A	
GAM119	LOC153077 3'	TGATACCAACTTGAGATAACTT 3366	CT _ C
		AAGT TC CAAGTTGG ATCA	

	TTCA AG GTTCAACC TAGT AT A A	
GAM119 LOC158382 3'	TGATAGCTGATAAGACTTA 3388 TAAGTCTT GT GC ATCA ATTCAGAA TA CG TAGT ____ GT A	CCAA TG _
GAM119 LOC158476 3'	TGATCTCGTCAGGAGACTTA 3391 TAAGTCTTC TGGC ATCA ATTCAGAGG ACTG TAGT ____ CTC	CAAGT ____
GAM119 LOC164397 5'	ATGTCTTCTGAAGACTTA 3249 TAAGTCTTC AG GGCAT ATTCAGAAG TC CTGTA ____ TT	CA TT
GAM119 LOC196510 3'	TGATCTGGCTTGGCAGACTTA 3416 TAAGTCT CCAAGT G ATCA ATTCAGA GGTTCTG C TAGT C GT _	T TG C
GAM119 LOC200220 3'	TGATCTGGCTTGGCAGACTTA 3445 TAAGTCT CCAAGT G ATCA ATTCAGA GGTTCTG C TAGT C GT _	T TG C
GAM119 LOC201477 5'	CAACTGAGGTCTGTAAGACTTA 3472 TAAGTCTT CC AGTTG ATTCAGAA GG TCAAC TGTCT AG	____ A_
GAM119 LOC201696 5'	TGATGCCATTGAAGACTT 2650 AAGTCTTC TGGCATCA TTCAGAAG ACCGTAGT TT____	CAAGT
GAM119 LOC220469 3'	GATGGCCAGAAGATTTA 3049 TAAGTCTTC TGGC ATC ATTTAGAAG ACCG TAG ____ G	CAAGT _
GAM119 LOC221272 3'	TGACACCAACTTTTGAGATTTA 3615 TAAGTCTT AAGTTGG TCA ATTTAGAG TTCAACC AGT TT AC	CC CA
GAM119 LOC222166 3'	TGAGGCCCCAGAGGACTTA 3636 TAAGTCTTC GGC TCA 	CAAGTT A

		ATTCAGGAG	CCG AGT		
		ACC__	G		
GAM119	LOC253220	5'	TGAGCAGCTCCTGGAAGAC	3706	__ G A
			GTCTTCCA AGTTG C TCA		
			CAGAAGGT TCGAC G AGT		
			CC __		
GAM119	LOC51275	5'	TGATGGAAGTGGAAGATT	1694	AG GG
			AGTCTTCCA TT CATCA		
			TTAGAAGGT AG GTAGT		
			GA __		
GAM119	LOC54505	5'	GATTTCTGGAAGACTTA	2800	AGTT C
			TAAGTCTTCCA GG ATC		
			ATTCAGAAGGT CT TAG		
			__ T		
GAM119	LOC90844	3'	TGATTGCATTGGAAGATCA	2682	A GTTG _
			A GTCTTCCAA GCA TCA		
			A TAGAAGGTT CGT AGT		
			C A__ T		
GAM119	LOC92697	5'	GATGCCACCAGACTTA	2882	TCCAA T
			TAAGTCT GT GGCATC		
			ATTCAGA CA CCGTAG		
			C__ _		
GAM120	KIF5C	3'	ACAAATTCTATTGAAGTATTT	1122	AC
			GAATAT TCAATAGAATTTGT		
			TTTATG AGTTATCTTAAACA		
			A_		
GAM120	DKFZP564M182	3'	ACAATTGTCAAGTATATTCTG	3097	CA AAT
			TAGAATATACT ATAG TTGT		
			GTCTTATATGA TGTT AACA		
			AC __		
GAM120	KIAA0852	5'	ACAAATTCGTAAGTATCCTCTA	1594	AT CAATA
			TAGA ATACT GAATTTGT		
			ATCT TATGA CTAAACA		
			CC ATG__		
GAM120	PRO0097	5'	CTATTGAGTAGTATTCTA	1472	_
			TAGAATAT ACTCAATAG		
			ATCTTATG TGAGTTATC		
			A		
GAM120	LOC222161	5'	TTGTATTAGTATATTCTA	3578	C G
			TAGAATATACT AATA AA		

ATCTTATATGA TTAT TT
 _ G
 GAM120 LOC255811 5' ACAAAGATGGCTATCGGTATAT 3662 CA AA____
 TCTA TAGAATATACT ATAG TTTGT
 ||||| ||| ||||
 ATCTTATATGG TATC AAACA
 C_ GG TAG
 GAM121 DPYD 3' TATTAAGTAAAATCCCCTTC 2569 TAT
 GA GGGATTTTACTTAATA
 || |||||
 CT CCCTAAAATGAATTAT
 TC_
 GAM121 KIAA1240 3' TATTAATGTTTAAATCCCATCT 2761 T T_ _
 C GA ATGGGATTT AC TTAATA
 || ||||| || |||||
 CT TACCCTAAA TG AATTAT
 C TT T
 GAM121 KIAA1843 3' TATTACAGAAAATCCCATATTC 2624 A A _
 A A GATATGGGATTTT CT TAATA
 | ||||| || |||||
 A TTATACCCTAAAA GA ATTAT
 C _ C
 GAM121 LOC122786 3' ATTAAGTAATCCACCATTCTT 2995 T GATT
 A TAAGA ATGG TTA CTTAAT
 |||| ||| |||||
 ATTCT TACC AATGAATTA
 T ACCT
 GAM122 FGF12 3' AACTAACTGTATTGTTATT 1935 TAG
 AATAACAGT TAGTTTAGTT
 ||||| |||||
 TTATTGTTA GTCAAATCAA
 T_
 GAM122 FGG 3' AACTGCTAACTTCTATTGA 1965 AC
 TCAATA AGTTAGTAGTT
 |||| |||||
 AGTTAT TCAATCGTCAA
 CT
 GAM122 NEBL 3' AACTAACTGTCAACTGTTG 1295 AG T
 TAACAGTT TAGTT AGTT
 ||||| |||| |||
 GTTGTCAA GTCAA TCAA
 CT _
 GAM122 RPE 3' AACTAAATATTTATACTGTTC 2623 AT GTA_
 TGA TCA AACAGTTA GTTTAGTT
 || ||||| |||||
 AGT TTGTCAAT TAAATCAA
 C_ ATTTA
 GAM122 TRHDE 3' AACTAAATTTCTCAACTGTTAT 1446 A _ T
 GA TCA TAACAGTT AG AGTTTAGTT
 || ||||| || |||||

AGT ATTGTCAA TC TTAAATCAA
 _ C T
 GAM122 BCMP1 3' AACTAAACATTCTCTGTTCTGA 2197 AT TT A
 TCA AACAG AGT GTTTAGTT
 ||| |||| ||| |||||
 AGT TTGTC TTA CAAATCAA
 C_ TC _
 GAM122 DKFZP434A0225 3' AACTAAACCTAATGCTGCTGTT 3624 T ____
 A TAACAGT AGTA GTTTAGTT
 ||||| ||| |||||
 ATTGTCG TCGT CAAATCAA
 _ AATC
 GAM122 FLJ12899 3' ACTAAAATACTGTTATTGG 2069 TAGTAG
 TCAATAACAGT TTTAGT
 ||||| ||| |||||
 GGTTATTGTCA AAATCA
 TA____
 GAM122 PREI3 3' AACTAAACTACTAAGTTA 2747 AG
 TAAC TTAGTAGTTTAGTT
 ||| |||||
 ATTG AATCATCAAATCAA
 _
 GAM122 PSIP2 3' AATTAAGCAACTGACATTGA 2323 AACA A
 TCAAT GTTAGT GTTTAGTT
 |||| ||||| |||||
 AGTTA CAGTCA CGAATTAA
 _ A
 GAM122 LOC220963 3' AACTAAACTACTTGTGTGTTG 3526 A TT
 A TCAATA CAG AGTAGTTTAGTT
 ||||| ||| |||||
 AGTTGT GTT TCATCAAATCAA
 _ GT
 GAM123 LOC143098 5' CGATGATCTGGCCGAAGAGCTT 3051 A_ _ TT
 AAGCT TCG TCA GATCATCG
 |||| ||| ||| |||||
 TTCGA AGC GGT CTAGTAGC
 GA C _
 GAM124 CALB2 3' AAAGAAGAGTTTACAGACAATA 853 ATTTA_
 A TTATTGTCTG TTTCTTT
 ||||| ||| |||||
 AATAACAGAC GAAGAAA
 ATTTGA
 GAM124 TRAF5 3' AAAGAAATAGGTTCAACAGG 1133 A CT
 A TCTT TTGT GATTTATTTCTTT
 ||| ||| |||||
 AGGA AACA TTGGATAAAGAAA
 C C_
 GAM124 C15orf5 3' AAAGAAAGGCACCATCAGACAA 2173 A TTA____
 AAGA TCTT TTGTCTGAT TTTCTTT
 ||| ||||| |||||

			AGAA AACAGACTA	AAAGAAA	
			— CCACGG		
GAM124	DKFZp761K1423	3'	AAAGAAATAAATCCAACAA	1826	CT
			TTGT GATTTATTTCTTT		
			AACA CTAAATAAAGAAA		
			AC		
GAM124	FLJ12892	5'	AAAGAAACATCATCTTCAGATA	2801	TTTA_____
			ATAAGA CTTATTGTCTGA	TTTCTTT	
			GAATAATAGACT	AAAGAAA	
			TCTACTAC		
GAM124	MGC15437	3'	AAAGAAATAAATGACAAT	2292	TG
			ATTGTC ATTTATTTCTTT		
			TAACAG TAAATAAAGAAA		
			—		
GAM124	MGC27016	3'	AAAGAAATGATGAGACAAAAAG	2503	A G T
			A TCTT TTGTCT ATT ATTTCTTT		
			AGAA AACAGA TAG TAAAGAAA		
			A G _		
GAM124	LOC154089	3'	AAGAAATATTACAATAAGG	3187	CTGATT
			TCTTATTGT TATTTCTT		
			GGAATAACA ATAAAGAA		
			TT_____		
GAM124	LOC159053	3'	AAAGAAATAAACTTTTGGACAG	3395	TG_____
			TTGTC A TTTATTTCTTT		
			GACAG T AAATAAAGAAA		
			GT TTC		
GAM125	XPR1	3'	CTGAGCATATCTCTCGTAACA	1152	AAATCA A
			TGTTACGA ATAT TTCAG		
			ACAATGCT TATA GAGTC		
			CTC_____ C		
GAM126	DFNA5	3'	TGCACGTAAAAAGTTGAC	1109	GC A
			GTCAAT TTAAACGT CA		
			CAGTTG AAATTGCA GT		
			A_ C		
GAM126	LRAT	3'	TGTCTTTTAAAGCATTTACTAA	2557	C CGT
			TTAGT AATGCTTTAA ACA		
			AATCA TTACGAAATT TGT		
			T TTC		
GAM126	PKHD1	3'	TACACTATAGCACTTTGACTAA	2449	___ T AC
			TTAGTCAA TGCT TA GTA		

			AATCAGTT	ACGA	AT	CAT		
			TC	T	CA			
GAM126	HSPC055	5'	CGTTGAAGCACA	ACTAA	1480	CAA		
			TTAGT	TGCTTTAACG				
			AATCA	ACGAAGTTGC				
			AC_					
GAM126	PRO0386	5'	TACTTTGAGAAACATTGACTA	1845		C_	C	
			TAGTCAATG	TTTAA	GTA			
			ATCAGTTAC	GAGTT	CAT			
			AAA	T				
GAM126	LOC121441	3'	TGTTTCTAAGCCATTGACTAA	2992		_	TAACGT	
			TTAGTCAATG	CTT	ACA			
			AATCAGTTAC	GAA	TGT			
			C	TCTT_				
GAM127	ADAMTS5	3'	ATTGGAAACTGAAATTCAGA	1351		CA	G	TG
			TC	AATT	CAGTTTC	GT		
			AG	TTAA	GTCAAAG	TA		
			AC	A	GT			
GAM127	BHLHB3	3'	GATACCAGATAATCACAA	2161		CA	_	
			TTG	GTT	TCTGGTATC			
			AAC	TAA	AGACCATAG			
			AC	T				
GAM127	CCR2	3'	GCTGAAAACGCAACTTG	767		A	CT	
			CAA	TTGCAGTTT	GGT			
			GTT	AACGTCAA	TCG			
			C	AG				
GAM127	DCN	3'	ACCTAACTGCAATGTGGA	868		A	TCT	
			TCCA	ATTGCAGTT	GGT			
			AGGT	TAACGTCAA	CCA			
			G	T_				
GAM127	DCN	3'	ACCTAACTGCAATGTGGA	2421		A	TCT	
			TCCA	ATTGCAGTT	GGT			
			AGGT	TAACGTCAA	CCA			
			G	T_				
GAM127	DCN	3'	ACCTAACTGCAATGTGGA	2422		A	TCT	
			TCCA	ATTGCAGTT	GGT			
			AGGT	TAACGTCAA	CCA			
			G	T_				
GAM127	DCN	3'	ACCTAACTGCAATGTGGA	2423		A	TCT	
			TCCA	ATTGCAGTT	GGT			

			AGGT TAACGTCAA CCA			
			G T__			
GAM127	DCN	3'	ACCTAACTGCAATGTGGA 2424	A	TCT	
			TCCA ATTGCAGTT GGT			
			AGGT TAACGTCAA CCA			
			G T__			
GAM127	DCN	3'	ACCTAACTGCAATGTGGA 2425	A	TCT	
			TCCA ATTGCAGTT GGT			
			AGGT TAACGTCAA CCA			
			G T__			
GAM127	EXTL1	5'	GGACACGGCCCTGCATTCTGGA 1116	AAT	TTT	GTA
			TCCA TGCAG CTG TCC			
			AGGT ACGTC GGC AGG			
			CTT CC_ AC_			
GAM127	FASN	3'	GGACACCAGAGCTGCCGACTTG 1088	A _	T	A
	GA		TCCAA TTG CAGTT CTGGT TCC			
			AGGTT AGC GTCGA GACCA AGG			
			C C _ C			
GAM127	INHBB	3'	GTCAGAAACTGCCATTTG 905	T		
			CAAAT GCAGTTTCTGGT			
			GTTTA CGTCAAAGACTG			
			C			
GAM127	NEDD4	3'	GATGGAAAACTGAAATTTGGA 2875	G	CTGG	
			TCCAAATT CAGTTT TATC			
			AGGTTTAA GTCAAA GTAG			
			A AG__			
GAM127	NFYA	3'	ACCAAAACTGCAATCAGGA 1955	AA	C	
			TCC ATTGCAGTTT TGGT			
			AGG TAACGTCAAA ACCA			
			AC _			
GAM127	NFYA	3'	ACCAAAACTGCAATCAGGA 933	AA	C	
			TCC ATTGCAGTTT TGGT			
			AGG TAACGTCAAA ACCA			
			AC _			
GAM127	RAD17	5'	ACCTGCAACTGTAATTTG 967		TCT	
			CAAATTGCAGTT GGT			
			GTTTAATGTCAA CCA			
			CGT			
GAM127	RAD17	5'	ACCTGCAACTGTAATTTG 2410		TCT	
			CAAATTGCAGTT GGT			

			GTTTAATGTCAA CCA		
			CGT		
GAM127	RAD17	5'	ACCTGCAACTGTAATTTG 2411	TCT	
			CAAATTGCAGTT GGT		
			GTTTAATGTCAA CCA		
			CGT		
GAM127	RAD17	5'	ACCTGCAACTGTAATTTG 2412	TCT	
			CAAATTGCAGTT GGT		
			GTTTAATGTCAA CCA		
			CGT		
GAM127	RAD17	5'	ACCTGCAACTGTAATTTG 2413	TCT	
			CAAATTGCAGTT GGT		
			GTTTAATGTCAA CCA		
			CGT		
GAM127	RAD17	5'	ACCTGCAACTGTAATTTG 2414	TCT	
			CAAATTGCAGTT GGT		
			GTTTAATGTCAA CCA		
			CGT		
GAM127	ZNF146	3'	GGACACCAGAAAATTTGTA 1358	—	A
			TGCAG TTTCTGGT TCC		
			ATGTT AAAGACCA AGG		
			TA C		
GAM127	CHST3	3'	GGACACCAGAAGACGATTCAGA 1096	CA	CAG A
			TC AATTG TTTCTGGT TCC		
			AG TTAGC GAAGACCA AGG		
			AC A_ C		
GAM127	DKFZp762E1511	3'	ATGCTACTGAATTTGGA 2531	G	TTCT
			TCCAAATT CAGT GGTAT		
			AGGTTTAA GTCA TCGTA		
			— ———		
GAM127	EIF5	5'	GATACCAAAAAGTTGCAAT 878	—	C
			ATTGCAG TTT TGGTATC		
			TAACGTT AAA ACCATAG		
			G A		
GAM127	LATS1	3'	GGATACCACAGCCAATT 2563	CA	TC
			AATTG GTT TGGTATCC		
			TTAAC CGA ACCATAGG		
			— C_		
GAM127	MGC27277	3'	CCAAAATTGCAATTCAGA 2505	CA	C
			TC AATTGCAGTTT TGG		

			AG TTAACGT TAAA ACC		
			AC _		
GAM127	POLD3	3'	ACTAAACTGAATTTG 3538	G	C
			CAAATT CAGTTT TGGT		
			GTTTAA GTCAAA ATCA		
			_ _		
GAM127	TSLRP	5'	GATACATCACTGAAATTTGGA 1435	G	TTCTG
			TCCAAATT CAGT GTATC		
			AGGTTTAA GTCA CATAG		
			A CTA__		
GAM127	LOC147463	3'	ATACCAGTGGCAAATTTGGA 3108	_	AGTTT
			TCCAAATT GC CTGGTAT		
			AGGTTTAA CG GACCATA		
			A GT__		
GAM127	LOC161734	3'	GGATACCGTTTTCAACTTGA 3400	A	C TTTC
			TCCAA TTG AG TGGTATCC		
			AGGTT AAC TT GCCATAGG		
			C _ TT__		
GAM127	LOC164173	3'	GATATTGAACTGCATCTGGA 3235	AAT	CT
			TCCA TGCAGTTT GGTATC		
			AGGT ACGTCAAG TTATAG		
			CT_ _		
GAM127	LOC199675	3'	GCCAAAGCCACA ACTTGA 3429	A	CA C
			TCCAA TTG GTTT TGGT		
			AGGTT AAC CGAA ACCG		
			C AC _		
GAM127	LOC200150	5'	GCCAACTGCAGTTTG 3439	TTC	
			CAAATTGCAGT TGGT		
			GTTTGACGTCA ACCG		
			_		
GAM127	LOC51185	3'	ATACCAGAAACATCTACTTGGG 1679	ATTGCA	
			TCCAA GTTTCTGGTAT		
			GGGTT CAAAGACCATA		
			CATCTA		
GAM127	LOC90459	3'	GCTGAAACTGCAATTGGA 2643	A	T
			TCCAA TTGCAGTTTC GGT		
			AGGTT AACGTCAAAG TCG		
			_ _		
GAM127	LOC91694	5'	ATACCAGAGGTCACTTCAG 2769	C	_
			TTG AGT TTCTGGTAT		

GAC TCA GAGACCATA
 T CTG
 GAM128 SCNN1G 3' ACCTGAACTATTAGCACGTC 793 ____ CA
 GA TGCTAATA TCAGGT
 || ||||| |||||
 CT ACGATTAT AGTCCA
 GC CA
 GAM128 YY1 3' ACCTGATGTGTACATC 1016 CTA
 GATG ATACATCAGGT
 ||| |||||
 CTAC TGTGTAGTCCA
 A____
 GAM128 FLJ21940 3' CCTGATGTGTACCTTA 2014 A TAAT
 TAAG TGC ACATCAGG
 ||| ||| |||||
 ATTC ATG TGTAGTCC
 C ____
 GAM128 PRO0159 5' ACCTGATGTATTGCTCT 1474 T T
 AGA GC AATACATCAGGT
 ||| || |||||
 TCT CG TTATGTAGTCCA
 - -
 GAM128 LOC200282 3' CCTGATGTAGGTCTTATT 3448 GCTAA
 AATAAGAT TACATCAGG
 ||||| |||||
 TTATTCTG ATGTAGTCC
 G____
 GAM129 PCDH9 5' ACATAGGGGATAGTAGCCAAC 3262 G C
 GTTGGCTACTATCTT TA GT
 ||||| ||||| || ||
 CAACCGATGATAGGG AT CA
 G A
 GAM129 ERO1L 3' GTACAATAACAACCTCA 1508 GC CTATC
 TGAGTTG TA TTGTAC
 ||||| || |||||
 ACTCAAC AT AACATG
 A_ ____
 GAM129 LOC253287 5' AAGATAATGCCAACTCA 3740 TAC
 TGAGTTGGC TATCTT
 ||||| |||||
 ACTCAACCG ATAGAA
 TA_
 GAM129 LOC254268 5' ACAACTGACAGCAGCCAGCTCA 3674 A A ____
 TGAGTTGGCT CT TC TTGT
 ||||| || || |||||
 ACTCGACCGA GA AG AACA
 C C TC
 GAM130 AP1B1 3' AGCCACAGAAGCTGTGCC 802 A
 GGCATGGTTTCTGTG CT
 ||||| ||||| ||

			CCGTGTCGAAGACAC GA		
			C		
GAM130	BBS2	5'	AGCCACAGAAGGCGCCG 2214	AT G	A
			CGGC G TTTCTGTG CT		
			GCCG C GAAGACAC GA		
			__ G C		
GAM130	FRK	5'	AGCCACAGAAAGCAAGCCG 890	A G	A
			CGGC TG TTTCTGTG CT		
			GCCG AC AAAGACAC GA		
			A G C		
GAM130	HSPD1	3'	TAGTCACAGAAATTCC 2560	CAT	
			GG GGTTTCTGTGACTA		
			CC TTAAAGACACTGAT		

GAM130	IL20RA	3'	TAGGAACTAACTATGCC 1501	CT GA	
			GGCATGGTTT GT CTA		
			CCGTATCAAA CA GAT		
			T_ AG		
GAM130	LAMC3	3'	TAGTCACACTCCCTGCCG 1269	T TTTC	
			CGGCA GG TGTGACTA		
			GCCGT CC ACACTGAT		
			C TC__		
GAM130	MEST	3'	TAGTCAAGTCACCATGCTG 2872	TT G	
			CGGCATGGT CT TGACTA		
			GTCGTACCA GA ACTGAT		
			CT _		
GAM130	MKI67	3'	AGCCACAGGAGATGTC 927	GG	A
			GGCAT TTTCTGTG CT		
			CTGTA GAGGACAC GA		
			__ C		
GAM130	MMP19	3'	AGCCACAGAAACCACGTT 2011	A	A
			GGC TGGTTTCTGTG CT		
			TTG ACCAAAGACAC GA		
			C C		
GAM130	MMP19	3'	AGCCACAGAAACCACGTT 2012	A	A
			GGC TGGTTTCTGTG CT		
			TTG ACCAAAGACAC GA		
			C C		
GAM130	MS4A8B	3'	AGTCTAGGAAACCATGCTG 2200	GT	
			CGGCATGGTTTCT GACT		

			GTCGTACCAAAGG CTGA		
			AT		
GAM130	PSMD9	3'	TAGCCACAGACATGCTG 957	GTT	A
			CGGCATG TCTGTG CTA		
			GTCGTAC AGACAC GAT		
			___ C		
GAM130	SH3GL2	3'	TAGTCACAGAACTGCTG 984	TGGT	
			CGGCA TTCTGTGACTA		
			GTCGT AAGACACTGAT		
			C___		
GAM130	SPTAN1	3'	AGTCACAATCATCATGTC 994	TTC	
			GGCATGGT TGTGACT		
			CTGTACTA ACACTGA		
			CTA		
GAM130	SYNGR1	3'	AGTCACAGACTGTCCTGCC 1146	T TT___	
			GGCA GG TCTGTGACT		
			CCGT CC AGACACTGA		
			_ TGTC		
GAM130	TRIM9	3'	AGTCACAGAACTGGGGGTC 2353	AT___ T	
			GGC GGTT CTGTGACT		
			CTG TCAA GACACTGA		
			GGGG _		
GAM130	TRPM2	5'	AGTTGCGAAACCATGTCTG 1011	TTG	
			CGGCATGGTTTC G ACT		
			GCTGTACCAAAG C TGA		
			_ GT		
GAM130	ATPAF1	3'	AGTCACAGAGATGAGCC 2582	ATG	
			GGC GTTTCTGTGACT		
			CCG TAGAGACACTGA		
			AG_		
GAM130	CENTG2	3'	TAGTCACGCGGCACGCGCCG 1587	A _ TC	
			CGGC TG GTT TGTGACTA		
			GCCG GC CGG GCACTGAT		
			C A C_		
GAM130	COL12A1	3'	AGCCACAGAAGATGTC 2381	GG	A
			GGCAT TTTCTGTG CT		
			CTGTA GAAGACAC GA		
			___ C		
GAM130	COL12A1	3'	AGCCACAGAAGATGTC 1103	GG	A
			GGCAT TTTCTGTG CT		

		CTGTA GAAGACAC GA		
		— C		
GAM130	DKFZp547I224 3'	AGCCGCTGCAAAATCATGCC	1902	CT__ A
		GGCATGGTTT GTG CT		
		CCGTACTAAA CGC GA		
		ACGT C		
GAM130	DKFZp566H0824 3'	AGTGAGCTGAGACCATGCC	1721	T G_
		GGCATGGTTTC GT ACT		
		CCGTACCAGAG CG TGA		
		T AG		
GAM130	FLJ11726 3'	AGTGAGCCGAGACCATGCC	2119	T G_
		GGCATGGTTTC GT ACT		
		CCGTACCAGAG CG TGA		
		C AG		
GAM130	FLJ12668 3'	TAGTCACTTGCCACCATGCC	2124	TTCT_
		GGCATGGT GTGACTA		
		CCGTACCA CACTGAT		
		CCGTT		
GAM130	FLJ13385 3'	TAGTCACAAAGATAATACC	2098	C G C
		GG AT GTTT TGTGACTA		
		CC TA TAGA ACACTGAT		
		A A A		
GAM130	FLJ14936 3'	TAGTCACAGACACAGGAGCC	2243	ATG_ T
		GGC GT TCTGTGACTA		
		CCG CA AGACACTGAT		
		AGGA C		
GAM130	FLJ14957 3'	AGTCACAGCTGGGCTTCC	2291	CAT _
		GG GGTTT CTGTGACT		
		CC TCGGG GACACTGA		
		T__ TC		
GAM130	HSU79275 3'	TAGTCACAAGATTTACCAT	2746	T__ _
		ATGGT TCT GTGACTA		
		TACCA AGA CACTGAT		
		TTT A		
GAM130	KALI 3'	AGTGAGCCAAAATCATGCC	2346	CT G_
		GGCATGGTTT GT ACT		
		CCGTACTAAA CG TGA		
		AC AG		
GAM130	KIAA0121 3'	TAGTCACAGAGTGGCTG	2957	ATGGT
		CGGC TTCTGTGACTA		

			GTCG GAGACACTGAT		
			GT___		
GAM130	KIAA0254	3'	AGTCACAGGGAAGTGCTG 1540	GG TT	
			CGGCAT T CTGTGACT		
			I		
			GTCGTG A GACACTGA		
			A_ GG		
GAM130	KIAA0820	3'	AGCACAAACCATGTC 2838	TC A	
			GGCATGGTT TGTG CT		
			CTGTACCAA ACAC GA		
			— —		
GAM130	KIAA0863	3'	AGTCATGGAGACCAGCC 3669	A	
			GGC TGGTTTCTGTGACT		
			CCG ACCAGAGGTACTGA		
			—		
GAM130	KIAA1023	3'	AGCCACAGGAGATGTC 1728	GG A	
			GGCAT TTTCTGTG CT		
			CTGTA GAGGACAC GA		
			— C		
GAM130	KIAA1161	5'	AGTCACAGAACATCTCC 3213	CAT _	
			GG GGT TTCTGTGACT		
			CC CTA AAGACACTGA		
			T__ C		
GAM130	KIAA1254	3'	TCACAGAAAGTAAAGCCG 2876	A_ G	
			CGGC TG TTTCTGTGA		
			GCCG AT AAAGACACT		
			AA G		
GAM130	KIAA1805	3'	TAGCTTGTGAAACCATTCC 3148	C T TG_	
			GG ATGGTTTC G A CTA		
			I		
			CC TACCAAAG T T GAT		
			T _ GT C		
GAM130	KIAA1866	3'	TCACAGGACCGTCATGCTG 2587	T__	
			CGGCATGG TTCTGTGA		
			GTCGTA CT AGGACACT		
			GCC		
GAM130	KIAA1958	3'	AGTGAGCCGAGACCATGCC 3218	T G_	
			GGCATGGTTTC GT ACT		
			CCGTACCAGAG CG TGA		
			C AG		
GAM130	LIMK2	5'	AGTCACAGACGGATTTGC 1709	T _	
			GCA GGTT TCTGTGACT		

			CGT TTAG AGACACTGA		
			— GC		
GAM130	MGC12921	5'	AGTCACAGCAGCTGCC	2666	TG T
			GGCA GTT CTGTGACT		
			CCGT CGA GACACTGA		
			— C		
GAM130	MGC5149	3'	TAGCCACAGAAATGTC	2939	GGT A
			GGCAT TTCTGTG CTA		
			CTGTA AAGACAC GAT		
			— C		
GAM130	MOST2	5'	AGCCACCTGGCCATGCTG	1909	TCT A
			CGGCATGGTT GTG CT		
			GTCGTACCGG CAC GA		
			TC_ C		
GAM130	MRPL9	3'	AGTAGACCGAAACCATCC	2195	C T G_
			GG ATGGTTTC GT ACT		
			CC TACCAAAG CA TGA		
			— C GA		
GAM130	NCBP2	3'	AGTCACAGAAGGTTCC	1397	C GG
			GG AT TTTCTGTGACT		
			CC TG GAAGACACTGA		
			T _		
GAM130	PCYT1B	3'	TAGTCACAGGAGCTGC	1160	TG
			GCA GTTTCTGTGACTA		
			CGT CGAGGACACTGAT		
			—		
GAM130	PIP3-E	3'	AGTCACAAACAATGTC	2764	G TC
			GGCAT GTT TGTGACT		
			CTGTA CAA ACACTGA		
			A _		
GAM130	PPP1R15B	5'	AGTCGGAACCATCGCCG	2288	_ CTG
			CGGC ATGGTTT TGACT		
			GCCG TACCAA GCTGA		
			C AG_		
GAM130	TFIP11	3'	TAGTCACAGTAATCCCC	1410	CAT T
			GG GGTT CTGTGACTA		
			CC CTAA GACACTGAT		
			C_ T		
GAM130	LOC132617	3'	AGTTTGAAATCATGCC	3039	TGT
			GGCATGGTTTC GACT		

		CCGTACTAAAG TTGA		
		T__		
GAM130	LOC147660 3'	AGTCACAGATCACGCC 3111	A TT	
		GGC TGG TCTGTGACT		
		CCG ACT AGACACTGA		
		C __		
GAM130	LOC149302 5'	AGTCACAGCAGCCGCC 3129	AT T	
		GGC GGTT CTGTGACT		
		CCG CCGA GACACTGA		
		__ C		
GAM130	LOC151720 5'	AGTCACAAAACCATGCTG 3160		C
		CGGCATGGTTT TGTGACT		
		GTCGTACCAA ACACTGA		
		A		
GAM130	LOC152215 3'	TAGTCACAAAGGGCTTACG 3167	GCAT C_	
		CG GGTTT TGTGACTA		
		GC TCGGG ACACTGAT		
		AT__ AA		
GAM130	LOC152426 3'	AGTCACAGGCAGGTGCC 3359	G_ TT	
		GGCAT GT CTGTGACT		
		CCGTG CG GACACTGA		
		GA __		
GAM130	LOC155179 3'	AGCCACAGGAGATGTC 3199	GG A	
		GGCAT TTTCTGTG CT		
		CTGTA GAGGACAC GA		
		__ C		
GAM130	LOC157562 5'	TAGTCACATGGCCACACC 3381	CA TC	
		GG TGGTT TGTGACTA		
		CC ACCGG ACACTGAT		
		AC T_		
GAM130	LOC163115 3'	AGTCACAGATCCGATGTC 3244	_ TT	
		GGCAT GG TCTGTGACT		
		CTGTA CC AGACACTGA		
		G T_		
GAM130	LOC169026 3'	TAGTCACAAAATTTTACC 3260	CAT C	
		GG GGTTT TGTGACTA		
		CC TTAAA ACACTGAT		
		ATT _		
GAM130	LOC170106 5'	AGCCACAGGAAGTGTCC 3255	C G A	
		GG ATG TTTCTGTG CT		

		CC TGT AAGGACAC GA		
		_ G C		
GAM130	LOC170425 5'	TAGTCACAACCCAATGC 3048	__	TTC
		GCAT GGT TGTGACTA		
		CGTA CCA ACACTGAT		
		AC _		
GAM130	LOC197342 3'	AGTCACAGAAGGACTCGCC 3423	AT	_
		GGC GGTT TCTGTGACT		
		CCG TCAG AGACACTGA		
		C_ GA		
GAM130	LOC200488 5'	AGTCATGATCATGCCG 3477		TCT
		CGGCATGGTT GTGACT		
		GCCGTACTAG TACTGA		
		_		
GAM130	LOC219667 3'	TAGTCACAAATCAGAACTG 3517	CA_	TC
		CGG TGGTT TGTGACTA		
		GTC ACTAA ACACTGAT		
		AAG _		
GAM130	LOC220980 5'	AGCCACGTGAGCCATGCC 3592		C A
		GGCATGGTTT TGTG CT		
		CCGTACCGAG GCAC GA		
		T C		
GAM130	LOC253461 3'	AGCCACAGAAAATATACC 3700	C G	A
		GG ATG TTTCTGTG CT		
		CC TAT AAAGACAC GA		
		A A C		
GAM130	LOC253502 3'	AGCCACAGAGGCCTGCC 3660	T	A
		GGCA GGTTTCTGTG CT		
		CCGT CCGGAGACAC GA		
		_ C		
GAM130	LOC254211 5'	AGTCACAGAGAGGTGCC 3707		GG
		GGCAT TTTCTGTGACT		
		CCGTG AGAGACACTGA		
		G_		
GAM130	LOC90785 3'	AGTGAGCCGAGACCATACC 2677	C	T G_
		GG ATGGTTTC GT ACT		
		CC TACCAGAG CG TGA		
		A C AG		
GAM130	LOC91050 3'	AGTCACAGAAATCATTCT 2701		C
		GG ATGGTTTCTGTGACT		

			TC TACTAAAGACACTGA		
			T		
GAM130	LOC91380	3'	AGTGAGCCGAGACCATGCC 2733	T G_	
			GGCATGGTTTC GT ACT		
			CCGTACCAGAG CG TGA		
			C AG		
GAM131	EIF2C1	3'	TTATTCCTCTCTGTCCACA 1414 A	T TACA	
			TG TGGACAGA GA AATAA		
			AC ACCTGTCT CT TTATT		
			_ _ CC_		
GAM131	PCDHA9	3'	TATCTATATCTGTCTATCA 1461	___	
			TGATGGACAGAT GATA		
			ACTATCTGTCTA CTAT		
			TAT		
GAM131	KIAA0923	3'	TATTTGTGTTGTCCATT 1463	GATG	
			GATGGACA ATACAAATA		
			TTACCTGT TGTGTTTAT		

GAM131	UBF-fl	3'	ATTTGTATATCTATCTACCA 2287 A C A		
			TG TGGAGATG TACAAAT		
			AC ATCT TCTAT ATGTTTA		
			C A _		
GAM131	LOC119548	3'	CTTATCTGTTATGTGTTCATCA 2983	G CAA	
			TGATGGACA ATGATA ATAAG		
			ACTACTTGT TATTGT TATTC		
			G C_		
GAM131	LOC120400	5'	CTTATCCATCTCTGTCCATTA 3027	T ACAA	
			TGATGGACAGA GAT ATAAG		
			ATTACCTGTCT CTA TATTC		
			_ CC_		
GAM132	NARS	3'	AAAGTTCGGGGAAAATACC 1125	TA CAA	
			GGTATTTTT TGG ACTTT		
			CCATAAAAG GCT TGAAA		
			GG _		
GAM132	BFAR	3'	TGCACATAAAAAAATACCG 2581	_	
			CGGTATTTTTTATG GCA		
			GCCATAAAAAATAC CGT		
			A		
GAM132	HSNOV1	3'	AAAGTTCAAAAGTAGAAATACC 1720	TATGGCA	
			GGTATTTTT AACTTT		

CCATAAAGA TTGAAA
 TGAAAAC
 GAM132 KIAA0628 3' AGGCTGCCATAACAAAATACC 1547 _ AA
 GGTATTTT TTATGGCA CT
 ||||| ||||| ||
 CCATAAAA AATACCGT GA
 C CG
 GAM132 KIAA1393 3' TAAAGTTTGATTGGAACATACC 2936 T TGG
 GGTAT TTTTA CAACTTTA
 ||||| ||||| |||||
 CCATA AAGGT GTTTGAAAT
 C TA_
 GAM132 LOC147054 5' TAAAGTTTACATGCTACAAAAA 3289 A ____
 ATAC GTATTTTTT TGGCA AACTTTA
 ||||| ||||| |||||
 CATAAAAAA ATCGT TTGAAAT
 C ACAT
 GAM133 TRIM 3' CAAATGTAAGGCCATGA 1684 AA GAC
 TCAT GCTT TACATTTG
 ||| ||| |||||
 AGTA CGGA ATGTAAAC
 C_ ____
 GAM133 MGC11296 3' CCAAATGTAAGTGCCATGA 2248 AA_ TGAC
 TCAT GCT TACATTTGG
 ||| ||| |||||
 AGTA TGA ATGTAAACC
 CCG ____
 GAM133 PRO2037 5' CAAATGCTGTTTATGATA 1853 TTGACTA
 TATCATAAGC CATTTG
 ||||| |||||
 ATAGTATTTG GTAAAC
 TC_____
 GAM134 PMX1 3' TCTATAGTGATGAAACATT 1996 A ACCGT
 AATG TTTCATCA TAGA
 ||| ||||| |||
 TTAC AAAGTAGT ATCT
 _ GAT_
 GAM134 FLJ22557 3' TCTGGCATGATAAAATCATGGA 2083 A C ACC
 TC ATGATTT ATCA GTTAGA
 || ||||| ||| |||||
 AG TACTAAA TAGT CGGTCT
 G A A_
 GAM134 KIAA0618 5' TCTAGTGGATGAGAATCA 1563 CA A
 TGATTT TCA CCGTTAGA
 ||||| ||| |||||
 ACTAAG AGT GGTGATCT
 _ A
 GAM134 LOC154215 3' AACGGTTGCCGCGCCATTG 3188 ATT AT
 CAATG TC CAACCGTT
 ||||| || |||||

		GTTAC GG GTTGGCAA	
		C__ CC	
GAM135	GARP	3' ATCAACAAATCTTCACTGAGC 1220	C TTA_
		GCTC GT ATTTGTTGAT	
		CGAG CA TAAACAATA	
		T CTTC	
GAM135	TEM8	3' AGGGAATTAAAGAAAGCCATG 1790	CCG G
		CATGGCT TTTAATTT TT	
		GTACCGA AAATTAAG GA	
		AAG G	
GAM135	TRHR	3' ATCAACAAAAGGGAGAACATG 1009	G_ G AATT
		CATG CTCC TTT TGTGAT	
		GTAC GAGG AAA ACAACTA	
		AA G ____	
GAM135	LGI2	3' ATCAACAAACAAATCAAAGCCA 1792	CC_ AA
		TGGCT GTTT TTTGTTGAT	
		ACCGA TAAA AAACAATA	
		AAC C_	
GAM135	MGC4638	3' TCAACAAATGTGAGTCAT 2212	CGTTTA
		ATGGCTC ATTTGTTGA	
		TACTGAG TAAACAATA	
		TG____	
GAM135	LOC139065	5' CAACAAACAAGAGCTATG 3035	CGTTTAA
		CATGGCTC TTTGTTG	
		GTATCGAG AAACAAC	
		AAC____	
GAM135	LOC154282	3' ATCAACAAAAAGGAGGACCA 3372	C G AA
		TGG TCC TTT TTTGTTGAT	
		ACC AGG AGG AAACAATA	
		_ _ AA	
GAM135	LOC91516	5' CAACAAAAAGGAGCTAT 2745	GTTTAA
		ATGGCTCC TTTGTTG	
		TATCGAGG AAACAAC	
		AA____	
GAM136	C20orf28	3' CCACTCCGGAGATCCGGGT 1629	G ATA_
		ACTCGGATCT CT TGG	
		TGGGCCTAGA GG ACC	
		_ CCTC	
GAM136	MGC5139	5' CCAAAGAAGATCCGAGTT 2994	G ATA
		AACTCGGATCT CT TGG	

			TTGAGCCTAGA GA ACC		
			A A__		
GAM136	PRO0899	3'	CCTGCAGCAGACCCGAGTTG 1847	A	A T
			TAACTCGG TCTGCT TA GG		
			GTTGAGCC AGACGA GT CC		
			C C _		
GAM136	PRO1386	3'	CCACATAGCAAGGTCTGA 2187	_	A
			TCGGATCT GCTAT TGG		
			AGTCTGGA CGATA ACC		
			A C		
GAM136	PTPRT	3'	CCATGTAAATCCGGGTTA 2399	CTGC	
			TAACTCGGAT TATATGG		
			ATTGGGCCTA ATGTACC		
			A__		
GAM136	TCL6	3'	CCATTGCAGATTCGAGT 1919	TAT	
			ACTCGGATCTGC ATGG		
			TGAGCTTAGACG TACC		
			T__		
GAM136	TCL6	3'	CCATTGCAGATTCGAGT 1433	TAT	
			ACTCGGATCTGC ATGG		
			TGAGCTTAGACG TACC		
			T__		
GAM136	TEX27	3'	CCATATAGCAAGTTTAGT 1968	C TC	
			ACT GGA TGCTATATGG		
			TGA TTT ACGATATACC		
			_ GA		
GAM136	LOC255759	5'	CCTGTCAGGATCCGAGT 3739	GCT T	
			ACTCGGATCT ATA GG		
			TGAGCCTAGG TGT CC		
			AC_ _		
GAM137	APXL	3'	ACTTACTTATTTTATCTA 842	CT C	
			TAGATAAA AT AGTAAGT		
			ATCTATTT TA TCATTCA		
			T_ T		
GAM137	CKN1	3'	ACTTCTGTATAGTTTATTTAGT 702	_ T	
	CA		TGACTAGATAAACTAT CAG AAGT		
			ACTGATTTATTTGATA GTC TTCA		
			T _		
GAM137	HMGA2	3'	ACCTACTAATAGTTTGTGATC 1032	CTA	C A
			GA GATAAACTAT AGTA GT		

			CT TTGTTTGATA TCAT CA	
			AG_ A C	
GAM137	ZNF36	3'	ACTTAAGGATCCTTCTAGTCA 3626	TAAACT AG
			TGACTAGA ATC TAAGT	
			ACTGATCT TAG ATTCA	
			TCC__ GA	
GAM137	FLJ23191	3'	GTTGATAGCCCTCTAGTCA 2065	TAAA
			TGACTAGA CTATCAGT	
			ACTGATCT GATAGTTG	
			CCC_	
GAM137	KIAA0841	3'	ACTTACTGAAATTCGCCAGTCA 2918	A_ TAAACTA
			TGACT GA TCAGTAAGT	
			ACTGA CT AGTCATTCA	
			CC TAA__	
GAM137	KIAA1243	3'	ACCTATGGGCAGTTTATCTG 2977	AT A A
			TAGATAAACT C GTA GT	
			GTCTATTTGA G TAT CA	
			CG G C	
GAM137	RNF20	3'	CTGTAGGACAGTTTATCAGTCA 1882	A A AGTA
			TGACT GATAAACT TC AG	
			ACTGA CTATTTGA AG TC	
			_ C GATG	
GAM137	LOC118851	3'	ACTTTGGGAAATTCATCTGGTC 3025	A CTA AGT
	A		TGACTAGAT AA TC AAGT	
			ACTGGTCTA TT AG TTCA	
			C AA_ GGT	
GAM137	LOC150005	3'	ACTAGCTGCTTCTAGTCA 3322	TAAACTAT A
			TGACTAGA CAGT AGT	
			ACTGATCT GTCG TCA	
			TC_ A	
GAM137	LOC221036	3'	ACTTACCGATAGTTTCAGT 3585	A TA A
			ACT GA AACTATC GTAAGT	
			TGA CT TTGATAG CATTCA	
			_ _ C	
GAM138	COG7	3'	AAAAGAGTTGTAAATTAAAGAT 2795	_ G
	G		TATCTTTAA TA AACTCTTTT	
			GTAGAAATT AT TTGAGAAAA	
			AA G	
GAM138	DUSP5	3'	GAAAAGAGTTCTTCAGAT 1111	TTAAT
			ATCT AGAACTCTTTTC	

				TAGA	TCTTGAGAAAAG		
				CT__			
GAM138	C6orf29	3'	AAAAGATTTTATTAAGATA	2278		C	
			TATCTTTAATAGAA	TCTTTT			
			ATAGAAATTATTTT	AGAAAA			
GAM138	CGR19	3'	GAAAAGTACACTTTCTACTAAA	1311	A	CT__	
			GATG	TATCTTTA TAGAA	CTTTTC		
			GTAGAAAT ATCTT	GAAAAG			
			C	TCACAT			
GAM138	DSCR6	3'	GAAAAGAGTAACAGAAAGATAG	1865		AATAGA	
			CTATCTTT	ACTCTTTTC			
			GATAGAAA	TGAGAAAAG			
			GACAA_				
GAM138	ETL	3'	GAAATAGTTCTGTCAAAAATAG	1982	C A	CT	
			T	ACTAT TTT ATAGAACT	TTTC		
			TGATA AAA TGTCTTGA	AAAG			
			A C	T_			
GAM138	FLJ21269	3'	GAGGCTTATTAATAAGT	2138	C	AA	
			ACTAT TTTAATAG	CTC			
			TGATA AAATTATT	GAG			
			A	CG			
GAM138	HNT	3'	GAAAAGAGTTTTAAAAAAGA	1692		AA	
			TCTTT TAGAACTCTTTTC				
			AGAAA ATTTTGAGAAAAG				
			AA				
GAM138	KCNB2	3'	AAAAGAGCTCTATTAGGA	3690	T	A	
			TCTT AATAGA	CTCTTTT			
			AGGA TTATCT	GAGAAAA			
			_	C			
GAM138	KIAA0794	3'	GAAAAGAACAAGAAAGATAG	3163		AATAGAAC	
			CTATCTTT	TCTTTTC			
			GATAGAAA	AGAAAAG			
			GAACA__				
GAM138	LOC123342	5'	GAAAAGAGTTCTAAACATGGT	3031	C	TAA	
			ACTAT TT TAGAACTCTTTTC				
			TGGTA AA	ATCTTGAGAAAAG			
			C	__			
GAM138	LOC144920	3'	AAAAGAGTTCTAAAGAAATAG	3270	C	AA	
			CTAT TTT TAGAACTCTTTT				

			GATA AAG ATCTTGAGAAAA		
			_ AA		
GAM138	LOC153688	3'	GAAAAGAGTTTCTGCAAGATA 3370	TAA	_
			TATCTT TAGAA CTCTTTTC		
			ATAGAA GTCTT GAGAAAAG		
			C_ T		
GAM138	LOC51336	5'	GAAAAGAATTCTGTTGAAATCA 1707	ATC	C
			GT ACT TTTAATAGAA TCTTTTC		
			TGA AAGTTGTCTT AGAAAAG		
			CTA A		
GAM139	SCN1A	3'	GAAAAACAAATTCTTAAATTTTC 3451	TA_	C
			A TGG TTAAGAATT GTTTTTC		
			ACT AATTCTTAA CAAAAG		
			TTA A		
GAM139	FLJ13315	5'	GAAAAACGGAGGATTAACCA 2127	A	GAA
			TGGT TTAA TTCGTTTTTC		
			ACCA AATT AGGCAAAAAG		
			A AGG		
GAM139	KIAA0940	3'	AAAATGGTATTATTAATACCAT 1584	G	_
			A TATGGTATTAA AAT TCGTTTT		
			ATACCATAATT TTA GGTA AAA		
			A T		
GAM139	SARM	3'	GAAATATAATTCTTAATATCAT 1608	C	T
			A TATGGTATTAAGAATT GT TTTC		
			ATACTATAATTCTTAA TA AAAG		
			_ T		
GAM139	LOC144231	5'	TGTAATTCTTAATACCAT 3266	_	
			ATGGTATTAAGAATT CG		
			TACCATAATTCTTAA GT		
			T		
GAM139	LOC148734	3'	GAAAATGGGGCCCTTAATAC 3124	AA_	
			GTATTAAG TTCGTTTTT		
			CATAATTC GGGTAAAAG		
			CCG		
GAM140	MBD1	3'	TTAAATATGCATCTGGCCCAGG 924	C	TTTAA
			AA TTCCT GGCCA ATATTTAA		
			AAGGA CCGGT TATAAATT		
			C CTACG		
GAM140	MBD1	3'	TTAAATATGCATCTGGCCCAGG 1644	C	TTTAA
			AA TTCCT GGCCA ATATTTAA		

			AAGGA CCGGT TATAAATT	
			C CTACG	
GAM140	MBD1	3'	TTAAATATGCATCTGGCCCAGG 1645	C TTTTA
	AA		TTCCT GGCCA ATATTTAA	
			AAGGA CCGGT TATAAATT	
			C CTACG	
GAM140	MBD1	3'	TTAAATATGCATCTGGCCCAGG 1646	C TTTTA
	AA		TTCCT GGCCA ATATTTAA	
			AAGGA CCGGT TATAAATT	
			C CTACG	
GAM140	LOC254734	3'	TTAAATATTCAGAACCGAGGA 3666	CCA T
			TCCTCGG TTT AATATTTAA	
			AGGAGCC AGA TTATAAATT	
			A__ C	
GAM140	LOC51026	3'	AAGTATTAACCAAGGAA 1659	C CCA
			TTCCT GG TTTTAATATTT	
			AAGGA CC AAAATTATGAA	
			A ____	
GAM141	AICDA	3'	TTGCAAGGAAATTGTGCTTTAT 1923	C____ C
	C		GATAAAGC TTCCT GCAA	
			CTATTTCTG AAGGA CGTT	
			TGTTA A	
GAM141	GCG	3'	GGAATAAAGTTTTATCAAA 895	C____
			TTTGATAAAGC TTCC	
			AAACTATTTTG AAGG	
			AAAT	
GAM141	PTPN1	3'	TTGCATCAAGGGCTTTATCAAA 960	CCTC
			TTTGATAAAGCCTT GCAA	
			AAACTATTTCTGGGA CGTT	
			ACTA	
GAM141	SCO2	5'	GCGAGGAGCATCAGA 1189	AAA CT
			TTTGAT GC TCCTCGC	
			AGACTA CG AGGAGCG	
			____ _	
GAM141	UNG	3'	TGTGAGCTTTATCAGA 2394	CTTCC
			TTTGATAAAGC TCGCA	
			AGACTATTTCTG AGTGT	
			____ _	
GAM141	UNG	3'	TGTGAGCTTTATCAGA 1013	CTTCC
			TTTGATAAAGC TCGCA	

AGACTATTTTCG AGTGT

GAM141 BM046 3' TGCAAGAAAAAGGACTTATTAA 1831 AG C__ C
A TTTGATAA CCTT CT GCA
||||||| ||| || |||
AAATTATT GGAA GA CGT
CA AAA A

GAM141 DKFZP761G1913 3' TGCCAGGCTTTGCCAAA 2209 A TCCTC
TTTG TAAAGCCT GCA
||| ||||| |||
AAAC GTTTCGGA CGT
C C____

GAM141 KIAA0057 3' GTGAGGAAGACTTTACCAA 1422 A C
TTG TAAAG CTCCTCGC
||| ||||| |||||
AAC ATTTC GAAGGAGTG
C A

GAM141 RTCD1 3' TTGCTGAGAAGGCTTCATTAAA 1053 A C _
TTTGAT AAGCCTTC TC GCAA
||||| ||||| || |||
AAATTA TTCGGAAG AG CGTT
C _ T

GAM141 LOC127396 3' TGAGAAGGCCTTATTAAA 3005 A C
TTTGATAA GCCTTC TCG
||||||| ||||| |||
AAATTATT CGGAAG AGT
C _

GAM141 LOC130074 3' TGAGAGGCTTTATGAAA 3044 G TC
TTT ATAAAGCCT CTCG
||| ||||| |||
AAA TATTTTCGGA GAGT
G _

GAM141 LOC149134 5' TGCAGGAAAGTTTACCAAA 3308 ATA C C
TTTG AAGC TTCCT GCA
||| ||| ||||| |||
AAAC TTTG AAGGA CGT
CA_ A _

GAM141 LOC219818 3' TTGCAAGGAAGGCCTAATCA 3503 AAA C
TGAT GCCTTCCT GCAA
||| ||||| |||
ACTA CGGAAGGA CGTT
ATC A

GAM141 LOC256714 3' TGCTGGGCTTTAGCAAA 3702 A TCCTC
TTTG TAAAGCCT GCA
||| ||||| |||
AAAC ATTTTCGGG CGT
G T____

GAM141 LOC91149 5' TGCAAAGAAGGTTTCCAGA 2714 ATA CTC
TTTG AAGCCTTC GCA
||| ||||| |||

AGAC TTTGGAAG CGT
 C__ AAA
 GAM142 ACADSB 3' CCATCATTTGGAAAAATAAAGG 838 __ C TA
 C GCCTTTATT TCCA AT GATGG
 ||||| ||| || ||||
 CGGAAATAA AGGT TA CTACC
 AA T __
 GAM142 EDAR 3' CCATTTAAATGGGAATAAA 1985 CA
 TTTATTTCCA TTAGATGG
 ||||| |||||
 AAATAAGGGT AATTTACC
 A_
 GAM142 MAX 3' CCATTCCATGGAAATAAA 2515 CATTA
 TTTATTTCCA GATGG
 ||||| ||||
 AAATAAAGGT TTACC
 ACC__
 GAM142 MAX 3' CCATTCCATGGAAATAAA 923 CATTA
 TTTATTTCCA GATGG
 ||||| ||||
 AAATAAAGGT TTACC
 ACC__
 GAM142 MPO 3' AATGTTTATGATAATAAAGGC 722 _ C__
 GCCTTTATT TC ACATT
 ||||| || ||||
 CGGAAATAA AG TGTA
 T TATT
 GAM142 NEK4 3' TAATGTAGAGATAAAAGC 995 C C
 GC TTTATTTTC ACATTA
 || ||||| |||||
 CG AAATAGAG TGTAAT
 A A
 GAM142 C20orf170 3' CCAAATAATAATGAAAATAAA 2608 C C_ GA_
 GGC GCCTTTATTT CA ATTA TGG
 ||||| || ||| ||
 CGGAAATAAA GT TAAT ACC
 A AA AAA
 GAM142 FLJ20435 3' CCATCTGGAGGAAATAAA 1756 ACA
 TTTATTTCC TTAGATGG
 ||||| |||||
 AAATAAAGG GGTCTACC
 A_
 GAM142 FLJ23071 3' CCATCTAATGTTTTAAAAGGC 2143 ATTTCC
 GCCTTT ACATTAGATGG
 |||| |||||
 CGGAAA TGTAATCTACC
 ATTT__
 GAM142 KIAA0562 3' CCACTATAGCAAGAAATAAAGG 1525 CACAT_ A
 C GCCTTTATTT TAG TGG
 ||||| || |||

CGGAAATAAAG ATC ACC
AACGAT _

GAM142 LRRFIP1 3' CCACTTAATAAAAATAGAGGC 1151 CCAC A
GCCTTTATTT ATTAG TGG
||||||| |||||
CGGAGATAAA TAATT ACC
AA__ C

GAM142 P115 3' CCATCTAATGTGATTGCTAAG 1051 TATTTC
CTT CACATTAGATGG
||| |||||||||
GAA GTGTAATCTACC
TCGTTA

GAM142 SDCCAG16 3' CATTTTAAAAATAAAGGC 1316 CCACATT
GCCTTTATTT AGATG
||||||| |||||
CGGAAATAAA TTTAC
AAT__

GAM142 TIAF1 3' GATGTATGGAAATAAAGGC 2370 _
GCCTTTATTTCC ACATT
||||||| |||||
CGGAAATAAAGG TGTAG
TA

GAM142 LOC149711 3' CCAAATAATAATGAAAATAAA 3314 C C_ GA_
GGC GCCTTTATTT CA ATTA TGG
||||||| || |||||
CGGAAATAAA GT TAAT ACC
A AA AAA

GAM142 LOC169933 5' CCAGTAGGTGAAGATAAAGGC 3251 C ATTAGA
GCCTTTATTT CAC TGG
||||||| ||| |||
CGGAAATAGA GTG ACC
A GATG__

GAM143 SNX9 3' ACAAATTGTAAAGAATATGT 1673 CCG
ACATAT TTACAATTTGT
||||| |||||||||
TGTATA AATGTAAACA
AGA

GAM143 TOX 5' AACAAACCACAAACGGATGTG 1533 ACAA_
CATATCCGTT TTTGTT
||||||| |||||
GTGTAGGCAA AAACAA
ACACC

GAM143 DKFZP434C212 3' AACAAATTGCATAGGAGTGT 2833 A GTTA
ACAT TCC CAATTTGTT
||| ||| |||||||
TGTG AGG GTTAAACAA
_ ATAC

GAM143 LOC151438 5' AACAAACCAAAAACGGATATG 3345 ACAA_
CATATCCGTT TTTGTT
||||||| |||||

GTATAGGCAA AAACAA
 AAACC
 GAM143 LOC221663 3' AACAAATTGCATGGATTTGT 3619 T TA
 ACA ATCCGT CAATTTGTT
 ||| ||||| |||||
 TGT TAGGTA GTTAAACAA
 T C_
 GAM143 LOC257358 5' AACATGACTAACGGATATTC 3730 C CAATT
 A ATATCCGTTA TGTT
 | ||||| |||
 C TATAGGCAAT ACAA
 T CAGT_
 GAM143 LOC56832 3' AACAAATTGTGGATCATG 2703 _ GTT
 CAT ATCC ACAATTTGTT
 ||| ||| |||||
 GTA TAGG TGTTAAACAA
 C _
 GAM144 SOX9 3' ATGATCCTAAAAATAACCG 732 TG C_
 CG TGTTT AGGATCAT
 || ||||| |||||
 GC ATAAA TCCTAGTA
 CA AA
 GAM144 FLJ14356 3' ATGAATGCAAACACATG 2171 _ GGA
 CGTGTGTTT CA TCAT
 ||||| || |||
 GTACACAAA GT AGTA
 C A_
 GAM144 KIAA0982 3' ATGACCCTGAAATGACTG 1464 C G A
 CA GT TGTTCAGG TCAT
 || || ||||| |||
 GT CA GTAAAGTCC AGTA
 _ _ C
 GAM144 KIAA1028 3' ATGATCCTGAAGAAAAAGGTGA 3546 ACGTGTG
 TCACC TTTCAGGATCAT
 |||| |||||
 AGTGG GAAGTCCTAGTA
 AAAAA_
 GAM144 PCQAP 3' CCTTAAACACACATGGGA 1649 A C C_
 TC CCA GTGTGTTT AGG
 || ||| ||||| |||
 AG GGT CACACAAA TCC
 _ A AT
 GAM144 PRKWINK2 3' GATCCTGAAATCAAGG 3488 ACG T
 CC TG GTTTCAGGATC
 || || |||||
 GG AC TAAAGTCCTAG
 A _ _
 GAM144 RCD-8 3' ATGACCCTGAGATCGTG 1491 TGT A
 CACG GTTTCAGG TCAT
 ||| ||||| |||

			GTGC TAGAGTCC AGTA		
			____ C		
GAM144	SMOC2	3'	ATGATCCTAAACTTTTTGG 2945	CGTGT	C
			CCA GTTT AGGATCAT		
			GGT CAAA TCCTAGTA		
			TTTT_ _		
GAM144	SYNJ2	3'	ATCCTGAGCCATGGTG 2605	CG T T	
			CACCA TG GTT CAGGAT		
			GTGGT AC CGA GTCCTA		
			____ _ _		
GAM144	TRABID	3'	ATGACCCTAAAGTTAGTGTGGT 2823	GTG C A	
	G		CACCACGT TTT AGG TCAT		
			GTGGTGTG GAA TCC AGTA		
			ATT A C		
GAM144	TSGA14	3'	CTGTGGACACACAAGGTGA 1861	AC	_
			TCACC GTGTGTTT CAG		
			AGTGG CACACAGG GTC		
			AA T		
GAM144	LOC197201	3'	TCTGGAAAACAACACACGGTGA 3421	AC	_____
			TCACC GTGTGT TTCAGG		
			AGTGG CACACA AGGTCT		
			____ ACAA		
GAM144	LOC219401	3'	ATGAAGCAAACACACGTAGG 3579	_	CAGGA
			CC ACGTGTGTTT TCAT		
			GG TGCACACAAA AGTA		
			A CGA__		
GAM145	INHBA	3'	ACTAGAACAACCCAAATAGCA 904	C C CCAG	
			TGCTATTT GG TG AGT		
			ACGATAAA CC AC TCA		
			C A AAGA		
GAM145	TBXAS1	5'	ACACTCTGAGAAAGAGCA 2182	A GGCTGC	
			TGCT TTTC CAGAGTGT		
			ACGA AAAG GTCTCACA		
			G A_____		
GAM145	TBXAS1	5'	ACACTCTGAGAAAGAGCA 798	A GGCTGC	
			TGCT TTTC CAGAGTGT		
			ACGA AAAG GTCTCACA		
			G A_____		
GAM145	KIAA1056	5'	ACACTTCAGCCGCAGCCAAATA 1576	C CA_____	
	GCA		TGCTATTT GGCTGC GAGTGT		

ACGATAAA CCGACG TTCACA
 _ CCGAC
 GAM145 LOC197342 3' GACACCTGGCTGAGCCGGAACA 3424 A _ A
 GCA TGCT TTTCGGCT GCCAG GTGTC
 ||| ||||| ||| ||||
 ACGA AAGGCCGA CGGTC CACAG
 C GT _
 GAM145 LOC91752 5' GACACTCTAGATGAAA 2779 G GCC
 TTTCG CT AGAGTGTC
 |||| || |||||
 AAAGT GA TCTCACAG
 A _
 GAM146 FLJ11838 3' ATGAATAAACATATCTTG 2078
 TAAGATATGTTTATTCAT
 ||||| |||||
 GTTCTATACAAATAAGTA

 GAM147 ATP10C 3' AATACAGGAAACAAGAGGTAC 2062 T _
 GT CCTC GTTTCCTGTATT
 || ||| |||||
 CA GGAG CAAAGGACATAA
 T AA
 GAM147 CASP10 3' ACAGGGAACAAAGAAACA 2304 C C_
 TGTT CT GTTTCCTGT
 ||| || |||||
 ACAA GA CAAGGGACA
 A AA
 GAM147 ZNF36 3' GGAAACAGAAACATAGA 3627 C C
 TCTATGTT CT GTTTC
 ||||| || |||||
 AGATACAA GA CAAAGG
 A _
 GAM147 DORFIN 3' AATACAGGAAATAGATAAACAT 1630 CC _
 G TATGTT TC GTTTCCTGTATT
 |||| || |||||
 GTACAA AG TAAAGGACATAA
 AT A
 GAM147 FLJ21313 3' AATACAGGATGAAAAACACTGA 2037 TA CC TT
 TC TGTT TCG TCCTGTATT
 || ||| || |||||
 AG ACAA AGT AGGACATAA
 TC AA _
 GAM147 KIAA1819 5' AATACAGGAGATAGAACCAGA 2865 AT CTC
 TCT GTTC GTTTCCTGTATT
 || ||| |||||
 AGA CAAG TAGAGGACATAA
 C_ A_
 GAM147 P37NB 3' ATGGGAAAAAAAACATAGA 1254 CCTCG
 TCTATGTT TTTCCTGT
 ||||| |||||

			AGATACAA AAAGGGTA	
			AAA__	
GAM147	RAP140	5'	ATACAGATAGAAACATAGA 1613	CC GTTTC
			TCTATGTT TC CTGTAT	
			AGATACAA AG GACATA	
			__ ATA__	
GAM147	LOC127002	3'	AATATAAAAACAGAAACATAGA 3002	C C CC
			TCTATGTT CT GTTT TGTATT	
			AGATACAA GA CAAA ATATAA	
			A _ A_	
GAM147	LOC132332	3'	AATACAGTTGCAGAGGAGCATA 3046	_ TTC
			TATGTTCCCTC GT CTGTATT	
			ATACGAGGAG CG GACATAA	
			A TT_	
GAM147	LOC145624	5'	ACTAGAAGAGGAACATA 3276	GT CT
			TATGTTCCCTC TTC GT	
			ATACAAGGAG AAG CA	
			_ AT	
GAM148	NR4A2	3'	AATAGTATTTTCAGACACTATG 1277	A CA
			TATAGT TCTGAAAT TATT	
			GTATCA AGACTTTA ATAA	
			C TG	
GAM148	PRKCN	3'	ATGATTATTCCAGATACTGTA 1252	A__
			TATAGTATCTG AATCAT	
			ATGTCATAGAC TTAGTA	
			CTTA	
GAM148	BIVM	3'	ATGGTGGGTGATTTTCAGATAT 1739	AT_
			GTATCTGAAATCAT TCAT	
			TATAGACTTTAGTG GGTA	
			GGT	
GAM148	DCLRE1A	3'	ATGAAGATTGTTTCAGATACT 2843	ATCATA
			AGTATCTGAA TTCAT	
			TCATAGACTT AAGTA	
			GTTAG_	
GAM148	EBF2	3'	ATGAAGCCTTTTCAGATAC 1995	TCATA
			GTATCTGAAA TTCAT	
			CATAGACTTT AAGTA	
			CCG__	
GAM148	FLJ10852	3'	GAATATTTTCAGATACTATA 1873	TC
			TATAGTATCTGAAA ATATTC	

ATATCATAGACTTT TATAAG

GAM148 FLJ20220 3' ATGAATAACATTTCAGATAC 1742 CA
GTATCTGAAAT TATTCAT
||||||| |||||
CATAGACTTTA ATAAGTA
CA

GAM148 FLJ21952 3' ATGATATTCTAGATACTATA 1992 _ _
TATAGTATCT GAA ATCAT
||||||| ||| |||||
ATATCATAGA CTT TAGTA
T A

GAM148 MGC10724 3' ATGAAGACCCAGATACTA 2274 AAA ATA
TAGTATCTG TC TTCAT
||||||| || |||||
ATCATAGAC AG AAGTA
CC_ _

GAM148 MGC4238 3' ATGGAAGGACTTCAGATAC 2247 A ATA
GTATCTGAA TC TTCAT
||||||| || |||||
CATAGACTT AG AGGTA
C GA_

GAM148 Rab11-FIP2 3' ATGACAGTATCTGCAGATACTA 1581 AAATCATAT
TA TATAGTATCTG TCAT
||||||| |||||
ATATCATAGAC AGTA
GTCTATGAC

GAM148 LOC90768 3' ATGAAGGTGTGTCCCAGATATT 2674 AAAT_ A
A TAGTATCTG CAT TTCAT
||||||| ||| |||||
ATTATAGAC GTG AAGTA
CCTGT G

GAM149 ANPEP 3' CTAAATCTGAGGAATCAAC 805 CT TA
GTTGAT CTCA GATTTAG
||||| ||||| |||||
CAACTA GAGT CTAAATC
AG _

GAM149 NP 3' TCTAAATCACCAGAGACCAAAC 724 GA_ CATA
GTT TCTCT GATTTAGA
||| ||||| |||||
CAA AGAGA CTAAATCT
ACC CCA_

GAM149 TFAP2C 3' CTAGATCAACAGATCAAC 1000 CTCATA
GTTGATCT GATTTAG
||||||| |||||
CAACTAGA CTAGATC
CAA_

GAM149 ZNF83 5' CTAAATGTGAGATCAAGGA 1813 G T AGAT
TC TTGATCTC CAT TTAG
|| ||||| ||| |||||

			AG AACTAGAG GTA AATC	
			G T _	
GAM149	MGC26766	3'	TTTACATCATGAGAGATCAA 2509	A T
			TTGATCTCTCAT GAT TAGA	
			AACTAGAGAGTA CTA ATTT	
			_ C	
GAM149	SCYB10	3'	TCTAAATGTTGAAAGATCAA 836	C TAG
			TTGATCT TCA ATTTAGA	
			AACTAGA AGT TAAATCT	
			A TG_	
GAM150	EBAF	3'	TACAGCTGAGCAATGCA 2721	CG AAATA
			TGCAT GT TAGCTGTA	
			ACGTA CG GTCGACAT	
			A_ A_	
GAM150	F7	3'	ATACGCAAACACACCGATGCA 706	AAATATA T
			TGCATCGGT GC GTAT	
			ACGTAGCCA CG CATA	
			CACAAA_ _	
GAM150	F7	3'	ATACGCAAACACACCGATGCA 1885	AAATATA T
			TGCATCGGT GC GTAT	
			ACGTAGCCA CG CATA	
			CACAAA_ _	
GAM150	MGC3771	3'	TAGAACATTTACCGATGC 2178	ATAG
			GCATCGGTAAAT CTG	
			CGTAGCCATTTA GAT	
			CAA_	
GAM150	LOC146438	3'	TAGAACATTTACCGATGC 3091	ATAG
			GCATCGGTAAAT CTG	
			CGTAGCCATTTA GAT	
			CAA_	
GAM151	BPGM	3'	TAAGAAGAAATGCAAAAG 852	CG
			CTT GCATTTCTTTTA	
			GAA CGTAAAGAAGAAT	
			AA	
GAM151	HAS2	3'	AAATGAAATGCCAAAGGAA 1198	C T
			TTCCTT GGCATTTT TTT	
			AAGGAA CCGTAAAG AAA	
			A T	
GAM151	HDAC2	3'	CATTAAAAAGAAAATATTGAAA 3507	_ CA_
	GGAA		TTCCTT CGG TTTCTTTTAAATG	

			AAGGAA GTT AAAGAAAAATTAC	
			A ATA	
GAM151	XRCC2	3'	CATTAAAAAGTGGGCAAAGGA 1208	CG ATTT
			TCCTT GC CTTTTTAATG	
			AGGAA CG GAAAAATTAC	
			A_ GGT_	
GAM151	APACD	3'	CATTAAAAAGAAACCAGGAA 1249	TC CA
			TTCCT GG TTTCTTTTAAATG	
			AAGGA CC AAAGAAAAATTAC	
			— —	
GAM151	SCIN	3'	CATTAAAATAACCTGAAGGAA 2313	CATTCT
			TTCCTTCGG TTTAATG	
			AAGGAAGTC AAAATTAC	
			CAAT_	
GAM151	USP16	3'	CATTAAATACATGCCAGAAG 1303	_ TTCTT
			CTTC GGCAT TTTAATG	
			GAAG CCGTA AAATTAC	
			A CAT_	
GAM151	LOC115004	3'	AAAAGAAATCCGAAAGAA 2970	C C
			TTC TTCGG ATTTCTTTT	
			AAG AAGCC TAAAGAAAA	
			A _	
GAM151	LOC146520	5'	GAAGAGAAATGCCATAGGAA 3096	TC
			TTCCT GGCATTTCTTTT	
			AAGGA CCGTAAAGAGAAG	
			TA	
GAM151	LOC219333	3'	CATTAAAAAAAACATGCCG 3607	_ C
			CGGCAT TT TTTTAAATG	
			GCCGTA AA AAAAATTAC	
			CA A	
GAM152	EIF1A	3'	CTTTGTGTTTTTGGTTTACCCT 3442	A_ TCT
			AG TAACTAAA CGCAAAG	
			TC ATTTGGTTT GTGTTTC	
			CC TT_	
GAM152	ENAM	3'	TTTGTTTTTAGTTATCTTA 2217	A TCTC
			TAAGATAA CTAAA GCAAA	
			ATTCTATT GATTT TGTTT	
			_ T_	
GAM152	MYCL1	3'	TTTGTTGGTAGCTTATCTTA 1204	A AATC
			TAAGATAA CTA TCGCAAA	

			ATTCTATT GAT GGTGTTT	
			C ____	
GAM152	ZNF42	5'	CTTTGATGTATTCTAGTTTATC 1018	AATCT _
	T		AGATAAACTA CG CAAAG	
			TCTATTTGAT GT GTTTC	
			CTTAT A	
GAM152	FLJ23604	3'	AGAATATAGTTTATCTTA 2134	AA_
			TAAGATAAACTA TCT	
			ATTCTATTTGAT AGA	
			ATA	
GAM152	HEY2	3'	AGATCTAGTTTATCTTA 1419	_ A
			TAAGATAAA CTA ATCT	
			ATTCTATTT GAT TAGA	
			T C	
GAM152	TSC22	3'	TGGGACCTAGGCTATCTTA 1265	AA AA
			TAAGATA CTA TCTCG	
			ATTCTAT GAT AGGGT	
			CG CC	
GAM153	FLJ20296	3'	ACATTAATAAATTTATTGATTC 1748	A CAA
	CA		TG AATC GGATTTATTAATGT	
			AC TTAG TTAAATAATTACA	
			C TTA	
GAM153	RAB22A	3'	ACATTAATAAATTCTAAGTTTC 2546	CCA
	A		TGAAAT AGGATTTATTAATGT	
			ACTTTG TCTTAAATAATTACA	
			AA_	
GAM153	UPLC1	3'	ACATTTGTTCTCTTGGATCTCA 1740	A _ TTTATT
			TGA ATCCAAG GA AATGT	
			ACT TAGGTTCT CT TTACA	
			C T TGT__	
GAM153	LOC122886	3'	ACACTGTGTTCCCTTGGACCTC 3028	AA TT TAA
			GA TCCAAGGA TAT TGT	
			CT AGGTTCCCT GTG ACA	
			CC T_ TC_	
GAM153	LOC222194	3'	ACATCATCTGTTCTTGGACCTC 3637	AA TTATTA
	A		TGA TCCAAGGAT ATGT	
			ACT AGGTTCTTG TACA	
			CC TCTAC_	
GAM154	ITGB1	3'	AGTAAATGTCCTGCTA 909	GA
			TAGCAGGACATT TGCT	

ATCGTCCTGTAA ATGA

GAM154 RHO 3' TCTAGAGCATGGAGCCTCTA 754 C ACA G
TAG AGG TT ATGCTCTAGA
||| ||| || |||||
ATC TCC AG TACGAGATCT
_ G_ G

GAM154 XPNPEP2 3' CTGGGTCCACATCCTGCTA 1015 CAT AT T
TAGCAGGA TG GC CTAG
||||| || || |||
ATCGTCCT AC TG GGTC
AC_ C_ _

GAM154 FLJ12700 3' CTAGAACAGGATGTCCTGC 2110 GA C
GCAGGACATT TG TCTAG
||||| || |||
CGTCCTGTAG AC AGATC
G_ A

GAM154 FLJ13291 3' GTCCAGAGTTAACTGCCCTGCT 2234 A TTGAT A
G TAGCAGG CA GCTCT GAC
||||| || ||| |||
GTCGTCC GT TGAGA CTG
C CAAT_ C

GAM154 FLJ20811 5' CTAGAGCACAAAGTCCTGCTA 2782 A A
TAGCAGGAC TTG TGCTCTAG
||||| ||| |||||
ATCGTCCTG AAC ACGAGATC

GAM154 KIAA1643 3' TCCAGAGCCTCTGTCCTGC 2693 TT T A
GCAGGACA GA GCTCT GA
||||| || ||| ||
CGTCCTGT CT CGAGA CT
_ C C

GAM154 KIAA1755 3' TCCAGAGCATTTATCTGC 2596 ACATT A
GCAGG GATGCTCT GA
|||| ||||| ||
CGTCT TTACGAGA CT
AT_ C

GAM154 KIAA1762 3' GTCTAGAGCACACACCGCT 2669 A ACAT A
AGC GG TG TGCTCTAGAC
||| || || |||||
TCG CC AC ACGAGATCTG
_ AC_ C

GAM154 MGC13033 5' TCCAGAGCATTCCTTCTA 2199 C CATTG A
TAG AGGA ATGCTCT GA
||| ||| ||||| ||
ATC TCCT TACGAGA CT
T _ C

GAM154 SLC7A3 5' TCTTCTTCAATTCCTGCTA 2281 C TGCTCT
TAGCAGGA ATTGA AGA
||||| ||| |||

ATCGTCCT TAACT TCT
 _ TCT_
 GAM154 LOC112609 3' GTCTAGAGTGATCCATCC 2960 CATT _
 GGA GAT GCTCTAGAC
 ||| ||| |||||
 CCT CTA TGAGATCTG
 AC_ G
 GAM154 LOC157349 5' GTCCAAAAGTTTAACTGTCCTG 3201 _ T CTA_
 C GCAGGACA TTGA GCT GAC
 ||||| ||| ||| |||
 CGTCCTGT AATT TGA CTG
 C _ AAAC
 GAM154 LOC90625 3' TCCAGATGATGCTCCTGCTA 2662 _ ATGC A
 TAGCAGGA CATTG TCT GA
 ||||| ||| ||| ||
 ATCGTCCT GTAGT AGA CT
 C _ C
 GAM155 MGAT4B 5' CCGCTACAAGGACAGTG 2360 ATAT TC
 CACT GTT TGTAGCGG
 ||| ||| |||||
 GTGA CAG ACATCGCC
 _ GA
 GAM155 PRKAR2A 3' GCCACAGAACACATACAG 1091 A _ A
 CT TATGT TTCTGT GC
 || |||| ||||| ||
 GA ATACA AAGACA CG
 C C C
 GAM155 SCD 3' GCCACGGAAACATACAGAGGA 1177 A A A
 TCC CT TATGTTTCTGT GC
 ||| || ||||| ||
 AGG GA ATACAAAGGCA CG
 A C C
 GAM155 DKFZp761H079 3' GCCACCTGAAACATAAAATGGA 2506 CTA T_ A
 TCCA TATGTTTC GT GC
 ||| ||||| ||| ||
 AGGT ATACAAAG CA CG
 AAA TC C
 GAM155 KIAA0417 3' GCCATGATGGAAACAGATAGTG 2910 A AGC
 CACTAT TGTTTCTGT GGC
 ||||| ||||| ||| ||
 GTGATA ACAAAGGTA CCG
 G GTA
 GAM155 LRBA 3' CCAATTATGGAAACATACAGTG 1327 A C_
 GA TCCACT TATGTTTCTGTAG GG
 ||||| ||||| ||| ||
 AGGTGA ATACAAAGGTATT CC
 C AA
 GAM155 SYAP1 3' GCCACAGAAACATAAGT 2279 A A
 ACT TATGTTTCTGT GC
 ||| ||||| ||| ||

TGA ATACAAAGACA CG
 _ C
 GAM155 LOC143188 5' ACAGAAACTATAGCAGA 3264 CA T
 TC CTATA GTTTCTGT
 || |||| |||||
 AG GATAT CAAAGACA
 AC _
 GAM155 LOC157292 3' GCCTCAGAAACATAAGTG 3378 A TA
 CACT TATGTTTCTG GC
 ||| ||||| ||
 GTGA ATACAAAGAC CG
 _ TC
 GAM156 C18orf1 3' AGTCATTATTGTTGCAGGA 2561 _ T TT
 TCC GCA AT TAATGACT
 ||| ||| || |||||
 AGG CGT TG ATTACTGA
 A _ TT
 GAM156 CRYZ 3' AAGAGTCATCATAGTAGGAA 866 GCA TTTA
 TTCC TAT ATGACTCTT
 ||| ||| |||||
 AAGG ATA TACTGAGAA
 ATG C__
 GAM156 TRPC5 3' GAAGTGTCAAAATATGAGAA 1434 CG TAA T
 TTC CATATTT TGAC CTTC
 ||| ||||| ||| |||
 AAG GTATAAA ACTG GAAG
 A_ _ T
 GAM156 DAP13 3' GAAGAACAGTTGAAACATGC 1862 A GAC
 GCAT TTTTAAT TCTTC
 ||| ||||| |||
 CGTA AAAGTTG AGAAG
 C ACA
 GAM156 DKFZP564O0463 3' GAAGAGCCATTACATGC 1481 ATTT A
 GCAT TAATG CTCTTC
 ||| ||||| |||||
 CGTA ATTAC GAGAAG
 C__ C
 GAM156 GRID1 3' AAGAACCATTAGGAGTGGA 2822 ATA AC
 TTCCGC TTTTAATG TCTT
 ||||| ||||| |||
 AAGGTG AGGATTAC AGAA
 _ CA
 GAM156 MGC30052 3' AAGACTTTTTTGAAAATATGCA 2499 C AAT__ C
 GAA TTC GCATATTTT GA TCTT
 ||| ||||| || |||
 AAG CGTATAAAA TT AGAA
 A GTTTT C
 GAM156 MGC32104 5' AAGAGTCATGCTGTGATGAA 2494 CG TTTTA
 TTC CATA ATGACTCTT
 ||| ||| |||||

			AAG GTGT TACTGAGAA		
			TA CG__		
GAM156	SCN9A	5'	GAAGAGGAATTTAAATATACAG 975	GC_	GA
	GA		TCC ATATTTTAAT CTCTTC		
			AGG TATAAAATTA GAGAAG		
			ACA AG		
GAM156	STK17A	3'	AGTCCAATTTAAATATGGAA 1154	GC	__
			TTCC ATATTTTAAT GACT		
			AAGG TATAAAATTA CTGA		
			__ AC		
GAM156	LOC148738	3'	AAGAATCATTAAAGGAAGC 2519	ATA	C
			GC TTTTAATGA TCTT		
			CG GAAATTACT AGAA		
			AAG A		
GAM157	BLMH	3'	GGTGGCCTAAGAGTTGAGCTC 734	A	CT
			GAGCTCAAC CTTA CCGCC		
			CTCGAGTTG GAAT GGTGG		
			A CC		
GAM157	BLVRB	3'	GGCAATAAATGTTGAGCC 768	A	C CTCC
			G GCTCAACA TTA GCC		
			C CGAGTTGT AAT CGG		
			_ A AA__		
GAM157	DHCR7	3'	GGTAGCGTGCACGGTGTGAAC 821	C	TACTC C
	T		AG TCAACACT CGC ACC		
			TC AGTTGTGG GCG TGG		
			A CACGT A		
GAM157	FGFR1	3'	GGTGACAGAGTGAGTGAGACTC 2032	_ AAC	__
			GAG CTC ACTTACTC CGCC		
			CTC GAG TGAGTGAG GTGG		
			A __ ACA		
GAM157	FGFR1	3'	GGTGACAGAGTGAGTGAGACTC 2034	_ AAC	__
			GAG CTC ACTTACTC CGCC		
			CTC GAG TGAGTGAG GTGG		
			A __ ACA		
GAM157	HEM1	3'	GGTGACTTGAGCTTGAGCTC 1200	CA	CTC
			GAGCTCAA CTTA CGCC		
			CTCGAGTT GAGT GTGG		
			C_ TCA		
GAM157	NT5C3	5'	GGTGGCGGGGGTGGTGCTGGCT 1689	T A	TA
	C		GAGC CA CACT CTCCGCCACC		

CTCG GT GTGG GGGGCGGTGG
_ C TG

GAM157 OTOR 3' GCGGGGAAATGTTGAGCTC 1894 C A
GAGCTCAACA TT CTCCGC
||||||| || |||||
CTCGAGTTGT AA GGGGCG
A _

GAM157 PRPSAP2 5' GCAATCAGTAAACATTGAGCT 954 CAC_ CC_
C GAGCTCAA TTACT GC
||||| ||| ||
CTCGAGTT AATGA CG
ACAA CTAA

GAM157 C14orf4 5' GGTGGCGGAGGCCCCCAGCTC 2788 CAACACTTA
GAGCT CTCCGCCACC
|||| |||||
CTCGA GAGGCGGTGG
CCCCCG__

GAM157 CG012 3' GGCGACAGAGTGAGTGAGACTC 3272 _ AAC _
GAG CTC ACTTACTC CGCC
||| ||| ||||| |||
CTC GAG TGAGTGAG GCGG
A _ ACA

GAM157 DKFZP434K2235 5' GGTGGCGGGTAACGCCGGA CT C 3278 C AACAC T
GAG TC TTAC CCGCCACC
||| || ||| |||||
CTC AG AATG GGCGGTGG
_ GCCGC _

GAM157 FLJ20699 3' GGTGCAAGGATTGAGCTC 1766 CA ACTC
GAGCTCAA CTT CGCC
||||| ||| |||
CTCGAGTT GAA GTGG
AG C__

GAM157 FLJ23129 3' GGCAACAGGAGAATGTCAAGCC 2088 A CA C A _
G GCT ACA TT CTCC GCC
| ||| ||| ||| |||
C CGA TGT AA GAGG CGG
_ AC _ _ ACAA

GAM157 HSPC065 3' GTGACGGAGTAGAAGCTT 1482 CAACAC C
GAGCT TTACTCCG CAC
|||| ||||| |||
TTCGA GATGAGGC GTG
A__ A

GAM157 KIAA0960 3' GGTAATTTAAGTGTGAAGT 3572 _ CTCC
GCT CAACACTTA GCC
||| ||||| |||
TGA GTTGTGAAT TGG
A TTAA

GAM157 MGC12466 3' GGTAAGGAGTGTTGAACTC 3127 C A CC
GAG TCAACACTT CT GCC
||| ||||| ||| |||

			CTC AGTTGTGAG GA TGG		
			A _ AA		
GAM157	MGC12904	3'	GCAGTGAGTGCTGAGCTC 2184	A	CC
			GAGCTCA CACTTACT GC		
			CTCGAGT GTGAGTGA CG		
			C _		
GAM157	MSTP028	3'	GGCAGTAAGTGTCCAGCTC 2224	CA	CC
			GAGCT ACACTTACT GCC		
			CTCGA TGTGAATGA CGG		
			CC _		
GAM157	RAB24	5'	TGACGGAGTAGCGAGCT 2397	AACAC	C
			AGCTC TTACTCCG CA		
			TCGAG GATGAGGC GT		
			C_ A		
GAM157	LOC113828	5'	TGAGGAGACGTTGAGCTC 2439	ACTTA	GC
			GAGCTCAAC CTCC CA		
			CTCGAGTTG GAGG GT		
			CA_ A_		
GAM157	LOC152300	5'	GTGGACAGCATTGAGCTC 3169	CA	TAC
			GAGCTCAA CT TCCGC		
			CTCGAGTT GA AGGTG		
			AC C_		
GAM157	LOC197125	3'	GGCAGGTAACATTGAGCTC 3420	CAC	CC
			GAGCTCAA TTACT GCC		
			CTCGAGTT AATGG CGG		
			AC_ A_		
GAM157	LOC219848	3'	GGTGACAGAGTAGGTGCTC 3528	TCAAC	_
			GAGC ACTTACTC CGCC		
			CTCG TGGATGAG GTGG		
			_ ACA		
GAM157	LOC51157	5'	GGTGGCGGGGTTTTGCAGAGCT 1671	AA	CTT
	C		GAGCTC CA ACTCCGCCACC		
			CTCGAG GT TGGGGCGGTGG		
			AC TT_		
GAM157	LOC92270	5'	GGTGACAGAGTGAGTGAGACTC 2828	_ AAC	_
			GAG CTC ACTTACTC CGCC		
			CTC GAG TGAGTGAG GTGG		
			A _ ACA		
GAM158	B3GALT3	3'	GCTGGTGTAAACAAACCTACTA 1057	A	C G_
	CA		TGTGGTAG TTTGTT TATA AGC		

ACATCATC AAACAA ATGT TCG
 C _ GG
 GAM158 KIAA1985 5' GCTCTGTATTAACAAATCCA 2066 A C____
 CCA TGGT GATTTGTT TATAGAGC
 |||| ||||| |||||
 ACCA CTAAACAA ATGTCTCG
 C AATT
 GAM158 MCM10 3' CTATGCAAATTACCACA 1835 A TCT
 TGTGGT GATTTGT ATAG
 ||||| ||||| |||
 ACACCA TTAAACG TATC

 GAM158 LOC149707 5' CTCCACAACATCTACCA 3137 _ TCTATA
 TGGTAGAT TTGT GAG
 ||||| ||| |||
 ACCATCTA AACA CTC
 C C____
 GAM158 LOC200227 5' CTCCACAACATCTACCA 3446 _ TCTATA
 TGGTAGAT TTGT GAG
 ||||| ||| |||
 ACCATCTA AACA CTC
 C C____
 GAM158 LOC255718 5' GCTCTATAGAACATGTCTAC 3741 T
 GTAGAT TGTTCTATAGAGC
 ||||| |||||
 CATCTG ACAAGATATCTCG
 T
 GAM159 DSG3 3' TTAAATGTTTGGGTTTCATAC 873 C_
 GTAT ATTTAAACATTTAA
 ||| |||||
 CATA TGGGTTTGTAATT
 CT
 GAM159 LPIN1 3' AAATGATAATGATACTG 2791 TAAA
 CAGTATCATT CATTT
 ||||| |||||
 GTCATAGTAA GTAAA
 TA_
 GAM159 TRPM1 3' AAATGAAAGTGATGATACTGT 928 TAAA_
 ACAGTATCATT CATTT
 ||||| |||||
 TGTCATAGTAG GTAAA
 TGAAA
 GAM159 DEPP 3' GTTAAATGTTTTCTGTCTTCTG 1347 TAT_ TTT
 TT AACAG CA AAACATTTAAC
 |||| || |||||
 TTGTC GT TTTGTAAATTG
 TTCT CT_
 GAM159 FLJ20668 3' TTAAATGGACCATGATACT 1764 TTAAA
 AGTATCAT CATTTAA
 ||||| |||||

			TCATAGTA	GTAAATT		
			CCAG_			
GAM159	KIAA1524	5'	TAAATGTTTAGAACCTACTGT	2975	TCA	
			ACAGTA	TTTAAACATTTA		
			TGTCAT	AGATTTGTAAAT		
			CCA			
GAM159	PRO1617	5'	AAATCAGTGAATGGTACTG	1850	AAC	
			CAGTATCATTTA	ATTT		
			GTCATGGTAAGT	TAAA		
			GAC			
GAM159	SDF1	3'	GTAAATGTGATGAATACTGT	3502	_	TAA
			ACAGTATCATT	ACATTTAAC		
			TGTCATA	GTAG	TGTAAATTG	
			A	___		
GAM159	LOC130074	3'	GTTAGGTGTCAATTGATACT	3043	TTTAA	
			AGTATCA	ACATTTAAC		
			TCATAGT	TGTGGATTG		
			TAAC_			
GAM159	LOC146952	5'	TAAATGTAATTTTATGTACTGT	3287	T	TT
		T	AACAGTA	CAT	AA	ACATTTA
			TTGTCAT	GTA	TT	TGTAAAT
			_	TT	AA	
GAM159	LOC157983	3'	TTGCATGTAAATGATACT	3208	A	T
			AGTATCATTTAA	CAT	TAA	
			TCATAGTAAATT	GTA	GTT	
			_	C		
GAM159	LOC203289	3'	TTGCATGTAAATGATACT	3463	A	T
			AGTATCATTTAA	CAT	TAA	
			TCATAGTAAATT	GTA	GTT	
			_	C		
GAM159	LOC256544	3'	TTGCATGTAAATGATACT	3695	A	T
			AGTATCATTTAA	CAT	TAA	
			TCATAGTAAATT	GTA	GTT	
			_	C		
GAM160	APPL	3'	AGAACAGAGATTTTACAGT	1405	A	CA
			ATTG	TAAAATCTC	TTCT	
			TGAC	ATTTTAGAG	AAGA	
			_	AC		
GAM160	F8	3'	AATGGAGAGAATACAATA	708	A	AAA
			TATTG	TA	TCTCCATT	

			ATAAC AT AGAGGTAA	
			_ AAG	
GAM160	RAB6A	3'	AGAATGGAAATAAACTCAATA 966	TAAA_ C
	TTA		TAATATTGA AT TCCATTCT	
			ATTATAACT TA AGGTAAGA	
			CAAAA A	
GAM160	RNF14	3'	AGAATGGAAATTTATAATAT 1097	ATA C
			ATATTG AAAT TCCATTCT	
			TATAAT TTTA AGGTAAGA	
			A_ A	
GAM160	SART2	3'	AGAATTGGGTTTTATTAATATT 1443	CC
	A		TAATATTGATAAAATCT ATTCT	
			ATTATAATTATTTTGGG TAAGA	
			T_	
GAM160	EEA1	3'	AATGGTTTTTGTTTTAACAATA 1035	A CT__
	TTA		TAATATTG TAAAAT CCATT	
			ATTATAAC ATTTTG GGTA	
			A TTTTT	
GAM160	FLJ10980	3'	AGAATGGAGTGTAACCAAATTA 2697	A A AAAT
			TAAT TTG TA CTCCATTCT	
			ATTA AAC AT GAGGTAAGA	
			_ C GT__	
GAM160	FLJ22794	3'	AATGGTCATCTTATCAATA 3532	A CT
			TATTGATAA AT CCATT	
			ATAACTATT TA GGTA	
			C CT	
GAM160	KIAA1328	3'	AGAATGGAGCCCACTAATATTA 2601	ATAAAAT
			TAATATTG CTCCATTCT	
			ATTATAAT GAGGTAAGA	
			CACCC__	
GAM160	PRO0902	3'	AATGGAGATCAATTTTA 2357	T TAAAA
			TAA ATTGA TCTCCATT	
			ATT TAACT AGAGGTAA	
			T _____	
GAM160	RASGRP4	3'	AGAACAGGGATTCTATCAATG 2348	_ CA
	T		ATATTGATA AAATCTC TTCT	
			TGTAACAT TTTAGGG AAGA	
			C AC	
GAM160	WBP4	3'	AGAATGGAGACTTATACA 1363	_ AA
			TG ATAA TCTCCATTCT	

		AC TATT AGAGGTAAGA	
		A C_	
GAM160	LOC116150 3'	AGAATGGAGCAGTTTAATA 2443	TAAAAT
		TATTGA CTCCATTCT	
		ATAATT GAGGTAAGA	
		TGAC_	
GAM160	LOC164200 5'	AATGAGGTTGTTATCAATA 3248	_ C
		TATTGATAA AATCTC ATT	
		ATAACTATT TTGGAG TAA	
		G _	
GAM160	LOC51320 3'	AGAATGATAAATTATCAATAT 1702	AATCTC
		ATATTGATAA CATTCT	
		TATAACTATT GTAAGA	
		AAATA_	
GAM161	SELPLG 3'	CCAAACAGGAAGTGGACATTCT 2539	A CG C
		AGAAT TCCAT TTTG TTGG	
		TCTTA AGGTG GGAC AACC	
		C AA A	
GAM161	FLJ21144 3'	CCAAAACATAAACAATAAATAT 2007	CC C C_
	TCTCA	TGAGAATAT AT GTTTG TTGG	
		ACTCTTATA TA CAAAT AACC	
		AA A ACAA	
GAM161	KIAA0676 3'	CAAAGTGATGGAACCCTCA 1603	AATA _
		TGAG TCCATCG TTTG	
		ACTC AGGTAGT AAAC	
		CCA_ G	
GAM161	KIAA1393 3'	CAAGTGATGAATATGCTCA 2935	A C GTTT
		TGAG ATAT CATC GCTTG	
		ACTC TATA GTAG TGAAC	
		G A _	
GAM161	UBN1 3'	CCAAGTCACAGATAGACATTCC 1716	A A C GTTT
	A	TG GAAT TC ATC GCTTGG	
		AC CTTA AG TAG TGAACC	
		_ C A ACAC	
GAM162	CELSR3 3'	AGAACTGAAGACTTTAA 824	TAT
		TTAAAGTCTTC TTCT	
		AATTCAGAAG AAGA	
		TC_	
GAM162	GPR85 3'	TAGAAGTTTGAAGACTTTAA 1868	T_
		TTAAAGTCTTC ATTTCTA	

			AATTTCAGAAG TGAAGAT		
			TT		
GAM162	ITGAV	3'	TAGAAATGGAGAGTTTAATA 908	G T	
			TATTAAA TCT CTATTTCTA		
			ATAATTT AGA GGTAAGAT		
			G _		
GAM162	MAPRE2	3'	TAGAAGTGAAGACCTTA 1487	A T	
			TAA GTCTTC ATTTCTA		
			ATT CAGAAG TGAAGAT		
			C _		
GAM162	PAX6	5'	AGGGGGAAGACTTTAA 837	AT	
			TTAAAGTCTTCT TTCT		
			AATTTCAGAAGG GGGA		
			—		
GAM162	PAX6	5'	AGGGGGAAGACTTTAA 726	AT	
			TTAAAGTCTTCT TTCT		
			AATTTCAGAAGG GGGA		
			—		
GAM162	SLC24A1	3'	TAGAAATAGAACAGCTTAATA 1150	A C_	
			TATTAA GT TTCTATTTCTA		
			ATAATT CG AAGATAAAGAT		
			_ AC		
GAM162	SLC31A1	3'	TAGAAATAGATATTTTTAA 864	TCT	
			TTAAAG TCTATTTCTA		
			AATTTT AGATAAAGAT		
			TAT		
GAM162	SLC4A7	3'	TAGAACAATAGAACTTTAATA 1043	C _	
			TATTAAAGT TTCTATT TCTA		
			ATAATTTCA AAGATAA AGAT		
			_ CA		
GAM162	ZNF22	3'	TAGAAATAGAGATGCTTTA 3527	C_	
			TAAAGT TTCTATTTCTA		
			ATTTCTG GAGATAAAGAT		
			TA		
GAM162	ARGBP2	5'	GGAAAAGTGAAGACTTTAATA 1041	TA_	
			TATTAAAGTCTTC TTTCT		
			ATAATTTCAGAAG AAAGG		
			TCA		
GAM162	C20orf7	3'	AGAAATGGATAGCTTTAA 2056	CT	
			TTAAAGT TCTATTTCT		

		AATTTTCG AGGTAAAGA	
		AT	
GAM162	FLJ12704 3'	AGAACGCTGGACTTTAATG 2125	TCTAT
		TATTAAAGTCT TTCT	
		GTAATTTTCAGG AAGA	
		TCGC_	
GAM162	FLJ13194 3'	TAGAAATGTTCTCAGACTTTAA 2141	TC__
		TTAAAGTCT TATTTCTA	
		AATTTTCAGA GTAAAGAT	
		CTCTT	
GAM162	FLJ20005 3'	AGAAAAAGACTTTAA 1731	CTA
		TTAAAGTCTT TTTCT	
		AATTTTCAGAA AAAGA	
		—	
GAM162	FLJ20417 5'	TAGAAATAAACAAGGCTTTA 1754	C__
		TAAAGTCTT TATTTCTA	
		ATTTTCGGAA ATAAAGAT	
		CAA	
GAM162	KIAA0712 3'	AGAAATTAAGACTTTAA 1529	CT
		TTAAAGTCTT ATTTCT	
		AATTTTCAGAA TAAAGA	
		T_	
GAM162	KIAA0750 5'	AGAAAGAGAAGACTTTAA 1510	A
		TTAAAGTCTTCT TTTCT	
		AATTTTCAGAAGA AAAGA	
		G	
GAM162	KIAA1128 3'	TAGAGTATTCAGACTTTGATA 2821	TCTAT
		TATTAAAGTCT TTCTA	
		ATAGTTTCAGA GAGAT	
		CTTAT	
GAM162	KIAA1281 3'	TAGAAGAGAGAGACTTTAA 3461	_ A
		TTAAAGTCT TCT TTTCTA	
		AATTTTCAGA AGA GAAGAT	
		G _	
GAM162	KIAA1841 3'	AGAGAACAGACTTTAATA 3151	TCTA
		TATTAAAGTCT TTTCT	
		ATAATTTTCAGA AGAGA	
		CA__	
GAM162	Rab11-FIP2 3'	AGATGTAGAAGCTTTAATA 1580	CT T
		TATTAAAGT TCTAT TCT	

			ATAATTTCA AGATG AGA	
			— T	
GAM162	RABEX5	3'	TAGTCGATGGAAGACTTTAA 1504	T_
			TTAAAGTCTTCTATT CTA	
			AATTCAGAAGGTAG GAT	
			CT	
GAM162	SGKL	3'	TAGAGGTAAGACTTTAATA 1438	TC
			TATTAAAGTCT TATTCTA	
			ATAATTCAGA ATGGAGAT	
			—	
GAM162	SYTL3	3'	TAGAAAATGGCCAGATTTTAAT 3183	T_ _
	A		TATTAAAGTCT CTATTT CTA	
			ATAATTTTAGA GGTAAA GAT	
			CC A	
GAM162	TTY7	3'	GAAAAAGACTTTTGATA 2220	CTA
			TATTAAAGTCTT TTTC	
			ATAGTTTCAGAA AAAG	
			—	
GAM162	LOC113612	3'	TAGAAATAGTTGACTTAATA 2968	A TT
			TATTAA GTC CTATTTCTA	
			ATAATT CAG GATAAAGAT	
			_ TT	
GAM162	LOC121457	3'	TAGAAATAGTTCTTTAA 2993	TCTT
			TTAAAG CTATTTCTA	
			AATTC GATAAAGAT	
			TT_	
GAM162	LOC133491	3'	TAGAATTGGGACTTTAGTA 3015	TT T
			TATTAAAGTC CTA TTCTA	
			ATGATTTCAG GGT AAGAT	
			— T	
GAM162	LOC143282	3'	AGAAATAGGCGTACTTTAA 3054	CT_
			TTAAAGT TCTATTTCT	
			AATTTCA GGATAAAGA	
			TGC	
GAM162	LOC143524	3'	TAGAGAAGGGAAAGACTTTA 3059	_ A_
			TAAAGTCTT CT TTTCTA	
			ATTCAGAA GG AGAGAT	
			A GA	
GAM162	LOC144559	5'	TAGAGAAGGGAAAGACTTTA 3066	_ A_
			TAAAGTCTT CT TTTCTA	

		ATTTCAGAA GG AGAGAT		
		A GA		
GAM162	LOC153222 3'	TAGAAATGGTTGTACTTTAATG 3180	CTT_	
		TATTAAAGT CTATTTCTA		
		GTAATTTCA GGTAAGAT		
		TGTT		
GAM162	LOC219623 5'	AGAAAAGAAGACTTCAAT 3525	A	A
		ATT AAGTCTTCT TTTCT		
		TAA TTCAGAAGA AAAGA		
		C _		
GAM162	LOC219918 5'	TAGAGAAGGGAAAGACTTTA 3530	_ A_	
		TAAAGTCTT CT TTTCTA		
		ATTTCAGAA GG AGAGAT		
		A GA		
GAM162	LOC220071 5'	TAGAGAAGGGAAAGACTTTA 3602	_ A_	
		TAAAGTCTT CT TTTCTA		
		ATTTCAGAA GG AGAGAT		
		A GA		
GAM162	LOC254431 3'	AGGTAAAGACTTTAGTA 3717	C	
		TATTAAAGTCTT TATTT		
		ATGATTTTCAGAA ATGGA		
		_		
GAM162	LOC255515 3'	TAGAGAAGGGAAAGACTTTA 3688	_ A_	
		TAAAGTCTT CT TTTCTA		
		ATTTCAGAA GG AGAGAT		
		A GA		
GAM162	LOC56959 5'	ATAGAAACAGAGGACGTGACTT 3219	_____ A III	
		TGATA TAAAGTC TTCT TTTCTA T		
		GTTTCAG GAGA AAAGAT A		
		TGCAG C III		
GAM162	LOC90906 3'	TAGAGAAGGGAAAGACTTTA 2685	_ A_	
		TAAAGTCTT CT TTTCTA		
		ATTTCAGAA GG AGAGAT		
		A GA		
GAM163	ENAM 5'	TATAGACCATTAAGAATA 2216	TC C C	
		TATTCTTA ATG GTC ATA		
		ATAAGAAT TAC CAG TAT		
		_ _ A		
GAM163	EFNA5 3'	CTATGGACAAGGAAGAATAGT 876	ATCATGC	
		ATTATTCTT GTCCATAG		

			TGATAAGAA	CAGGTATC	
			GGAA__		
GAM163	LOC159199	5'	CTATGGACAAGCCAAGAA	3236	ATCAT __
			TTCTT GC GTCCATAG		
			AAGAA CG CAGGTATC		
			C__ AA		
GAM163	LOC90321	3'	ATGGAGGTGGACAGAGAATAA	2630	ATCA G
			TTATTCTT TGC TCCAT		
			AATAAGAG GTG AGGTA		
			ACAG G		
GAM164	KRAS2	3'	AATATTATATTTTTTCTATAAA	1166	GAT
	AA		TTTTTA AAAAAATATAATATT		
			AAAAAT TTTTTTATATTATAA		
			ATC		
GAM164	KRAS2	3'	AATATTATATTTTTTCTATAAA	2331	GAT
	AA		TTTTTA AAAAAATATAATATT		
			AAAAAT TTTTTTATATTATAA		
			ATC		
GAM165	APXL	3'	AGGACTTTCTCTTCTACAC	843	TATA
			GTGTGGGA AAAGTCCT		
			CACATCTT TTTCAGGA		
			CTC_		
GAM165	ASTN	3'	AGGTGCTTATATCCCACCAAC	2852	__ AA _
			GT GTGGGATATA AGT CCT		
			CA CACCCTATAT TCG GGA		
			AC _ T		
GAM165	GALK2	3'	AGGACTTTCTGTGCCACA	891	G TA
			TGTGG ATA AAAGTCCT		
			ACACC TGT TTTCAGGA		
			G C_		
GAM165	MCL1	3'	AGGACTTTTATACCTGT	1970	TG A
			G GG TATAAAAGTCCT		
			T CC ATATTTTCAGGA		
			GT _		
GAM165	PACE4	5'	AGGACTTTTACTACCATGGTA	2434	TG ATA
			TACCGTG GG TAAAAGTCCT		
			ATGGTAC TC ATTTTCAGGA		
			CA _		
GAM165	PODXL	3'	AGGACTTTTATGGGCTCGGC	1206	G A_
			GT TGGG TATAAAAGTCCT		

CG GCTC GTATTTTCAGGA
 _ GG
 GAM165 TNFSF8 3' GGA CTCTCTCACACAGG 811 _ TATAAA
 CC GTGTGGGA AGTCC
 || ||||| ||||
 GG CACTCT TCAGG
 A C____

GAM165 ATP1B4 3' GACCTCTATATCCTGGTG 1401 GTGT AAA
 TACC GGGATATA GTC
 ||| ||||| ||
 GTGG TCCTATAT CAG
 _____ CTC

GAM165 CDC14A 3' AGGACCCTTATAGGTACTCACA 1047 A__ AA
 TGTGGG TATAA GTCCT
 ||||| ||||| ||||
 ACACTC ATATT CAGGA
 ATGG CC

GAM165 DKFZP434C171 3' GGACTCTTATGTCACTGCA 1641 TG_ A
 TG G GATATAA AGTCC
 || | ||||| ||||
 AC C CTGTATT TCAGG
 GT A C

GAM165 EMR2 3' AGGACTTTCATACCGACAAC 1453 _ G A A
 GT GT GG TAT AAAGTCCT
 || ||| || |||||
 CA CA CC ATA TTTCAGGA
 A G _ C

GAM165 FYCO1 3' AGGACTTTTGTGGGGCCACAAG 2063 CG GA_
 TA TAC TGTGG TATAAAAGTCCT
 ||| ||||| |||||
 ATG ACACC GTGTTTTCAGGA
 A_ GGG

GAM165 GGA2 3' AGGACTTTCCCGTCCACACAC 2448 _ ATA
 GTGTG GGAT AAAGTCCT
 ||||| ||||| |||||
 CACAC CCTG TTTCAGGA
 A CCC

GAM165 GGA2 3' AGGACTTTCCCGTCCACACAC 1604 _ ATA
 GTGTG GGAT AAAGTCCT
 ||||| ||||| |||||
 CACAC CCTG TTTCAGGA
 A CCC

GAM165 ICT1 3' AGGACTTTCACACCATAAGG 834 G GATATA
 CC TGTGG AAAGTCCT
 || ||||| |||||
 GG ATACC TTTCAGGA
 A ACAC__

GAM165 ZFP100 3' AGGACTCCCTATCCCACA 2877 TAAA
 TGTGGGATA AGTCCT
 ||||| |||||

ACACCCTAT TCAGGA
 CCC_
 GAM165 LOC64744 3' GACTTTATGAAGATCCACAC 2607 ATA____
 GTGTGGGAT AAAGTC
 ||||| ||||
 CACACCCTA TTTCAG
 GAAGTA
 GAM166 MEF-2 3' TGCTATTAAATAGTAAAC 2688 T ATAAC
 GTTTACTATTTA TG GCA
 ||||| || ||
 CAAATGATAAAT AT CGT
 T ____
 GAM166 LOC146184 5' TATCAATAAATAGCAAAC 3281 A
 GTTT CTATTTATTGATA
 ||| |||||
 CAAA GATAAATAACTAT
 C
 GAM167 CDH5 3' CAGTGATGACTATTCTCAAATG 858 G A ATTC
 CAT TGA AATAGTCAT CTG
 ||| ||||| ||
 GTA ACT TTATCAGTA GAC
 A C GT_
 GAM167 LNK 3' CAGAGAACACTATTTTACAT 1216 CATA _
 ATGTGAAAATAGT TTC CTG
 ||||| || ||
 TACATTTTATCA AAG GAC
 C__ A
 GAM167 NPR2 3' CAGAAATGGACATTTTCATATG 786 A A C
 CATGTGAAAAT GTC TATT CTG
 ||||| || || ||
 GTATACTTTTA CAG GTAA GAC
 _ _ A
 GAM167 CLLD8 3' GCAGGAACACAATTAGGATATT 2219 G A _____ |||
 TTCATA AAATA TC TA TTCCTG C
 |||| || |||| |
 TTTAT AG AT AAGGAC G
 _ G TAACAC |||
 GAM167 FLJ22301 3' CAGGTGAGGACCATTTCAC 2094 A ATATT
 GTGAAAAT GTC CCTG
 ||||| || ||
 CACTTTTA CAG GGAC
 C GAGT_
 GAM167 FLJ22833 3' AGGGAACACCAGTTTTCACATG 2016 AGTCATA
 CATGTGAAAAT TTCCT
 ||||| || ||
 GTACACTTTTG AGGGA
 ACCACA_
 GAM167 KIAA0125 3' GAAATGACATTTCACATG 1548 AATA A
 CATGTGAA GTCAT TTC
 ||||| || || ||

			GTACACTT CAGTA AAG		
			A__ _		
GAM167	KIAA0125	3'	GAAATGACATTCACATG 1549	AATA	A
			CATGTGAA GTCAT TTC		
			GTACACTT CAGTA AAG		
			A__ _		
GAM167	KIAA0125	3'	GAAATGACATTCACATG 1550	AATA	A
			CATGTGAA GTCAT TTC		
			GTACACTT CAGTA AAG		
			A__ _		
GAM167	KIAA0125	3'	GAAATGACATTCACATG 1551	AATA	A
			CATGTGAA GTCAT TTC		
			GTACACTT CAGTA AAG		
			A__ _		
GAM167	KIAA0125	3'	GAAATGACATTCACATG 1552	AATA	A
			CATGTGAA GTCAT TTC		
			GTACACTT CAGTA AAG		
			A__ _		
GAM167	KIAA1199	3'	CAGAAATCTGCTGCATTTTCA 2951	A_	T T C
			TG CATGTGAAA TAG CA ATT CTG		
			GTACACTTT GTC GT TAA GAC		
			AC _ C A		
GAM167	LANCL2	3'	ATATGACTTCTTCACAT 1860	AAT	
			ATGTGAA AGTCATAT		
			TACACTT TCAGTATA		
			CT_		
GAM167	SEZ6	3'	CAGGAGTACCTTTCTCCACATG 2997	AAAAT	TCA
			CATGTG AG TATTCCTG		
			GTACAC TC ATGAGGAC		
			CTCTT C__		
GAM167	SNX10	3'	AGGAAGATATTTTCAGAT 1442	G	GTCATA
			AT TGAAAATA TTCCT		
			TA ACTTTTAT AAGGA		
			G AG__		
GAM167	TNFRSF21	3'	AGTGTGACTTTTCCCACA 1502	AA	T
			TGTG AA AGTCATATT		
			ACAC TT TCAGTGTGA		
			CC T		
GAM167	TTY11	5'	CAGGAATAGTCAGCATTTTCA 2221	ATAGTCA	
			T ATGTGAAA TATTCCTG		

		TACACTTT ATAAGGAC	
		ACGACTG	
GAM167	LOC143879 3'	GAATACTTAGTATTTTCACATG 3063	GTCA_
		CATGTGAAAATA TATTC	
		GTACACTTTTAT ATAAG	
		GATTC	
GAM167	LOC145439 5'	CAGGAATACAGAGATTTTCGCAT 3078	ATAGTCA
	G	CATGTGAAA TATTCCTG	
		GTACGCTTT ATAAGGAC	
		AGAGAC_	
GAM167	LOC147353 3'	CAGGAATAGAACTTGCACATG 3293	AAAAT CA
		CATGTG AGT TATTCCTG	
		GTACAC TCA ATAAGGAC	
		GT__ AG	
GAM167	LOC221584 5'	GAATATGGGCTACTTCATATG 3620	AA _
		CATGTGAA TAGTC ATATTC	
		GTATACTT ATCGG TATAAG	
		C_ G	
GAM167	LOC257054 3'	CAGGAATGTGTCATTTCCCACA 3682	A_ AGT
		TGTG AAAT CATATTCCTG	
		ACAC TTTA GTGTAAGGAC	
		CC CT_	
GAM167	LOC91145 5'	CAGGAATGTACACTTTACAT 2713	AATA C
		ATGTGAA GT ATATTCCTG	
		TACATTT CA TGTAAGGAC	
		CA__ _	
GAM167	LOC93297 3'	GAATATGTTTGTGTATGTTTAC 2929	A____ T
	ATG	CATGTGAA ATAG CATATTC	
		GTACACTT TGTT GTATAAG	
		GTATG T	
GAM168	BACH2 3'	AAGCTGTTTCGTTGTATCA 1961	A _
		TGA TACAACGAATA CTT	
		ACT ATGTTGCTTGT GAA	
		_ C	
GAM168	GAN 3'	TGAAGTATAGGGATGTATTTA 1974	ACGA_
		TGAATACA ATACTTCA	
		ATTTATGT TATGAAGT	
		AGGGA	
GAM168	MHC2TA 3'	TGAAGCATTACTTTGTGTTCA 720	C__ A
		TGAATACAA GAAT CTTCA	

			ACTTGTGTT TTTA GAAGT		
			TCA C		
GAM168	MTM1	3'	TGAAGTATTGTGTTTA 723	ACGA	
			TGAATACA ATACTTCA		
			ATTTGTGT TATGAAGT		

GAM168	AWP1	3'	TGAAGTAATTGTGCTGTATTTA 1872	___ A	
			TGAATACA ACGA TACTTCA		
			ATTTATGT TGTT ATGAAGT		
			CG A		
GAM168	BLCAP	3'	TGAAGTATGGTGTGTTCA 1324	ACGA	
			TGAATACA ATACTTCA		
			ACTTGTGT TATGAAGT		
			GG__		
GAM168	C5orf3	3'	TGAAGTATTCAGGTTCTCA 1859	AT AAC	
			TGA AC GAATACTTCA		
			ACT TG CTTATGAAGT		
			CT GA_		
GAM168	CRK7	3'	AAGCTGTCCGTTGTATTC 1690	A _	
			GAATACAACG ATA CTT		
			CTTATGTTGC TGT GAA		
			C C		
GAM168	FLJ11101	3'	TGAAGTTTTGATTGTATTTA 1814	_ T	
			TGAATACAA CGAA ACTTCA		
			ATTTATGTT GTTT TGAAGT		
			A _		
GAM168	FLJ12876	3'	TGAAGTGTAGATCATTGTATTC 2004	C ____	
	A		TGAATACAA GA ATACTTCA		
			ACTTATGTT CT TGTGAAGT		
			A AGA		
GAM168	KLF12	3'	TGAAGTGTAGATTTGTATTTA 1374	CGA_	
			TGAATACAA ATACTTCA		
			ATTTATGTT TGTGAAGT		
			TAGA		
GAM168	MGC4734	3'	AAGTGTTCTGTATTCA 2513	AC	
			TGAATACA GAATACTT		
			ACTTATGT CTTGTGAA		

GAM168	PRO2000	3'	GAGTATTCTTTATATTCA 1469	C C	
			TGAATA AA GAATACTT		

			ACTTAT TT CTTATGAG		
			A T		
GAM168	RAB33B	3'	TGAAGTGTTCACATTCA 2191	ACAAC	
			TGAAT GAATACTTCA		
			ACTTA CTTGTGAAGT		
			CA__		
GAM168	RGS12	3'	TGAAGCCCGCTGTGTTC 972	A AATA	
			TGAATACA CG CTTCA		
			ACTTGTGT GC GAAGT		
			C CC__		
GAM168	ZNF387	3'	TGAAGTATGTTTGTATTTA 1522	CGA	
			TGAATACAA ATACTTCA		
			ATTTATGTT TATGAAGT		
			TG_		
GAM168	LOC158381	3'	TGAAGTAATTGTGCTGTATTTA 2905	__ A	
			TGAATACA ACGA TACTTCA		
			ATTTATGT TGTT ATGAAGT		
			CG A		
GAM168	LOC196411	3'	AAGTTTCTTTGTGTTCA 3412	C T	
			TGAATACAA GAA ACTT		
			ACTTGTGTT CTT TGAA		
			T _		
GAM168	LOC51186	5'	GAAGTCATTGTATTCA 1680	C ATA	
			TGAATACAA GA CTTC		
			ACTTATGTT CT GAAG		
			A __		
GAM169	RDX	3'	TAGAGATTAAACCAATTA 971	G	
			TAATTGGTTTAATC TTTA		
			ATTAACCAAATTAG AGAT		
			-		
GAM169	TRPC3	3'	AATAAATGTTGAAACCAACTGA 1010	A AAT	
			TTA TTGGTTT CGTTTATT		
			AGT AACCAAA GTAAATAA		
			C GTT		
GAM169	LOC131000	3'	TAATAACGATTTAATGAA 3038	G T	
			TT GTT AATCGTTTATTA		
			AA TAA TTAGCAAATAAT		
			G T		
GAM170	ACTA2	3'	TGTGAATGTCCTGTGGAA 839	AG CTAAT _	
			TTCCACAG CA TTC CA		

			AAGGTGTC GT AAG GT		
			CT _____ T		
GAM170	ASPH	3'	GAAATAATTGCTCTGTTGAA 2251	C	CTA
			TTC ACAGAGCA ATTTC		
			AAG TGTCTCGT TAAAG		
			T TAA		
GAM170	ASPH	3'	GAAATAATTGCTCTGTTGAA 2253	C	CTA
			TTC ACAGAGCA ATTTC		
			AAG TGTCTCGT TAAAG		
			T TAA		
GAM170	BRCA1	3'	TGGAAGTTAGCACTCTAGGGAA 1392	AC	CA
			TTCC AGAG CTAATTTCCA		
			AAGG TCTC GATTGAAGGT		
			GA AC		
GAM170	CDC42	3'	GAAGACAGACATCTGTGGAA 856	GCA	AA
			TTCCACAGA CT TTTC		
			AAGGTGTCT GA GAAG		
			ACA CA		
GAM170	CLASP1	3'	TTGGAAATAAAGAAGTGCTCTG 2718	A_____	
			CAGAGCACT ATTTCCAA		
			GTCTCGTGA TAAAGGTT		
			AGAAA		
GAM170	CPNE3	3'	GAAATTAGTGTGGGGAA 1069	ACAGA	
			TTCC GCACTAATTC		
			AAGG TGTGATTAAAG		
			GG_____		
GAM170	DACH	3'	TTGGAAATTTTCTATGG 2388	C	CACT
			CCA AGAG AATTTCCAA		
			GGT TCTT TTAAAGGTT		
			A T_____		
GAM170	ECM2	5'	GAAATTGGCTGGTGGAA 823	AG	AC
			TTCCAC AGC TAATTC		
			AAGGTG TCG GTTAAAG		
			G_ _		
GAM170	EDNRA	3'	TAGACTGTCTCTGTGGAA 2681	_ _	
			TTCCACAGAG CA CTA		
			AAGGTGTCTC GT GAT		
			T CA		
GAM170	ENC1	3'	TTGGAAATCAGTTGTG 1045	GAGC	A
			CACA ACT ATTTCCAA		

			GTGT TGA TAAAGGTT		
			____ C		
GAM170	FANCF	3'	TTGGTGGCTGCCCTGTGGAA 1999	A _	ATTT
			TTCCACAG GCA CTA CCAA		
			AAGGTGTC CGT GGT GGTT		
			C C ____		
GAM170	FCAR	3'	GAAAACTTAGTCTGTGGAG 2405	GCA _	
			TTCCACAGA CTAA TTTC		
			GAGGTGTCT GATT AAAG		
			____ CA		
GAM170	FCAR	3'	GAAAACTTAGTCTGTGGAG 2407	GCA _	
			TTCCACAGA CTAA TTTC		
			GAGGTGTCT GATT AAAG		
			____ CA		
GAM170	GAS7	3'	TTGGAAATATACAGCTCTGTG 1259	ACTA_	
			CACAGAGC ATTTCCAA		
			GTGTCTCG TAAAGGTT		
			ACATA		
GAM170	KCNJ5	5'	GAAATTAATCTCTGGGGAA 784	A CAC	
			TTCC CAGAG TAATTC		
			AAGG GTCTC ATTAAG		
			G TA_		
GAM170	MEF2A	3'	GAGAAAATGCTTTGTAGAA 1228	C CTAA	
			TTC ACAGAGCA TTTC		
			AAG TGTTCGT AGAG		
			A AAA_		
GAM170	MIR16	3'	GGAAACTAACTCTGTGGAA 1704	CAC A	
			TTCCACAGAG TA TTTCC		
			AAGGTGTCTC AT AAAGG		
			AA_ C		
GAM170	P4HB	3'	TTGAAAATTCCGTCTGTGGGA 787	G ACT C	
			TTCCACAGA C AATTT CAA		
			AGGGTGTCT G TTAAA GTT		
			CC A		
GAM170	RAF1	3'	TTGGAATCAGCTTCTGGAGGA 3168	A_ CA A	
	A		TTCC CAGAG CT ATTTCCAA		
			AAGG GTCTT GA TAAAGGTT		
			AG C_ C		
GAM170	RPS6KA5	3'	TTGGAATTTTTCTGTTGAA 1153	C CACT	
			TTC ACAGAG AATTTCCAA		

AAG TGTCTT TTAAAGGTT
 T T__
 GAM170 TBL1X 3' GAAATGGCCTGTGGAA 1233 A ACTA
 TTCCACAG GC ATTC
 ||||| || ||||
 AAGGTGTC CG TAAAG
 _ G__
 GAM170 ARHGAP10 5' GGAGCCTGCTTGTGGAA 1926 G CTAAT
 TTCCACA AGCA TTCC
 ||||| ||| ||||
 AAGGTGT TCGT GAGG
 _ CC__
 GAM170 ATP9A 3' TTGGAAATCAGTCTGT 2619 GCA A
 ACAGA CT ATTTCCAA
 |||| || |||||
 TGTCT GA TAAAGGTT
 _ C
 GAM170 Di-Ras2 3' TTGGAAATATGTTCCCTGGAA 1725 CA CTA
 TTCCA GAGCA ATTTCCAA
 |||| |||| |||||
 AAGGT CTTGT TAAAGGTT
 C_ A__
 GAM170 FHOD2 3' GAGAACGATGCTCTGTGAGA 2981 _ CTAA
 TC CACAGAGCA TTTC
 || ||||| ||||
 AG GTGTCTCGT AGAG
 A AGCA
 GAM170 FLJ10704 3' TTGGAAATTAGTGTTATCTGGA 1795 CAG
 A TTCCA AGCACTAATTTCCAA
 |||| |||||
 AAGGT TTGTGATTAAAGGTT
 CTA
 GAM170 FLJ12085 3' TTGGAAATTATGCACTTTG 2006 C A C
 CA AG GCA TAATTTCCAA
 || || || |||||
 GT TC CGT ATTAAGGTT
 T A _
 GAM170 FLJ20209 3' AGATTGGTTGCTCTGGAA 3351 CA _
 TTCCA GAGCA CTAATT
 |||| |||| |||||
 AAGGT CTCGT GGTTAGA
 _ T
 GAM170 FLJ22174 5' TTGGAAATTGAAGCTGTAGAG 1969 C AGCAC
 TTC ACAG TAATTTCCAA
 || ||| |||||
 GAG TGTC GTTAAAGGTT
 A GAA__
 GAM170 HSPC129 3' TTGGAAATTAAAGGTGGA 1685 AGAGCAC
 TCCAC TAATTTCCAA
 |||| |||||

		AGGTG	ATTAAGGTT		
		GAA_____			
GAM170	KIAA0632	3'	GGCCCCCAGTGCTCTGTGGGA	1634	AATTT
			TTCCACAGAGCACT	CC	
			AGGGTGTCTCGTGA	GG	
			CCCCC		
GAM170	KIAA1184	3'	TTGGAAATCAGAAGTCTGTGAG	1994	_ GCA A
	A		TC CACAGA	CT ATTTCCAA	
			AG GTGTCT	GA TAAAGGTT	
			A	GAA C	
GAM170	KIAA1671	3'	GAAATCAGTGTGTGGAG	2725	GA A
			TTCCACA	GCACT ATTTC	
			GAGGTGT	TGTGA TAAAG	
			—	C	
GAM170	KIAA1728	3'	TGGTAGTGCTCCTGGAA	2818	CA ATTT
			TTCCA	GAGCACTA CCA	
			AAGGT	CTCGTGAT GGT	
			C_	—	
GAM170	KIAA1737	3'	TTGGAAAAACCTCTGTGGAG	2789	CACTAA
			TTCCACAGAG	TTTCCAA	
			GAGGTGTCTC	AAAGGTT	
			CCAA_		
GAM170	KIAA1750	3'	ATTGGAAATTGTTGCTGTGTTC	2811	_____
	TGTG		CAGAGCAC	TAATTTCCAA T	
					I
			GTCTTGTG	GTTAAAGGTT A	
			TCGTT		
GAM170	KIAA1900	3'	TGGAACATGTTGTGGAA	2972	GA CTAA
			TTCCACA	GCA TTTCCA	
			AAGGTGT	TGT AAAGGT	
			—	AC_	
GAM170	KIAA1946	3'	AAGTTAGTGCTCTGCTGAA	3246	CA
			TTC	CAGAGCACTAATTT	
			AAG	GTCTCGTGATTGAA	
			TC		
GAM170	LALP1	3'	AAATGAATGGTCTGTGGAA	1915	G CTA
			TTCCACAGA	CA ATTT	
			AAGGTGTCT	GT TAAA	
			G	AAG	
GAM170	LRRFIP2	3'	TTGGAAATCTGCCTGCAGA	1743	CA A CTA
			TC	CAG GCA ATTTCCAA	

			AG GTC CGT TAAAGGTT		
			AC _ C__		
GAM170	MGC1842	3'	TGGCAGCAGTGCTCTGGGAA 2724	A	AATTT
			TTCC CAGAGCACT CCA		
			AAGG GTCTCGTGA GGT		
			_ CGAC_		
GAM170	MGC9753	5'	TGGCCTGGTGCCTGTGGAA 2333	A	ATT
			TTCCACAG GCACTA CCA		
			AAGGTGTC CGTGGT GGT		
			_ CC_		
GAM170	PEG10	3'	GAATTGGTCTGTGGAA 1606	GCA	
			TTCCACAGA CTAATT		
			AAGGTGTCT GGTAAAG		

GAM170	PGRMC2	3'	TTGGAAATTAGGAGAAGGAA 1287	ACAGAGCA	
			TTCC CTAATTTCCAA		
			AAGG GATTAAAGGTT		
			AAGAG__		
GAM170	PPP4R1L	5'	GGAAAGCCCTGTGGAA 3139	A	ACTAA
			TTCCACAG GC TTTCC		
			AAGGTGTC CG AAAGG		
			C _____		
GAM170	PRO0386	5'	GAACATAATGTTCTGTGGAA 1843	C	A
			TTCCACAGAGCA TA TTT		
			AAGGTGTCTTGT AT AAG		
			A C		
GAM170	PRO0456	3'	TGGAATTCATACTCTGTGGAA 1476	CACTAAT	
			TTCCACAGAG TTCCA		
			AAGGTGTCTC AAGGT		
			ATACTT_		
GAM170	SLC26A8	5'	AGTCAGTATCTGTGGAA 2455	GC	A
			TTCCACAGA ACT ATT		
			AAGGTGTCT TGA TGA		
			A_ C		
GAM170	SNTG1	5'	TTGGAAATAGCTTTGTG 1867	ACTA	
			CACAGAGC ATTTCCAA		
			GTGTTTCG TAAAGGTT		
			A__		
GAM170	ZNF396	3'	TTGGAAATAAGTCAATGGAA 3034	CA	GCA A
			TTCCA GA CT ATTTCCAA		

		AAGGT CT GA TAAAGGTT		
		AA ____ A		
GAM170	LOC145098 5'	TTGGAAATATCTTCTGTG 3074	CACTA	
		CACAGAG ATTTCCAA		
		GTGTCTT TAAAGGTT		
		CTA__		
GAM170	LOC146136 5'	GAAAAGGCCTCTGTGGAG 2964	CA AA	
		TTCCACAGAG CT TTTC		
		GAGGTGTCTC GA AAAG		
		CG ____		
GAM170	LOC148195 3'	GGAAGGCATCCTGTGGAA 3298	A__ A AATT	
		TTCCACAG GC CT TCC		
		AAGGTGTC CG GA AGG		
		CTA _ ____		
GAM170	LOC149086 5'	TGGAGATGATCCGTGGAA 3306	A GCACTA	
		TTCCAC GA ATTTCCA		
		AAGGTG CT TAGAGGT		
		C AG ____		
GAM170	LOC149420 3'	TTGGAAATTAGAGGTGGAA 3133	AGAGCA	
		TTCCAC CTAATTTCCAA		
		AAGGTG GATTAAAGGTT		
		GA ____		
GAM170	LOC149912 5'	TGGAAAGTGCTCTGTGG 3317	AAT	
		CCACAGAGCACT TTCCA		
		GGTGTCTCGTGA AAGGT		

GAM170	LOC151816 5'	GGAGTGTGCTCTGGGAA 3350	A TAAT	
		TTCC CAGAGCAC TTCC		
		AAGG GTCTCGTG GAGG		
		_ T ____		
GAM170	LOC152991 5'	GAAATGGGTCATACTCTGTGGA 3365	C__ A	
		TCCACAGAG ACT ATTTT		
		AGGTGTCTC TGG TAAAG		
		ATAC G		
GAM170	LOC157556 3'	TGGAGGGGTGCTCTGTGGAA 3382	AA	
		TTCCACAGAGCACT TTTCCA		
		AAGGTGTCTCGTGG GGAGGT		

GAM170	LOC157697 5'	AAATCTTGTGCTCTGCGAA 3204	CA TA_	
		TTC CAGAGCAC ATTT		

		AAG GTCTCGTG TAAA		
		C_ TTC		
GAM170	LOC158431 3'	TGGAAATTGTTTCTGTAGAA 3390	C	C T
		TTC ACAGAG AC AATTTCCA		
		AAG TGTCTT TG TTAAAGGT		
		A _ _		
GAM170	LOC200488 5'	GAAATGAGTCTGTGGGA 3478	GCA	A
		TTCCACAGA CT ATTTT		
		AGGGTGTCT GA TAAAG		
		___ G		
GAM170	LOC220565 3'	GAAAAGGCCTCTGTGGAG 3494	CA	AA
		TTCCACAGAG CT TTTC		
		GAGGTGTCTC GA AAAG		
		CG _		
GAM170	LOC221751 5'	TTGGAAATTGAAGCTGTAGAG 3552	C	AGCAC
		TTC ACAG TAATTTCCAA		
		GAG TGTC GTTAAAGGTT		
		A GAA_		
GAM170	LOC253978 5'	TTGGAATCTGTGCTTTGCAGAA 3743	CA	TAAT
		TTC CAGAGCAC TTCCAA		
		AAG GTTTCGTG AAGGTT		
		AC TCT_		
GAM170	LOC257319 3'	GAAATTAATCCTTTGTGG 3683	CAC	
		CCACAGAG TAATTTT		
		GGTGTTC ATTAAAG		
		CTA		
GAM170	LOC92162 5'	GGAGGCGCCTGTGGAA 2816	A A	AATT
		TTCCACAG GC CT TCC		
		AAGGTGTC CG GG AGG		
		_ C _		
GAM170	LOC92391 3'	GGAACAGCTCTGTGGAA 2842	ACTAAT	
		TTCCACAGAGC TTCC		
		AAGGTGTCTCG AAGG		
		AC_		
GAM171	BACH2 3'	CCGTGTTGGCCCCAGCCACG 1963	CA	ACAA AA_
		CG GC TG CCAACACGG		
		GC CG AC GGTTGTGCC		
		AC _ CCC		
GAM171	NCL 3'	CGTGTGTTGTTTGGACTG 2552	_	CAAT
		CAG CA GAACCAACACG		

GTC GT TTTGGTTGTGC
 A ____
 GAM171 NEO1 3' CGTGTCTTTGTGCTGTG 932 T ACCAA
 CGCAGCACAA GA CACG
 ||||| || |||
 GTGTCGTGTT CT GTGC
 T ____
 GAM171 SLC21A3 3' CTGTTGGTGTGCTGC 1183 AATGA C
 GCAGCAC ACCAACA G
 ||||| ||||| |
 CGTCGTG TGGTTGT C
 ____ A
 GAM171 UGCG 5' CCGTGTTGGCGGCCGCAGCGG 1012 A ACAA AA
 CCGC GC TG CCAACACGG
 ||| || || |||||
 GGCG CG GC GGTGTGCC
 A CCG_ _
 GAM171 MGC3101 3' CCGCGTTTTCTGTGCTGC 2047 AT CC A
 GCAGCACA GAA AAC CGG
 ||||| ||| ||| |||
 CGTCGTGT CTT TTG GCC
 C_ _ C
 GAM171 MGC3413 3' CCATGTTAGTGCTACATTGTGC 2269 A_ _ C C
 GCACAATG AC AACA GG
 ||||| || ||| ||
 CGTGTTAC TG TTGT CC
 ATCG A A
 GAM171 LOC151568 5' CCGTGTTGGCCTTGGCTAGG 2444 GC A TGAA
 CC AGC CAA CCAACACGG
 || ||| || |||||
 GG TCG GTT GGTGTGCC
 A_ _ CC_
 GAM171 LOC152765 5' GTGTGTCTTGTGCTGC 3175 T ACCA
 GCAGCACAA GA ACAC
 ||||| || |||
 CGTCGTGTT CT TGTG
 _ G_
 GAM171 LOC158314 5' CCACCCTTCACTGTGCTGCGG 3387 A CCAACAC
 CCGCAGCACA TGAA GG
 ||||| ||| || ||
 GGCGTCGTGT ACTT CC
 C CCCA_
 GAM171 LOC57086 3' CTGTTGGTGTGCTGC 1914 AATGA C
 GCAGCAC ACCAACA G
 ||||| ||||| |
 CGTCGTG TGGTTGT C
 ____ A
 GAM172 ABCE1 3' TTGACATTTGATAAATAACAT 2533 A A CATC
 CA C ATGT TATTTATC GTCAA
 | ||| ||||| |||||

			A TACA ATAAATAG CAGTT		
			C A TTTA		
GAM172	DMC1	3'	TGATTTATGATAACTATACATT 1356	T	CATC
	G		CAATGTATA TTATC GTCA		
			GTTACATAT AATAG TAGT		
			C TATT		
GAM172	PHEMX	3'	GTGGTCAAATATACATCA 2467	A	AT
			C ATGTATATTT CCAT		
			A TACATATAAA GGTG		
			C CT		
GAM172	PHEMX	3'	GTGGTCAAATATACATCA 2468	A	AT
			C ATGTATATTT CCAT		
			A TACATATAAA GGTG		
			C CT		
GAM172	PHEMX	3'	GTGGTCAAATATACATCA 2469	A	AT
			C ATGTATATTT CCAT		
			A TACATATAAA GGTG		
			C CT		
GAM172	PHEMX	3'	GTGGTCAAATATACATCA 1237	A	AT
			C ATGTATATTT CCAT		
			A TACATATAAA GGTG		
			C CT		
GAM172	H-L(3)MBT	3'	ACGATGGGGATACATT 1632	ATTTA	
			AATGTAT TCCATCGT		
			TTACATA GGGTAGCA		
			G____		
GAM172	KIAA0979	3'	GGTGGGATCAACATACATTG 1602	A T _	
			CAATGTAT TT ATCC ATC		
			GTTACATA AA TAGG TGG		
			C C G		
GAM172	LOC220672	3'	TTGACATTTGATAAATAACAT 2566	A A	CATC
	CA		C ATGT TATTTATC GTCAA		
			A TACA ATAAATAG CAGTT		
			C A TTTA		
GAM172	LOC257336	5'	TTGAAAAAATAAATGTACATT 3694		CCATCG
			AATGTATATTTAT TCAA		
			TTACATGTAAATA AGTT		
			AAAAA_		
GAM173	MGC16169	3'	AGCACCAACAGCACAGTTCTTC 2312	C__ _	TAACAA
	A		TGAAGAGC GC GTT TGCT		

		ACTTCTTG CG CAA ACGA	
		ACA A CC_____	
GAM173	LOC151414 3'	AGCATTA AAAACGAGCTCT 3156	C ____ AAC
		TCA TGAAGAGC GC GTTT AATGCT	
		ACTTCTCG CG CAAA TTACGA	
		A AC AA_	
GAM173	LOC153817 5'	AGCATTGTAAAGTCTCTCTTC 2591	CC G
		A TGAAGAG GC TTTAACAATGCT	
		ACTTCTC TG AAATTGTTACGA	
		TC _	
GAM173	LOC51145 3'	AGCTGCAAAAACGAGCTCTTCA 1665	CG AACAAT
		TGAAGAGC CGTTT GCT	
		ACTTCTCG GCAAA CGA	
		A_ AACGT_	
GAM174	ENAM 5'	CAAAGGCAAGCTAACAAAGTTC 2215	ACTAAT C
	AA	TTGAATTT CTTGCC TTG	
		AACTTGAA GAACGG AAC	
		ACAATC A	
GAM174	DOCK3 3'	CAAGGACAAGGAGAATGAATTC 2750	CTAA C
	AA	TTGAATTTA TCTTG CCTTG	
		AACTTAAGT GGAAC GGAAC	
		AAGA A	
GAM174	GAPCENA 3'	AAGGGATCAGAAATTCAA 1412	A AATCTTG
		TTGAATTT CT CCCTT	
		AACTTAAA GA GGGAA	
		_ CTA_____	
GAM175	HNRPA2B1 3'	ATTTTGTGAATGGATTGGA 902	G AGC
		TCCAATC CAT TATAAAAT	
		AGGTTAG GTA GTGTTTTA	
		_ A_	
GAM175	HNRPA2B1 3'	ATTTTGTGAATGGATTGGA 2186	G AGC
		TCCAATC CAT TATAAAAT	
		AGGTTAG GTA GTGTTTTA	
		_ A_	
GAM175	bA430M15.1 3'	TATTTTATTACAGATTGGA 3073	GCATAGCT
		TCCAATC ATAAAAATA	
		AGGTTAG TATTTTAT	
		ACAT_____	
GAM175	LOC146481 3'	CTATTTTATAGCCACCCAGGTA 3092	A GCATA_
	GG	CC ATC GCTATAAAATAG	

			GG TGG CGATATTTTATC		
			A ACCCAC		
GAM176	LOC146229	3'	ACAGCAATCAAAACATCAA 3087	GC	T
			TTGATGTTTTG TGCT GT		
			AACTACAAAAC ACGA CA		
			TA _		
GAM177	FLJ20413	3'	ATAGACGAAAATCAACT 1753	AT	
			AGTT ATTTTCGTCTAT		
			TCAA TAAAAGCAGATA		
			C_		
GAM178	CRP	3'	AGAAAATAACACCCAGAAAGG 2920	GAA_	ATAC
	AG		CTCT TGG TAGTTTTCT		
			GAGG ACC ATCAAAAGA		
			AAAG CACA		
GAM178	DBY	3'	AAAACAGCAGCCCTATTCAGA 1140	ATA__	A
			TCTGAATGG CT GTTTT		
			AGACTTATC GA CAAAA		
			CCGAC _		
GAM178	ERBB2	3'	AAAGCGACCCATTTCAGAGA 1115	ATACTA	
			TCTCTGAATGG GTTTT		
			AGAGACTTACC CGAAA		
			CAG__		
GAM178	ITGA1	3'	AGAACATGTATTCATCCAGA 2660	A	TA
			TCTG ATGGATAC GTTTT		
			AGAC TACTTATG CAAGA		
			C TA		
GAM178	MS4A1	3'	AGAAAATAAGTATCCATCAGAG 710	A	A
	A		TCTCTGA TGGATACT GTTTTCT		
			AGAGACT ACCTATGA TAAAAGA		
			_ A		
GAM178	ARSDR1	3'	AAAACAATTCTTCATTCAGA 1656	TACTA	
			TCTGAATGGA GTTTT		
			AGACTTACTT CAAAA		
			CTTAA		
GAM178	ATP1B4	3'	AAACTAGTATGTGGAAAG 1400	GAA	G
			CT TG ATACTAGTTTT		
			GA GT TATGATCAAAA		
			AAG G		
GAM178	FLJ00024	3'	AGAAAACCGTCCATTTAGA 2665	ACTA	
			TCTGAATGGAT GTTTTCT		

AGATTTACCTG CAAAAGA
 C____
 GAM178 FLJ10493 3' AAAGCATATCCGTTCA 1782 CTA
 TGAATGGATA GTTTT
 ||||| ||||
 ACTTGCCTAT CGAAA
 A____
 GAM178 FLJ11175 3' AGACTAACATCCATTCTGA 1816 T AC
 TC GAATGGAT TAGTTT
 || ||||| |||||
 AG CTTACCTA ATCAGA
 T CA
 GAM178 KIAA0977 3' AGAAAACTAGTGATACCA 1578 A____
 TGG TACTAGTTTTCT
 ||| |||||
 ACC GTGATCAAAAGA
 ATA
 GAM178 TRIP3 3' AGAAAACTTGACATTCAGATGA 3102 _ GATACT
 TC TCTGAATG AGTTTTCT
 || ||||| |||||
 AG AGACTTAC TCAAAAGA
 T AGT____
 GAM178 LOC149117 3' AAAACTTTATCCATTGAGA 3307 G CT
 TCT AATGGATA AGTTTT
 ||| ||||| |||||
 AGA TTACCTAT TCAAAA
 G T_
 GAM178 LOC196993 5' AGAAAACTTTCCATTC 3471 TACT
 GAATGGA AGTTTTCT
 ||||| |||||
 CTTACCT TCAAAAGA
 T____
 GAM178 LOC56965 5' AGAACTCTGTATCCATCAGAGA 1900 A T TT
 TCTCTGA TGGATAC AG TTCT
 ||||| ||||| || ||||
 AGAGACT ACCTATG TC AAGA
 _ _ TC
 GAM179 NUMA1 3' AGTCACTTCTCCATCACA 3604 A A
 TGTGATGGA AA TGA
 ||||| || |||||
 ACACTACCT TT ACTGA
 C C
 GAM179 SLC15A1 3' ATTGGTCATCTTCCCTATCACA 1182 A_ A
 TGTGATGG AA ATGACTAAT
 ||||| || |||||
 ACACTATC TT TACTGGTTA
 CC C
 GAM179 CNOT3 5' AAAATTCAGTTCCTCCATTACA 1505 AAAAT _
 TGTGATGGA GACT AATTTT
 ||||| ||| |||||

ACATTACCT TTGA TTAAAA
 CC__ C
 GAM179 FLJ10898 5' AGTCATTTCTCCATCACA 2527 A
 TGTGATGGA AAATGACT
 ||||| |||||
 ACACTACCT TTTACTGA
 C
 GAM179 FLJ14686 3' AAAATTAGTTGTTACCTCCTCA 2286 T AA_ TG
 CA TGTGA GGA AA ACTAATTTT
 ||||| || || |||||
 ACACT CCT TT TGATTAAAA
 _ CCA GT
 GAM179 HDAC9-PENDING 3' AAAATTGTATATTTTTTCCATC 1526 T TG__ T
 TCA TG GATGGAAAAA AC AATTTT
 || ||||| || |||||
 AC CTACCTTTTT TG TTAAAA
 T TATA _
 GAM179 ZAK 3' GGTCACCTTCCCATCACA 2427 A A
 TGTGATGG AAA TGA
 ||||| || |||||
 ACATTACC TTT ACTGG
 C C
 GAM179 LOC119548 5' TGGGCCATTTTTCCACAACA 2984 GA A_
 TGT TGGAAAAATG CTA
 || ||||| ||
 ACA ACCTTTTAC GGT
 AC CG
 GAM179 LOC153937 5' AAAATGCAGTTTTTCCTTCACA 3185 T GACTA
 TGTGA GGAAAAAT ATTTT
 ||||| ||||| |||||
 ACACT CCTTTTGG TAAAA
 T ACG__
 GAM179 LOC221895 3' GGTACTTTTCTCATCACA 3568 _ ATG
 TGTGATG GAAAA ACT
 ||||| ||||| ||
 ACACTAC CTTTT TGG
 T CA_
 GAM180 BLNK 5' GACGTGACCACTGGACAGTTAT 1441 ATTTTTAA
 T GATAACTGT TCACGTC
 ||||| |||||
 TTATTGACA AGTGCAG
 GGTCACC_
 GAM180 FLJ20152 3' GACAGGAAGAAAAATACAGTTA 1870 AA AC
 TAACTGTATTTTT TC GTC
 ||||| || |||||
 ATTGACATAAAAA AG CAG
 GA GA
 GAM181 BTG2 3' GAAAAGACAAAGGTTAC 1330 AA C
 GTGA CTTTGTC TTTC
 ||||| ||||| |||||

			CATT GAAACAG AAAG		
			G_ A		
GAM181	CELSR2	3'	GGAAAGGACAAAGCCACA 826	AAA	
			TGTG CTTTGTCTTTCC		
			ACAC GAAACAGGAAAGG		
			C_		
GAM181	GAB2	3'	AAAGGACAAGGACATGAG 1424	GAAA	
			TTCATGT CTTTGTCTTT		
			GAGTACA GGAACAGGAAA		

GAM181	GAB2	3'	AAAGGACAAGGACATGAG 2375	GAAA	
			TTCATGT CTTTGTCTTT		
			GAGTACA GGAACAGGAAA		

GAM181	GOLGA4	5'	AGAGTTTGAAATCTTCACATGA 2553	AC_ TC	
	A		TTCATGTGAA TTTG CTTT		
			AAGTACACTT AAGT GAGA		
			CTA TT		
GAM181	MEF2D	3'	GAAAAGACAAAGTCCTCG 3721	A_ C	
			TGA ACTTTGTC TTTC		
			GCT TGAAACAG AAAG		
			CC A		
GAM181	NEBL	5'	AAAGGACGCCACATGAG 1294	AAACTT	
			TTCATGTG TGTCCTTT		
			GAGTACAC GCAGGAAA		
			C_		
GAM181	PCSK1	3'	GAAAATATGATGTTTCACAT 743	T TG CC	
			ATGTGAAAC T T TTTC		
			TACACTTTG A A AAAG		
			T GT TA		
GAM181	PRKAR2B	3'	GGAAAAGAGAGCTCTCTACATG 951	AAACT G C	
	AA		TTCATGTG TT TC TTTC		
			AAGTACAT GA AG AAAGG		
			CTCTC G A		
GAM181	SCGB3A2	3'	AAAGGACAAATAAGCAATGAA 2361	_ GAAAC	
			TTCAT GT TTTGTCTTT		
			AAGTA CG AAACAGGAAA		
			A AAAT_		
GAM181	SMP1	3'	AGAGGAAACTTTTCACATGAA 1490	CTTTG	
			TTCATGTGAAA TCCTTT		

			AAGTACACTTT AGGAGA		
			CAA__		
GAM181	SYNGR1	3'	GGAAAAAAGGTTTCACAT 1147	G__	
			ATGTGAAACTTT TCC		
			TACACTTTGGAA AGG		
			AAA		
GAM181	TGFA	3'	GGAAACTGTTTAATATCACATG 1001	_____	TTTG
	AA		TTCATGTGA AAC TCC		
			AAGTACACT TTG AGG		
			ATAAT TCAA		
GAM181	ACAA2	5'	GGCAAAGTCTCACCTGAA 3540	T A	
			TTCA GTGA ACTTTGTC		
			AAGT CACT TGAAACGG		
			C C		
GAM181	C1orf34	3'	AAAGGACAAAGCCTCAGGGAA 2576	ATG AA	
			TTC TGA CTTTGTCTTT		
			AAG ACT GAAACAGGAAA		
			GG_ CC		
GAM181	CAMKK2	3'	GGAAAGGACCTGCCCCACATGA 1310	AAACTTT	
	A		TTCATGTG GTCCTTTCC		
			AAGTACAC CAGGAAAGG		
			CCCGTC_		
GAM181	FLJ10849	3'	GAAAGGATAACATTTCTCATGA 1803	T CT	
	A		TTCATG GAAA TTGTCCTTTC		
			AAGTAC CTTT AATAGGAAAG		
			T AC		
GAM181	FLJ13262	3'	GGAATAAATTTACATGAA 2112	C _	
			TTCATGTGAAA TTTGT CC		
			AAGTACACTTT AAATA GG		
			_ A		
GAM181	FLJ21977	5'	GGACAAAGCTCACATGAA 2237	AA	
			TTCATGTGA CTTTGTCC		
			AAGTACACT GAAACAGG		
			C_		
GAM181	FLJ22301	3'	GAAAGCTCACTTCCATGAA 2095	T ACTT TC	
			TTCATG GAA TG CTTTC		
			AAGTAC CTT AC GAAAG		
			_ C__ TC		
GAM181	HERC1	3'	GAAAGGACAGTTTTACATGAA 1071	TT	
			TTCATGTGAAACT GTCCTTTC		

AAGTACATTTTGA CAGGAAAG

GAM181 KIAA0280 3' AAAGGAATCACATGAA 3536 AACTTTG
TTCATGTGA TCCTTT
||||||| |||||
AAGTACACT AGGAAA

A_____

GAM181 KIAA0391 3' GAAAAGATAATTACTTACATGA 1517 AACT C
A TTCATGTGA TTGTC TTTC
||||||| ||||| |||||
AAGTACATT AATAG AAAG

CATT A

GAM181 PRO1386 3' GAAAAAACAAAGTTCTGCATGA 2188 GA CC
G TTCATGT AACTTTGT TTTC
||||||| ||||| |||||
GAGTACG TTGAAACA AAAG

TC AA

GAM181 RBMS1 3' GAAAGGTGTTCTTACATGAA 1711 _ TTTGT
TTCATGTGA AAC CCTTTC
||||||| ||| |||||
AAGTACATT TTG GGAAAG

C T_____

GAM181 RBMS1 3' GAAAGGTGTTCTTACATGAA 1712 _ TTTGT
TTCATGTGA AAC CCTTTC
||||||| ||| |||||
AAGTACATT TTG GGAAAG

C T_____

GAM181 RBMS1 3' GAAAGGTGTTCTTACATGAA 1713 _ TTTGT
TTCATGTGA AAC CCTTTC
||||||| ||| |||||
AAGTACATT TTG GGAAAG

C T_____

GAM181 RBMS1 3' GAAAGGTGTTCTTACATGAA 970 _ TTTGT
TTCATGTGA AAC CCTTTC
||||||| ||| |||||
AAGTACATT TTG GGAAAG

C T_____

GAM181 ROBO2 5' AAAAGACAAAGTTCGAATTGA 2635 TG_ A C
TCA TGAA CTTTGTC TTT
||| ||| ||||| |||
AGT GCTT GAAACAG AAA

TAA _ A

GAM181 SGP28 3' AAAGAACAATATAATTTTCACA 1270 CT_____ C
TGAA TTCATGTGAAA TTGT CTTT
||||||| ||| |||||
AAGTACACTTT AACAA GAAA

TAATAT A

GAM181 ST7L 3' AAAGGACAACACTGTAGATGAA 1746 G AAAC
TTCAT TG TTGTCCTTT
||||| || |||||

			AAGTA AT AACAGGAAA	
			G GTC__	
GAM181	ST7L	3'	AAAGGACAACACTGTAGATGAA 2456	G AAAC
			TTCAT TG TTGTCCTTT	
			AAGTA AT AACAGGAAA	
			G GTC__	
GAM181	ST7L	3'	AAAGGACAACACTGTAGATGAA 2475	G AAAC
			TTCAT TG TTGTCCTTT	
			AAGTA AT AACAGGAAA	
			G GTC__	
GAM181	LOC152263	3'	GAAAGGACAAAATAAACACA 3356	AAAC_
			TGTG TTTGTCCTTTC	
			ACAC AAACAGGAAAG	
			AAATA	
GAM181	LOC157507	5'	ACAAAGCTATCACATGAA 3202	AA_
			TTCATGTGA CTTTGT	
			AAGTACACT GAAACA	
			ATC	
GAM181	LOC158158	3'	GAAAGGACATCTACACCGAA 3211	AT AAAC
			TTC GTG TGTCCTTTC	
			AAG CAC ACAGGAAAG	
			C_ ATCT__	
GAM181	LOC219730	3'	GGAAAGGACAAAATGGAGAGTG 3588	GTGAAAC
	A		TCAT TTTGTCCTTTCC	
			AGTG AAACAGGAAAGG	
			AGAGGTA	
GAM181	LOC255158	3'	GAAAAACAAAAAGTTATATAT 3693	A __ CC
	GAA		TTCATGTG AACTT TGT TTTC	
			AAGTATAT TTGAA ACA AAAG	
			A AA AA	
GAM182	PTPRM	3'	ATGCAAACTCAACGATC 963	G _ C
			GAT CGT GAGT TTGCAT	
			CTA GCA CTCA AACGTA	
			_ A A	
GAM182	HCA4	3'	AATGCAAGAAGGAACACATAAG 2450	CG C GAG_
	TA		TACT ATG GT TCTTGCATT	
			ATGA TAC CA AGAACGTAA	
			A_ A AGGA	
GAM182	HCA4	3'	AATGCAAGAAGGAACACATAAG 3086	CG C GAG_
	TA		TACT ATG GT TCTTGCATT	

			ATGA TAC CA AGAACGTAA		
			A_ A AGGA		
GAM183	FLJ13154	3'	ACCAGAATCTCCACTGTAGT 2070	___	A
			ACTGCA GAGATTCT GT		
			TGATGT CTCTAAGA CA		
			CAC C		
GAM183	HDAC9-PENDING	3'	ACTAGAATCTCTTAAGTAT 1527		GC
			ATACT AGAGATTCTAGT		
			TATGA TCTCTAAGATCA		
			AT		
GAM183	KIAA0232	3'	TTACTAGCATTGCAGTGTC 2958		AGATT
			GATACTGCAG CTAGTAA		
			CTGTGACGTT GATCATT		
			AC___		
GAM183	KIAA1010	3'	ACTAGAATCTCTAGAATTTGA 2933		TACTGC
			TCGA AGAGATTCTAGT		
			AGTT TCTCTAAGATCA		
			TAAGA_		
GAM183	LOC219894	3'	TGCTGTCTCTGCAGTACTGA 3596	A	TCT
			TCG TACTGCAGAGAT AGTA		
			AGT ATGACGTCTCTG TCGT		
			C ___		
GAM184	PABPC4	3'	AATAAAGAAAAAAATCTCCA 1064	A	AG
			TGGAGA TTTTTTTC TTGTT		
			ACCTCT AAAAAAAG AATAA		
			A A_		
GAM184	SH3GL2	3'	GACTGAAAAGAAATTCTCCA 983	_	
			TGGAGAATTTTTTT CAGTT		
			ACCTCTTAAAGAAA GTCAG		
			A		
GAM184	IMP-2	3'	CAAACAAAGAAAAAATTCCACA 1309	GA	CAG
			TG GAATTTTTTT TTGTTTG		
			AC CTAAAAAAG AACAAAC		
			AC A_		
GAM184	KIAA0872	3'	CAAAAGAAAAAAATTCCTCC 1593	_	AG
			GGAGAATTTTTTT C TTG		
			CCTCTTAAAAAAA G AAC		
			A AA		
GAM184	MGC19570	5'	CAAACAACCGACTCCTTTCCA 2514		ATTTTTT A
			TGGAGA TC GTTGTTTG		

ACCTTT AG CAACAAAC
 CCTC__ C
 GAM184 PTPN4 3' CAAACAAGGCTCAAAATTCTC 961 TTTCAG
 GAGAATTTT TTGTTTG
 ||||| |||||
 CTCTTAAAA AACAAAC
 CTCGG_
 GAM184 TIX1 5' CAAACAAGTGAAGCTGCA 2604 G AAT
 TG AG TTTTTCAGTTGTTTG
 || || |||||
 AC TC GAAAAAGTCAACAAAC
 G __
 GAM185 PSG5 3' AAAAAACTCCATGTTATTGGAC 955 TC_ AC
 TAA TTAGTTCA ATATGGA TTTT
 ||||| ||||| |||||
 AATCAGGT TGTACCT AAAAA
 TAT CA
 GAM185 FAPP2 3' AAAAAGCTGGTGGTGAAC 2267 ATGGAA
 GTTCATCAT CTTTT
 ||||| |||||
 CAAGTGGTG GAAAAA
 GTC__
 GAM185 LOC145820 3' AAGTGCCACAAAATGAACTAA 3084 CATA A
 TTAGTTCAT TGG ACTT
 ||||| |||||
 AATCAAGTA ACC TGAA
 AAAC G
 GAM185 LOC83690 3' AAAAAGTTGAACAAAGATGAAC 2202 ATATGG_
 TAA TTAGTTCATC AACTTTTT
 ||||| |||||
 AATCAAGTAG TTGAAAAA
 AAACAAG
 GAM186 IGF1 3' TATACTACAGCAGAATGACT 762 A ACG C
 AGTTATTC TG GTAG ATA
 ||||| || |||||
 TCAGTAAG AC CATC TAT
 _ GA_ A
 GAM186 FLJ20035 3' ATGTTCTGTCATGAATACT 1733 T T
 AGT ATTCATGACGG AGCAT
 || ||||| |||||
 TCA TAAGTACTGTC TTGTA
 - -
 GAM186 FXYD3 3' TATGCTACCCTTAATAAC 1966 TCA C
 GTTAT TGA GGTAGCATA
 |||| || |||||
 CAATA ATT CCATCGTAT
 __ C
 GAM186 FXYD3 3' TATGCTACCCTTAATAAC 1263 TCA C
 GTTAT TGA GGTAGCATA
 |||| || |||||

			CAATA ATT CCATCGTAT		
			___ C		
GAM186	GMFB	3'	TATTGAGCCATGAATAATTTA 1090	A___	
			TAAGTTATTCATG CGGTA		
			ATTTAATAAGTAC GTTAT		
			CGA		
GAM187	ADCY2	3'	ATGTTGAATGTATCTAGTG 2710	TT G	
			CACTAG TA ATTCAACAT		
			GTGATC AT TAAGTTGTA		
			T_ G		
GAM187	CCNA1	3'	GTTGGATCAACTAATG 1070	C TA	
			CA TAGTT GATTCAAC		
			GT ATCAA CTAGGTTG		
			A _		
GAM187	COG6	3'	ATGTTGACCTGAGCTAGT 2961	AT	
			ACTAGTTTAG TCAACAT		
			TGATCGAGTC AGTTGTA		
			C_		
GAM187	DACH	3'	GTATATTGAACCCCTAGGCTAGT 2387	A_ C	
	G		CACTAGTTTAG TTCAA ATAC		
			GTGATCGGATC AAGTT TATG		
			CC A		
GAM187	FKBP1A	3'	GTGTGTTTACCTAAACTA 775	ATTC	
			TAGTTTAG AACATAC		
			ATCAAATC TTGTGTG		
			CAT_		
GAM187	HSPD1	3'	ATGTTCTAACTCCTAGACTAGT 2559	ATTC___	
	G		CACTAGTTTAG AACAT		
			GTGATCAGATC TTGTA		
			CTCAATC		
GAM187	JJAZ1	3'	TATGTTGAATTGATCTAG 1622	TTTA	
			CTAG GATTCAACATA		
			GATC TTAAGTTGTAT		
			TAG_		
GAM187	MAN1A1	3'	GTATGTCAAAGAATAAATTAGT 3543	GA_ CA	
			ACTAGTTTA TT ACATAC		
			TGATTAAAT AA TGTATG		
			AAG AC		
GAM187	PKIB	3'	ATGTTGAAAGACTTAGTG 2254	_ AGA	
			CACTA GTTT TTCAACAT		

			GTGAT CAGA AAGTTGTA	
			T _	
GAM187	RRM2B	3'	GTATGTTGAAATAAACTA 2799	GA
			TAGTTTA TTCAACATAC	
			ATCAAAT AAGTTGTATG	
			A_	
GAM187	SWAP70	3'	GTATGTGCTGTAAACTAG 2917	ATTCA
			CTAGTTTAG ACATAC	
			GATCAAATT TGTATG	
			GTCG_	
GAM187	ABHD3	3'	GTTTTAATTAACTAGT 2436	C_
			ACTAGTTTAGATT AAC	
			TGATCAAATTTAA TTG	
			TT	
GAM187	ATIP1	3'	ATGTTCTTTTAAATTAGTG 1924	TTC
			CACTAGTTTAGA AACAT	
			GTGATTAAATTT TTGTA	
			TC_	
GAM187	DKFZP564F013	3'	TATGTTGAATTATGTCAGTG 3640	AG TTA
			CACT T GATTCAACATA	
			GTGA G TTAAGTTGTAT	
			CT TA_	
GAM187	FN5	3'	TATGTTGAATCAAAGTG 1898	AGT A
			CACT TT GATTCAACATA	
			GTGA AA CTAAGTTGTAT	
			_ _	
GAM187	KIAA0416	3'	TATGCTGAAGACTGGT 1637	TAGA A
			ACTAGTT TTCA CATA	
			TGGTCAG AAGT GTAT	
			_ C	
GAM187	KIAA0455	3'	TATGTTGATTCTACCTGTG 2948	T TT T
			CAC AG TAGA TCAACATA	
			GTG TC ATCT AGTTGTAT	
			_ C_ T	
GAM187	KIAA0912	3'	GTATGTTTTACTTAACTAG 2689	ATTC
			CTAGTTTAG AACATAC	
			GATCAAATT TTGTATG	
			CATT	
GAM187	KIAA0981	3'	ATGTTGAATTTTAACTAG 2597	_
			CTAGTTTAGA TTCAACAT	

			GATCAAATTT AAGTTGTA		
			T		
GAM187	KIAA1911	3'	TATGTTGAAAACTGCTGTG 2976	T	TTAGA
			CAC AGT TTCAACATA		
			GTG TCG AAGTTGTAT		
			_ TCAAA		
GAM187	KRTHB2	3'	GTATGTTGAACCCAACTGTG 2310	T	AGA
			CAC AGTTT TTCAACATAC		
			GTG TCAAA AAGTTGTATG		
			_ CCC		
GAM187	RPS6KC1	3'	GTATGTTGAATGTGGTCCCAG 1429	AGT_	G
			CT TTA ATTCAACATAC		
			GA GGT TAAGTTGTATG		
			CCCT G		
GAM187	TOMM70A	3'	ATGTTGATTTTAAATTA 1558	T_	
			TAGTTTAGA TCAACAT		
			ATTAAATTT AGTTGTA		
			TT		
GAM188	CDC23	3'	TGCACAGTAGATGCTATGGA 1141		AAC
			TCTATAGCATCTACT TGTA		
			AGGTATCGTAGATGA ACGT		
			C_		
GAM188	EGLN3	3'	TGGAGGTGGTAGATGCCACAGA 2330	ATA	A G
			TCT GCATCTACTA CT TA		
			AGA CGTAGATGGT GA GT		
			CAC G G		
GAM188	EGLN3	3'	TGGAGGTGGTAGATGCCACAGA 1976	ATA	A G
			TCT GCATCTACTA CT TA		
			AGA CGTAGATGGT GA GT		
			CAC G G		
GAM188	JAM3	3'	GTACACAGATGCTACAGA 2280	A	ACTAAC
			TCT TAGCATCT TGTAC		
			AGA ATCGTAGA ACATG		
			C C_		
GAM188	RNF7	3'	ACAGCTTAGAAGTGCTATA 1485	T A _	
			TATAGCA CT CTAA CTGT		
			ATATCGT GA GATT GACA		
			_ A C		
GAM188	WBSCR5	3'	GTACAGTTAACTTATAGA 1973	CATCTAC	
			TCTATAG TAACTGTAC		

			AGATATT	ATTGACATG	
			CA_____		
GAM188	WBSCR5	3'	GTACAGTTAACTTATAGA	2250	CATCTAC
			TCTATAG	TAACTGTAC	
			AGATATT	ATTGACATG	
			CA_____		
GAM188	WBSCR5	3'	GTACAGTTAACTTATAGA	1479	CATCTAC
			TCTATAG	TAACTGTAC	
			AGATATT	ATTGACATG	
			CA_____		
GAM188	C8orf13	3'	TGCACAGCTGTTTAGGCTATAG	3206	ATCT TAA A
	A		TCTATAGC	AC CTGT CA	
			AGATATCG	TG GACA GT	
			GATT TC_	C	
GAM188	CDT6	3'	TATAGTTAATAATAAATGCTGT	1945	C C___
	A		TATAGCAT TA	TAACTGTA	
			ATGTCGTA AT	ATTGATAT	
			A AATA		
GAM188	DKFZp566D234	3'	TGCAGCATGCTATAGA	2613	CTACTAA
			TCTATAGCAT	CTGTA	
			AGATATCGTA	GACGT	
			C_____		
GAM188	FLJ10525	3'	GTACAGTTTTAGTATAGA	1786	GCAT CT
			TCTATA	CTA AACTGTAC	
			AGATAT	GAT TTGACATG	
			_____	T_	
GAM188	FLJ12078	5'	TGCTAGAGTAATGCTATA	2121	C AACT
			TATAGCAT TACT	GTA	
			ATATCGTA ATGA	CGT	
			_	GAT_	
GAM188	KIAA0007	3'	TGTACAGTTATATTTGTCTATA	3154	_ TC C
			TATAG CA TA	TAACTGTACA	
			ATATC GT AT	ATTGACATGT	
			T TT	_	
GAM188	KIAA1728	3'	TGTACAATTAGTACTTTATAG	2819	CATC C
			CTATAG	TACTAA TGTACA	
			GATATT	ATGATT ACATGT	
			TC_	A	
GAM188	MGC4643	3'	TGTACAGTCTAAAGCTACAGA	2272	A ATCTACTA
			TCT TAGC	ACTGTACA	

			AGA ATCG	TGACATGT		
			C	AAATC__		
GAM188	MPPE1	3'	TGTACAGTATGTAAATGCTAT	2029	C	TA
			ATAGCAT TAC	ACTGTACA		
			TATCGTA ATG	TGACATGT		
			A	TA		
GAM188	RNPS1	3'	TGTACAGTCAGTACTATA	2376	CATC	A
			TATAG	TACT ACTGTACA		
			ATATC	ATGA TGACATGT		
			__	C		
GAM188	RNPS1	3'	TGTACAGTCAGTACTATA	1326	CATC	A
			TATAG	TACT ACTGTACA		
			ATATC	ATGA TGACATGT		
			__	C		
GAM188	TUSP	3'	AGTAGAAGATGCTACAGA	1907	A	A A
			TCT TAGCATCT	CTA CT		
			AGA ATCGTAGA	GAT GA		
			C	A _		
GAM188	LOC153027	3'	TGTACAGTCAGTTCTATA	2792	CATCT	A
			TATAG	ACT ACTGTACA		
			ATATC	TGA TGACATGT		
			T__	C		
GAM188	LOC153114	5'	GTGAGCAGACTGCTATAGA	3367	_	A A
			TCTATAGCA	TCT CT AC		
			AGATATCGT	AGA GA TG		
			C	C G		
GAM189	SORT1	3'	CATCAAAGCCAAAAGGACCTAC	974	A C	AAA
	A		TGTA G	TCTTTTTG TTGATG		
			ACAT C	AGGAAAAC AACTAC		
			_ C	CGA		
GAM189	ATP9A	3'	CATCAATCTGGAAAGAACTTAC	2618	C	GAA
	A		TGTAAG	TCTTTTT ATTGATG		
			ACATTC	AGAAAGG TAACTAC		
			A	TC_		
GAM189	DKFZP434K1772	3'	TTTCAAAAAGAGGTTACA	2797	G	
			TGTAA	CTCTTTTTGAAA		
			ACATT	GAGAAAACTTT		
			G			
GAM189	UNC5D	3'	CAATTTCAAAGAGAACCCACA	2392	AAGC	
			TGT	TCTTTTTGAAATTG		

			ACA AGAGAACTTTAAC	
			CCCA	
GAM190	SCD	3'	AGCCAGACAAAATTTGAGAATA 1176	CA TG CCA
			TAT T A TTTGTCTGGCT	
			ATA A T AAACAGACCGA	
			AG GT TA_	
GAM190	SOS2	3'	AGCCATATGTAGTCATTGA 2824	T CATT C
			TCA TGAC TGT TGGCT	
			AGT ACTG GTA ACCGA	
			T AT__ T	
GAM190	BANP	3'	CCAGACAAGTGCCCAACGA 2744	A AC
			TC TTG CATTTGTCTGG	
			AG AAC GTGAACAGACC	
			C CC	
GAM190	KIAA0446	5'	AGCCAGACAAAAAGAATGATTC 2831	T GACCA
			A ATCATT TTTGTCTGGCT	
			C TAGTAA AAACAGACCGA	
			T GAA__	
GAM190	LOC115110	3'	GGCTGAAATGGTCAAT 2924	GTC
			ATTGACCATTT TGGCT	
			TAACTGGTAAA GTCGG	
			—	
GAM190	LOC148443	3'	AGCCAACACATATGGTCAATGA 3118	T C_
			TCATTGACCAT TGT TGGCT	
			AGTAACTGGTA ACA ACCGA	
			T CA	
GAM190	LOC151826	3'	TTATTCAAAGGCCAATGATA 3161	A A TC
			TATCATTG CC TTTG TGG	
			ATAGTAAC GG AAAC ATT	
			C _ TT	
GAM190	LOC200609	5'	CCACCACCAATGGTCAAGATAT 3479	A T C_
			ATATC TTGACCATT GT TGG	
			TATAG AACTGGTAA CA ACC	
			_ C CC	
GAM191	BHLHB3	3'	TCAAGTGCATCTATTCCCA 2163	AAATAC GT
			TGGGAATA TACT TGA	
			ACCCTTAT GTGA ACT	
			CTAC__ _	
GAM191	ITK	3'	CATGAGGTAATATTATTATTC 1223	_ C GT_
	CA		TGGGAATAA AATA TACT TG	

			ACCCTTATT TTAT ATGG AC		
			A A AGT		
GAM191	MPV17	3'	CTTGATAATAGTCTTATTCCCA 2888	AAT C TG	
			TGGGAATAA ACTA TGT AG		
			ACCCTTATT TGAT ATA TC		
			C__ A GT		
GAM191	MSR1	3'	TCAGCATT TTTTATTCCCA 930	TACTAC	
			TGGGAATAAAA TGTTGA		
			ACCCTTATTTT ACGACT		
			T_____		
GAM191	RNMT	3'	TCAGCACCATTATTCCCA 1061	AATACTAC	
			TGGGAATAA TGTTGA		
			ACCCTTATT ACGACT		
			ACC_____		
GAM191	SCP2	3'	CAGAAACAGTATTTTCTTCCCA 976	T ACTG	
			TGGGAA AAAATACT TTG		
			ACCCTT TTTTATGA GAC		
			C CAAA		
GAM191	DKFZP564K0822	3'	CTCAACAATTTTGTATTCCCA 3630	AAATACTAC	
			TGGGAATA TGTTGAG		
			ACCCTTAT ACAACTC		
			GTTTTA__		
GAM191	KIAA0564	3'	CAAAATGTACCTTATTCCCA 2742	AA TACTG	
			TGGGAATAA TAC TTG		
			ACCCTTATT ATG AAC		
			CC TAA__		
GAM191	KIAA0769	3'	CGGCATTATTTTATTCCCA 1560	CTAC	
			TGGGAATAAAATA TGTTG		
			ACCCTTATTTTAT ACGGC		
			T_____		
GAM191	KIAA1163	3'	CTTGGTTAGTATTTGATTCCCA 3122	A CTG TG	
			TGGGAAT AAATACTA T AG		
			ACCCTTA TTTATGAT G TC		
			G T__GT		
GAM191	KIAA1332	3'	CAACAAAGGATTTTATTCC 2909	A AC	
			GGAATAAAAT CT TGTTG		
			CCTTATTTTA GG ACAAC		
			_ AA		
GAM191	SFRS11	3'	AGTAATAATTTATTCCCA 1155	A C	
			TGGGAATAAA TA TACT		

			ACCCTTATTT AT ATGA	
			A A	
GAM191	ZNF387	3'	CTCAACAGTAATTCCTCCCA 1521	ATAAAATAC
			TGGGA TACTGTTGAG	
			ACCCT ATGACAACTC	
			CACCTTA__	
GAM191	LOC138639	3'	CTCAACACACCAAGCCTTATTC 3020	AATACTAC_
			CCA TGGGAATAA TGTTGAG	
			ACCCTTATT ACAACTC	
			CCGAACCAC	
GAM191	LOC147299	3'	CAACATTTTATTTCCA 3107	TACTAC
			TGGGAATAAAA TGTTG	
			ACCTTTATTTT ACAAC	

GAM191	LOC90019	5'	CTCAACAGCTGCTTATTCCTCG 2445	AATACTA
			TGGGAATAA CTGTTGAG	
			GCCCTTATT GACAACTC	
			CGTC__	
GAM192	B3GALT5	5'	AGATCAGAGACTGTAAAAAGT 2320	C_ C
			GCTT TACAGTCTTT GTTT	
			TGAA ATGTCAGAGA TAGA	
			AA C	
GAM192	BTEB1	3'	GAAACGAAAGAAAGCAAAGC 808	CTACAG
			GCTT TCTTTCGTTTC	
			CGAA AGAAAGCAAAG	
			ACGAA_	
GAM192	RP2	3'	GCTAAAACTGTAGAAGC 1340	C C
			GCTTCTACAGT TTT GT	
			CGAAGATGTCA AAA CG	
			_ T	
GAM192	C12orf22	3'	AAACAAAACCTGTAGAAGC 2169	C C
			GCTTCTACAGT TTT GTTT	
			CGAAGATGTCA AAA CAAA	
			- -	
GAM192	C20orf26	3'	GGAAACGCGCTCTGTAGAA 2879	TCTTT
			TTCTACAG CGTTTCC	
			AAGATGTC GCAAAGG	
			TCGC_	
GAM192	FLJ14627	5'	GAACCTGAAGACTGCAGAGC 2283	T A C_
			GCT CT CAGTCTTT GTTT	

			CGA GA GTCAGAAG CAAG		
			_ C TT		
GAM192	GPR72	3'	GGAAACACACTCCTGCAGAAGC 2867	A	TCTTTC
	TG		TAGCTTCT CAG GTTTCC		
			GTCGAAGA GTC CAAAGG		
			C CTCACA		
GAM192	GPT2	3'	GAAAAGGTTAAATCGTAGAAGC 2418	A	CTT_ G
	TA		TAGCTTCTAC GT TC TTTC		
			ATCGAAGATG TA GG AAAG		
			C AATT A		
GAM192	KIAA0470	5'	GCCAAAGACTTAGAAGCTA 1556	C	C
			TAGCTTCTA AGTCTTT GT		
			ATCGAAGAT TCAGAAA CG		
			_ C		
GAM192	KIAA1328	5'	GAAATCATACCTGCAGAAGCTA 2602	A	TCTTTC
			TAGCTTCT CAG GTTTC		
			ATCGAAGA GTC TAAAG		
			C CATACT_		
GAM192	KIAA1981	3'	AGATGAAACCATGGAAGC 3430	CA	CT
			GCTTCTA GT TTCGTTT		
			CGAAGGT CA AAGTAGA		
			AC _		
GAM192	MGC17330	3'	GGAAACGAGTTTGTACAGAAGT 2342	_	TCT
			GCTTCT ACAG TTCGTTTCC		
			TGAAGA TGTT GAGCAAAGG		
			CA T_		
GAM192	MRPL35	3'	GAAACGAAAAAGTTAAGC 1701	CT	AGTC
			GCTT AC TTTCGTTTC		
			CGAA TG AAAGCAAAG		
			T_ AA_		
GAM192	LOC205011	5'	GAAAACAAGAGTAGAGGC 3492	AG	TCG
			GCTTCTAC TCTT TTTC		
			CGGAGATG AGAA AAAG		
			_ CA_		
GAM193	KIAA1228	3'	CGGAACACACCCTCTCA 2712	AAA	
			TGAGA GTGTGTTCTG		
			ACTCT CACACAAGGC		
			CC_		
GAM193	KIAA1655	5'	GCGACTCGGGGCACTGCTCCTC 2754	AAA _	A
	A		TGAG AGT GTGTTCTGA TCGC		

ACTC TCG CACGGGGCT AGCG
 C__ T C
 GAM193 NDST3 3' TAGAACACACCTTTTCCA 1157 A _
 TG GAAAAG TGTGTTCTG
 || ||||| |||||
 AC CTTTTC ACACAAGAT
 _ C
 GAM193 PP1057 3' GCAATTTACACACTTGTCTCA 2189 A TCT C
 TGAGA AAGTGTGT GAAT GC
 ||||| ||||| |||||
 ACTCT TTCACACA TTTA CG
 G _ A
 GAM193 RNP24 3' CGACTCAGCATACATTTTCCCA 1333 A G T A
 TG GAAAA TGTGT CTGA TCG
 || ||||| ||||| |||||
 AC CTTTT ACATA GACT AGC
 C _ C C
 GAM193 LOC150142 5' CAGAACACCACCTCTCA 3142 AAA _
 TGAGA GTG TGTCTG
 ||||| ||||| |||||
 ACTCT CAC ACAAGAC
 C__ C
 GAM193 LOC199899 5' ATTCAAAACACACATTC 3473 AA C
 GAA GTGTGTT TGAAT
 ||||| ||||| |||||
 CTT CACACAA ACTTA
 A_ A
 GAM193 LOC222068 3' ATTTTAATACACTTCCCTCA 3573 AA CT
 TGAG AAGTGTGTT GAAT
 ||||| ||||| |||||
 ACTC TTCACATAA TTTA
 CC T_
 GAM194 HUS1 3' TTCCTATTATAATTACATCT 3509 A TC
 GGAT TAGTT ATAATAGGAA
 ||||| ||||| |||||
 TCTA ATTAA TATTATCCTT
 C _
 GAM194 TRPM8 3' TCCTATTGAAGGAACCACCCCC 2052 ATATA A_
 GG GTTTC TAATAGGA
 || ||||| |||||
 CC CAAGG GTTATCCT
 CCCAC AA
 GAM194 LOC148936 3' CCTACCTGATATTACATCCTA 3304 A T TAA
 TAGGAT TAGT TCA TAGG
 ||||| ||||| |||||
 ATCCTA ATTA AGT ATCC
 C T CC_
 GAM194 LOC148938 3' CCTACCTGATATTACATCCTA 3303 A T TAA
 TAGGAT TAGT TCA TAGG
 ||||| ||||| |||||

		ATCCTA ATTA AGT ATCC		
		C T CC_		
GAM194	LOC200803 3'	TTCCTATTATATGGTATCC 3452	AGTTTC	
		GGATAT ATAATAGGAA		
		CCTATG TATTATCCTT		
		GTA__		
GAM194	LOC255332 5'	TTCCTATTACTCTGCATATCTT 3696	A TTCA	
	A	TAGGATAT GT TAATAGGAA		
		ATTCTATA CG ATTATCCTT		
		_ TCTC		
GAM194	LOC90459 3'	CTAGATGAAACCATATCTTA 2641	A AA	
		TAGGATAT GTTTCAT TAG		
		ATTCTATA CAAAGTA ATC		
		C G_		
GAM195	DKFZp434E0519 5'	TGGAAATCCGTGTGTAA 2241	ACG	
		TTACACACGGA TTTA		
		AATGTGTGCCT AGGT		
		AA_		
GAM195	HSU84971 3'	GTTATAAACATTCTTATGTGTA 1439	C_ C	
	AT	ATTACACA GGAA GTTTATAAC		
		TAATGTGT TCTT CAAATATTG		
		AT A		
GAM195	LOC157663 3'	AGCTTCCCATTGTGTAATA 3203	C_ C	
		TATTACACA GGAA GTT		
		ATAATGTGT CCTT CGA		
		TAC _		
GAM196	EXT2 3'	GAGAAGAGAAGCGTGTTA 737	G	
		TAACACGCTTCT TTCTC		
		ATTGTGCGAAGA AAGAG		
		G		
GAM196	MBNL 3'	ATAGATGAGAGCGTGCATGC 1936	TTC_	
		GC TGTTCTCATCTAT		
		CG GCGAGAGTAGATA		
		TACGT		
GAM196	PLN 3'	AGATGAGAACTGGTGGTTA 946	A TCT	
		TAAC CGCT GTTCTCATCT		
		ATTG GTGG CAAGAGTAGA		
		_ T_		
GAM196	SLC12A2 3'	AGCAATAAAAGCGTGTTA 796	C _	
		TAACACGCTT TGTT CT		

ATTGTGCGAA ATAA GA
 A C
 GAM196 SLC1A3 3' AGATGAGAAGACTAGCAGC 1092 T ____
 GCT CTG TTCTCATCT
 ||| ||| |||||
 CGA GAT AAGAGTAGA
 C CAG
 GAM196 BTBD3 3' ATAGATGATGAAAAGCTGTTA 1600 C CTG _
 TAACA GCTT TTC TCATCTAT
 |||| ||| ||| |||||
 ATTGT CGAA AAG AGTAGATA
 _ ____ T
 GAM196 KIAA1237 3' AGATGAGGATGAGCGT 3166 CT
 ACGCTT GTTCTCATCT
 |||| |||||
 TGCGAG TAGGAGTAGA
 _
 GAM196 NAALAD2 3' ATAGATGAGAATTTTCCGT 1215 CTTCT
 ACG GTTCTCATCTAT
 || |||||
 TGC TAAGAGTAGATA
 CTTT_
 GAM196 PEG10 3' ATAGATGAATTAGTAAGC 1605 _ TTC
 GCTT CTG TCATCTAT
 ||| ||| |||||
 CGAA GAT AGTAGATA
 T TA_
 GAM197 RAI2 5' AGAATTAGGCTTAAAAAATGCC 1959 CG TATGAT
 T AGGCATTT TAA ATTCT
 ||||| ||| |||||
 TCCGTAAA ATT TAAGA
 AA CGGAT_
 GAM197 UMPK 3' CATGGAGATGAAATGCCT 1436 AA_
 AGGCATTTCTG TATG
 ||||| |||
 TCCGTAAAGTA GTAC
 GAG
 GAM197 ZNF134 3' GAAAATCATGAAATGCCT 1021 GTAAT A
 AGGCATTTTC ATGAT TTC
 ||||| ||| |||
 TCCGTAAAG TACTA AAG
 ____ A
 GAM197 ARL8 3' AGAATATCACATTATTCAATGC 3594 TC A
 GCATT GTAAT TGATATTCT
 |||| ||| |||||
 CGTAA TATTA ACTATAAGA
 CT C
 GAM197 KIAA0546 3' AATGTTAATTATGAAACACCT 2911 CA A
 AGG TTTCGTAAT TGATATT
 || ||||| |||||

TCC AAAGTATTA ATTGTAA
 AC _
 GAM197 KIAA0644 3' AGAACATCACTGAAAATGCCT 1557 _ TAATA A
 AGGCATTT CG TGAT TTCT
 ||||| || ||| |||
 TCCGTAAA GT ACTA AAGA
 A C _ C
 GAM197 KIAA1508 3' GGATATCACATAATGCC 2614 TCGTA A
 GGCATT AT TGATATTC
 |||| | |||||
 CCGTAA TA ACTATAGG
 _ C
 GAM197 MTHFS 3' ATTGTAATTATGAAATACCT 1302 C _ TG
 AGG ATTTCGTAAT A AT
 || ||||| | ||
 TCC TAAAGTATTA T TA
 A A GT
 GAM197 SUCLA2 3' GTCATATTAAGAAACACCT 1066 CA G
 AGG TTTC TAATATGAT
 || ||| |||||
 TCC AAAG ATTATACTG
 AC A
 GAM197 LOC149910 3' AGAACTTTATTTACCATGAAAT 3140 AAT _ TA
 GCCT AGGCATTTCTG ATGA TTCT
 ||||| ||| |||
 TCCGTAAAGTA TATT AAGA
 CCATT TC
 GAM197 LOC222171 3' GAATATTTACACAATGCCT 3575 TC ATAT
 AGGCATT GTA GATATTC
 ||||| || |||||
 TCCGTAA CAT TTATAAG
 CA _
 GAM198 ZNF24 3' GACAAATACATTATTTCTG 1342 _ AA
 TAGAAATAATG AT GTC
 ||||| || |||
 GTCTTTATTAC TA CAG
 A AA
 GAM198 ALS2CR12 3' GATGGTTGGCACACCATTCTG 2471 AA ATAAGT
 TA TATAGAAAT TG CCATC
 ||||| || |||
 ATGTCTTTA AC GGTAG
 CC ACGGTT
 GAM198 FLJ10508 3' GATGGCTCTTATCATCATCTTT 1783 A A T_
 ATA TATAGA AT ATGATAAG CCATC
 |||| | ||||| |||
 ATATTT TA TACTATTC GGTAG
 C C TC
 GAM198 FLJ13197 3' GATTCATCATTATTCCTA 2072 A A
 TAG AATAATGAT AGTC
 || ||||| |||

		ATC TTATTACTA TTAG		
		C C		
GAM198	FLJ21934	3' GATGATGTCATTACTTCTATA	2085	A A_
		TATAGAA TAATGATA GTC		
		ATATCTT ATTACTGT TAG		
		C AG		
GAM198	FLJ23132	3' ATGGACTTAATCTCTG	3691	AATAAT _
		TAGA GAT AAGTCCAT		
		GTCT CTA TTCAGGTA		
		_____ A		
GAM198	KIAA0470	3' ATGGACTTCTTCATCTGTA	1555	AATAA T_
		TATAGA TGA AAGTCCAT		
		ATGTCT ACT TTCAGGTA		
		_____ TC		
GAM198	LEPROTL1	3' GCTGCGTATTATTTCTATA	1620	ATA
		TATAGAAATAATG AGT		
		ATATCTTTATTAT TCG		
		GCG		
GAM198	LYSAL1	5' GACCCCAGCATTATTTCTATA	1164	ATAA_
		TATAGAAATAATG GTC		
		ATATCTTTATTAC CAG		
		GACCC		
GAM198	RAB40A	5' GATGGATGCATGCATTATTTT	3229	ATAA_
		GAAATAATG GTCCATC		
		CTTTATTAC TAGGTAG		
		GTACG		
GAM198	STK38L	3' GATAGGGTTTCATTTATTTCTA	2845	_ TA GT _
	TA	TATAGAAATAA TGA A CC ATC		
		ATATCTTTATT ACT T GG TAG		
		T _ TG A		
GAM198	ZNF363	3' GATAGACTTATCATAGCTCTAT	2974	AA A C
	A	TATAGA TA TGATAAGTC ATC		
		ATATCT AT ACTATTCAG TAG		
		CG _ A		
GAM198	LOC146481	3' GACAGTCATGCATTTCTATA	3093	A_ AA
		TATAGAAAT ATGAT GTC		
		ATATCTTTA TACTG CAG		
		CG A_		
GAM198	LOC152008	3' ATGGAGGCATTATTTCTA	3165	ATAAG
		TAGAAATAATG TCCAT		

ATCTTTATTAC AGGTA
 GG____
 GAM198 LOC153020 3' GATGGACCCCTCAAGCAATTTC 3178 AA__ TAA
 TATA TATAGAAAT TGA GTCCATC
 ||||| || |||||
 ATATCTTTA ACT CAGGTAG
 ACGA TCC
 GAM198 LOC199786 3' GCTTAAGCCATTATTTCTG 3433 A__
 TAGAAATAATG TAAGT
 ||||| ||||
 GTCTTTATTAC ATTCG
 CGA
 GAM198 LOC220766 3' ATGGACTTCTTCATCTGTA 3498 AATAA T_
 TATAGA TGA AAGTCCAT
 |||| || |||||
 ATGTCT ACT TTCAGGTA
 ____ TC
 GAM199 ADAM12 3' CTAGAGCACTGCCACCAGTA 1029 A A AAT _
 TACT GGT GCA TG TCTAG
 ||| ||| || |||||
 ATGA CCA CGT AC AGATC
 _ C C__ G
 GAM199 HOXC13 3' CTAGATGTAGATGCTGCCTA 2538 AAT_
 TAGGTAGCA TGTCTAG
 ||||| |||||
 ATCCGTCGT GTAGATC
 AGAT
 GAM199 NRIP1 3' CTAGACAATTTCTTCTA 2549 T C
 TAGG AG AAATTGTCTAG
 ||| || |||||
 ATCT TC TTTAACAGATC
 _ _
 GAM199 RRM2B 3' CTAAACAATTTGCATTTA 2798 A C
 TAGGT GCAAATTGT TAG
 |||| ||||| |||
 ATTTA CGTTTAACA ATC
 _ A
 GAM199 BIRC4 3' TTAGCATTTGCTACCAAGTA 806 A T T
 TACT GGTAGCAAAT G CTAG
 ||| ||||| |||
 ATGA CCATCGTTTA C GATT
 A _ _
 GAM199 FLJ11301 3' GCGGTATTTACTACCTAG 1822 C _
 CTAGGTAG AAAT TGT
 ||||| ||| |||
 GATCCATC TTTA GCG
 A TG
 GAM199 LAP1B 5' AGGCAGGTTTGCTACACAG 2696 AG _
 CT GTAGCAAAT TGTCT
 || ||||| |||||

			GA CATCGTTTG ACGGA		
			CA G		
GAM199	MGC11324	3'	TAGATCTGTACCTAGTA 2273	G AATT	
			TACTAGGTA CA GTCTA		
			ATGATCCAT GT TAGAT		
			_ C _		
GAM199	PRO2958	3'	ACACCTTTGCTACCAGTA 1841	A T_	
			TACT GGTAGCAAA TGT		
			ATGA CCATCGTTT ACA		
			_ CC		
GAM199	SH3BGRL2	3'	CTAGACAAAGCTACCCAG 2208	A AAA	
			CT GGTAGC TTGTCTAG		
			GA CCATCG AACAGATC		
			C A_		
GAM199	LOC144997	3'	CTAGACAGATATCCACTTAGTA 3271	AGCAAA	
			TACTAGGT TTGTCTAG		
			ATGATTCA GACAGATC		
			CCTATA		
GAM199	LOC148809	3'	CTAGACAACATGACCCTACC 3125	_ AA	
			GGTAG CA TTGTCTAG		
			CCATC GT AACAGATC		
			CCA AC		
GAM199	LOC219540	3'	CTAGACAATTTTTTTTAG 3612	TAGC	
			CTAGG AAATTGTCTAG		
			GATT TTAAACAGATC		
			TT_		
GAM200	PTGER3	3'	CTATAGAGTATTCCATAATTTG 790	T AC _	
	AA		TTCAA TTAT GGAT TTCTATAG		
			AAGTT AATA CTTA GAGATATC		
			T C_ T		
GAM200	SIRT1	3'	CTATAGATGATATTTTAAATTG 1416	TACGGATT	
	AA		TTCAATTTA TCTATAG		
			AAGTTAAAT AGATATC		
			TTTATAGT		
GAM200	FLJ10898	3'	AGAACTGTAAATTGAA 2526	T A	
			TTCAATTTA ACGG TTTCT		
			AAGTTAAAT TGTC AAAGA		
			_ _		
GAM201	FLJ10511	3'	ATGCCTATAATACCATAATGCC 1784	C _ ACACC	
	AG		CT GT TTATG ATAGGCAT		

		GA CG AATAC TATCCGTA	
		C T CATAA	
GAM201	KIAA1462	3' ATGCCTATAATTAGGAAGGAGT 3521	G A CACC
		ACTC TTT TGA ATAGGCAT	
		TGAG AAG ATT TATCCGTA	
		G G AA__	
GAM201	MESDC2	3' CCCTGGTGGCATAAACGAGT 2950	A TA
		ACTCGTTTATG CACCA GG	
		TGAGCAAATAC GTGGT CC	
		G C_	
GAM201	LOC149620	5' ATGCCTACAAAGGAAATGAGT 3135	ATGACACCA
		ACTCGTTT TAGGCAT	
		TGAGTAAA ATCCGTA	
		GGAAAC__	
GAM201	LOC219988	5' ATGCCTACAGTGTCTGTATTAG 3534	GTT _ CA
	A	TC TAT GACAC TAGGCAT	
		AG ATG CTGTG ATCCGTA	
		ATT T AC	
GAM202	BHMT2	3' CTGAAATAATCGAACAGGAAA 1730	A TA
		TTTCT GTTC ATTATTT CAG	
		AAAGG CAAG TAATAAAGTC	
		A C_	
GAM202	COL15A1	3' AAATAATCTGAAACTAGAAA 862	_ TA
		TTTCTAGTT C ATTATTT	
		AAAGATCAA G TAATAAA	
		A TC	
GAM202	PDGFRA	3' TCTGAAATAATGGGATTAGAAA 1280	A
		TTTCTAGTTCTA TTATTT CAGA	
		AAAGATTAGGGT AATAAAGTCT	
		-	
GAM202	DORFIN	5' TTCTGGCCTCCAGAACTAGA 1631	AATTATT
		TCTAGTTCT TCAGAA	
		AGATCAAGA GGTCTT	
		CCTCC__	
GAM202	FLJ20034	5' TCTGTGATAAGCAGAACTAGAA 1732	AA T
	A	TTTCTAGTTCT TTATT CAGA	
		AAAGATCAAGA AATAG GTCT	
		CG T	
GAM202	KIAA0831	5' TCTGCATTGAAGTAGAAA 1589	T TATTT
		TTTCTAGTTC AAT CAGA	

			AAAGATCAAG TTA	GTCT	
			— C—		
GAM202	MBLL39	3'	TTCTGAAATAATCAGCAGAAA	1243	A CTA
			TTTCT GTT ATTATTT CAGAA		
			AAAGA CGA TAATAAAGTCTT		
			— C—		
GAM202	TSP-NY	3'	CTGGGAGCAGAACTAGAAA	2261	AATTA TT
			TTTCTAGTTCT T CAG		
			AAAGATCAAGA A GTC		
			CG— GG		
GAM202	LOC112840	3'	CTGAAAGTAGAACTGAAA	2384	T ATTA
			TTTC AGTTCTA TTTCAG		
			AAAG TCAAGAT AAAGTC		
			— G—		
GAM202	LOC136895	3'	AAATATTAGAACTAGAAA	2458	T
			TTTCTAGTTCTAAT ATTT		
			AAAGATCAAGATTA TAAA		
			—		
GAM202	LOC145790	5'	TTCTGAAATAATCTCTGGAGG	3083	TTCTA
			TTTCTAG ATTATTT CAGAA		
			GGAGGTC TAATAAAGTCTT		
			TC—		
GAM202	LOC151040	3'	TCAGGGATCTAGAACTAGAAA	3153	ATT TT A
			TTTCTAGTTCTA AT C GA		
			AAAGATCAAGAT TA G CT		
			C— GG A		
GAM202	LOC157869	3'	TTCTGAAATAATTTCAAGC	3207	CT_
			GTT AATTATTT CAGAA		
			CGA TTAATAAAGTCTT		
			ACT		
GAM202	LOC222028	3'	TTCTAAGTAGTTAAAATTAGAA	3631	C C
	A		TTTCTAGTT TAATTATTT AGAA		
			AAAGATTAA ATTGATGAA TCTT		
			A —		
GAM202	LOC222252	3'	TCAGGGATCTAGAACTAGAAA	3652	ATT TT A
			TTTCTAGTTCTA AT C GA		
			AAAGATCAAGAT TA G CT		
			C— GG A		
GAM203	FLJ20485	3'	TGTGATGGAGTATAC	1875	CGA T
			GTATACT CCATC ACG		

CATATGA GGTAG TGT

GAM203 LOC132617 3' CGTAGATGATGTGAATGA 3040 A TCGAC
TCGT TAC CATCTACG
||||| ||| |||||
AGTA GTG GTAGATGC
A TA__

GAM204 PER2 3' AGATATGTAAATAAGCTCTCA 2013 A T AC
A AG GC GTTTACATATCT
| || || |||||
A TC CG TAAATGTATAGA
C T AA

GAM204 SLC14A2 3' AGATATGTTTAGTTTAGACTTT 1360 GC__ GTTT
ATA TATAAAGT AC ACATATCT
||||| || |||||
ATATTTCA TG TGTATAGA
GATT ATT_

GAM204 C20orf82 3' ATGTAAACGCCACCTTA 3316 A CA
TAA GTG CGTTTACAT
||| ||| |||||
ATT CAC GCAAATGTA
C CC

GAM204 DKFZp566D234 3' ATATGTAAATTATGCTTTA 2610 CAC
TAAAGTG GTTTACATAT
||||| |||||
ATTTCTG TAAATGTATA
AT_

GAM204 EFS2 3' AGACATGGGTGTGCACCTTA 1257 A TTTA A
TAA GTGCACG CAT TCT
||| ||||| ||| |||
ATT CACGTGT GTA AGA
C GG__ C

GAM204 FLJ13194 3' ATGTTTATGCACACTTTATA 2140 CA TT
TATAAAGTG CGT ACAT
||||||| ||| |||
ATATTTTAC GTA TGTA
AC TT

GAM204 ZNF291 3' AGATATGGCATGTACTTTA 1930 C TTA
TAAAGTGCA GT CATATCT
||||||| || |||||
ATTTTCATGT CG GTATAGA
A __

GAM204 LOC157503 3' ATGAAACCATGCACTTTGTA 3380 C_ A
TATAAAGTGCA GTTT CAT
||||||| ||| |||
ATGTTTCACGT CAAA GTA
AC _

GAM204 LOC254431 3' AGATATGTAAACACTGGTAC 3716 AC__
GTGC GTTTACATATCT
||| |||||

			CATG CAAATGTATAGA		
			GTCA		
GAM205	BRCA1	3'	CTAATGAAGTGGGCTCCA 1390	A A T	
			TG GA GTCT TTTCATTAG		
			AC CT CGGG GAAGTAATC		
			_ _ T		
GAM205	C18orf1	3'	AGTGAAGGACCTCTCA 2562	A TT	
			TGAGA GTCT TTCATT		
			ACTCT CAGG AAGTGA		
			C _		
GAM205	CENTD1	3'	GCTAATGATGACATCTCA 1614	A TTTT	
			TGAGA GTC TCATTAGC		
			ACTCT CAG AGTAATCG		
			A T _		
GAM205	CENTD1	3'	GCTAATGATGACATCTCA 2473	A TTTT	
			TGAGA GTC TCATTAGC		
			ACTCT CAG AGTAATCG		
			A T _		
GAM205	CPNE3	3'	CTAATGAAAACTGCTTA 1068	A CT	
			TGAG AGT TTTCATTAG		
			ATTC TCA AAAAGTAATC		
			G _		
GAM205	EPB72	3'	CTAATGAAAAACATTACTC 1086	A C	
			GAG AGT TTTTTCATTAG		
			CTC TTA AAAAAGTAATC		
			A C		
GAM205	GBP1	3'	GCTAATGAAGAAAACTTCTC 894	C	
			GAGAAGT TTTTTCATTAGC		
			CTCTTCA AAGAAGTAATCG		
			A		
GAM205	MMP2	3'	GCCAATGGAGACTGTCTCA 1124	_ TTT A	
			TGAGA AGTCTT CATT GC		
			ACTCT TCAGAG GTAA CG		
			G _ C		
GAM205	PSCD4	3'	CTAACAGGAAACACTTCTCA 1447	C CA	
			TGAGAAGT TTTT TTAG		
			ACTCTTCA AAAGG AATC		
			C AC		
GAM205	SLC7A6	3'	GCTAATGAAATGGGAACCTC 1077	AAG T	
			GAG TCT TTTCATTAGC		

			CTC GGG AAAGTAATCG		
			CAA T		
GAM205	XKRY	5'	CTAATGAAAATTATTCTC 1142	GTCT	
			GAGAA TTTTCATTAG		
			CTCTT AAAAGTAATC		
			ATT_		
GAM205	XKRY	5'	CTAATGAAAATTATTCTC 2551	GTCT	
			GAGAA TTTTCATTAG		
			CTCTT AAAAGTAATC		
			ATT_		
GAM205	C1orf16	3'	GCCAATGGGAACCTTCTCA 1568	CTT TT A	
			TGAGAAGT T CATT GC		
			ACTCTTCA A GTAA CG		
			___ GG C		
GAM205	C3orf4	3'	GCTAATGTCTGTTAGACTTTTC 1890	TTTT__	
	A		TGAGAAGTCT CATTAGC		
			ACTTTTCAGA GTAATCG		
			TTGTCT		
GAM205	FLJ10483	3'	GCCAATGAAAATGTGCTTC 1781	CT_ A	
			GAAGT TTTTCATT GC		
			CTTCG AAAAGTAA CG		
			TGT C		
GAM205	FLJ12568	3'	GCTAATGAAAATGTTTTCT 2122	TCT	
			AGAAG TTTTCATTAGC		
			TCTTT AAAAGTAATCG		
			TGT		
GAM205	FLJ20340	3'	GCTTTGAAAAACTTTTCA 1750	CT TT	
			TGAGAAGT TTTTCA AGC		
			ACTTTTCA AAAAGT TCG		
			___ T_		
GAM205	FLJ20727	5'	GCTAATGGACTTGACTCTCA 1769	A TTT	
			TGAGA GTC TTCATTAGC		
			ACTCT CAG AGGTAATCG		
			_ TTC		
GAM205	FLJ20736	3'	CTAATGGACATCTTCTCA 1770	TCTTT	
			TGAGAAG TTCATTAG		
			ACTCTTC AGGTAATC		
			TAC__		
GAM205	PDE1C	3'	GCTAATGACCTGGCTTTCA 1172	A TTTT	
			TGAGA GTC TCATTAGC		

			ACTTT CGG AGTAATCG		
			_ TCC_		
GAM205	TOB2	5'	GCTAAGGGTGAAACTTTTCA 3680	C T A	
			TGAGAAGT TT TTC TTAGC		
			ACTTTTCA AG GGG AATCG		
			A T _		
GAM205	TSC22	3'	CTAATGAAATGGATTTCCTCA 1264	A T	
			TG GAAGTCT TTTTCATTAG		
			AC CTTTAGG AAAGTAATC		
			C T		
GAM205	TSP-NY	3'	GCTAAGAATGAAAAAGACTTCT 2262		___
	C		GAGAAGTCTTTTTCAT TAGC		
			CTCTTCAGAAAAAGTA ATCG		
			AGA		
GAM205	TUCAN	3'	GCTAACAAAAGCTTCTCA 1598	T TCA	
			TGAGAAG CTTTT TTAGC		
			ACTCTTC GAAAA AATCG		
			_ C_		
GAM205	LOC138241	5'	GCCAATGGGGGAATTCTCA 3019	GTC TT A	
			TGAGAA TTT CATT GC		
			ACTCTT AGG GTAA CG		
			A_ GG C		
GAM205	LOC152345	3'	AATGGAGAGACTTCCG 3170	A T	
			TG GAAGTCTTTT CATT		
			GC CTTCAGAGAG GTAA		
			_ _		
GAM205	LOC154214	5'	CTAATGAAAAGGACCTTA 3189	AA	
			TGAG GTCTTTTTCATTAG		
			ATTC CAGGAAAAGTAATC		
			_		
GAM205	LOC154790	5'	AATGAAAAGAACTTCCCA 3192	A CT	
			TG GAAGT TTTTCATT		
			AC CTTCA AAAAGTAA		
			C AG		
GAM205	LOC158427	3'	CTAATGAAAATAACTCCCA 2478	A A CT	
			TG GA GT TTTTCATTAG		
			AC CT CA AAAAGTAATC		
			C _ AT		
GAM205	LOC161003	5'	AGTATAAAAGCTTCTCA 2520	T TC	
			TGAGAAG CTTTT ATT		

		ACTCTTC GAAAA TGA		
		— TA		
GAM205	LOC200830 3'	GCTAATGGGCTGACTACTCA 3480	A	TTT
		— TGAG AGTC TTCATTAGC		
		ACTC TCAG GGGTAATCG		
		A TC_		
GAM205	LOC221421 3'	GCTAATGAAAGAGATTCT 3558	G	
		AGAA TCTTTTTCATTAGC		
		TCTT AGAGAAAGTAATCG		
		—		
GAM205	LOC257017 5'	CTAAGTTAAGACTTTTCA 3736		TTTCA
		TGAGAAGTCTT TTAG		
		ACTTTTCAGAA AATC		
		TTG_		
GAM205	LOC257353 5'	GCTAATAATGATGGCCTCTCA 3738	A	T TTC
		TGAGA GTC TT ATTAGC		
		ACTCT CGG AG TAATCG		
		C T TAA		
GAM205	LOC90459 3'	GCCAATGAATTTCTGCTTTTCA 2642	CTTT_	A
		TGAGAAGT TTCATT GC		
		ACTTTTCG AAGTAA CG		
		TCTTT C		
GAM206	CXADR 3'	TATTGAGATGACACTAGGTGC 820	_	CA CCC
		GCAC TAG TC TTTCAATA		
		CGTG ATC AG AGAGTTAT		
		G AC T_		
GAM206	EPB72 3'	TATTGAGGATTGAGCCAGTGC 1087	A	A CCC
		GCACT GC TC TTTCAATA		
		CGTGA CG AG GGAGTTAT		
		C _ TTA		
GAM206	FCAR 5'	ATTGAAAGGAGAGCAACGG 880	CACTA	A C
		CCG GC TC CCTTTCAAT		
		GGC CG AG GGAAAGTTA		
		AA_ _ A		
GAM206	FCAR 5'	ATTGAAAGGAGAGCAACGG 2400	CACTA	A C
		CCG GC TC CCTTTCAAT		
		GGC CG AG GGAAAGTTA		
		AA_ _ A		
GAM206	FCAR 5'	ATTGAAAGGAGAGCAACGG 2401	CACTA	A C
		CCG GC TC CCTTTCAAT		

			GGC CG AG GGAAAGTTA		
			AA__ _ A		
GAM206	FCAR	5'	ATTGAAAGGAGAGCAACGG 2402	CACTA A C	
			CCG GC TC CCTTTCAAT		
			GGC CG AG GGAAAGTTA		
			AA__ _ A		
GAM206	FCAR	5'	ATTGAAAGGAGAGCAACGG 2403	CACTA A C	
			CCG GC TC CCTTTCAAT		
			GGC CG AG GGAAAGTTA		
			AA__ _ A		
GAM206	FCAR	5'	ATTGAAAGGAGAGCAACGG 2404	CACTA A C	
			CCG GC TC CCTTTCAAT		
			GGC CG AG GGAAAGTTA		
			AA__ _ A		
GAM206	FCAR	5'	ATTGAAAGGAGAGCAACGG 2406	CACTA A C	
			CCG GC TC CCTTTCAAT		
			GGC CG AG GGAAAGTTA		
			AA__ _ A		
GAM206	KCNAB1	3'	TGAAAATGCTAGTGGG 2585	G CCCC	
			CC CACTAGCAT TTTCA		
			GG GTGATCGTA AAAGT		
			— —		
GAM206	NCOA6	3'	TATTGAAAGGAGCTAATGC 1468	C ATCC	
			GCA TAGC CCTTTCAATA		
			CGT ATCG GGAAAGTTAT		
			A A__		
GAM206	SDHC	3'	TATTGAAAGAAGAGAGGTGGGG 2856	G AGCA CC	
			CC CACT TC CTTTCAATA		
			GG GTGG AG GAAAGTTAT		
			G AG__ AA		
GAM206	CBLN1	5'	GGAGGGGACGCTAGTCGCGG 1101	_ A	
			CCGC ACTAGC TCCCCTTT		
			GGCG TGATCG AGGGGAGG		
			C C		
GAM206	CSTF2	3'	TATTGAAAAAAGATGACCTGC 819	CTAG CCC	
			GCA CATC TTTCAATA		
			CGT GTAG AAAGTTAT		
			CCA_ AAA		
GAM206	GS3955	5'	AAAGGGGGTGCAGCGCGG 1953	A A	
			CCGC CT GCATCCCCTTT		

GGCG GA CGTGGGGGAAA
C _
GAM206 KIAA0184 3' ATTGAAAGAGGTGTGCTGG 2715 TC _
CTAGCA CC CTTTCAAT
||||| || |||||
GGTCGT GG GAAAGTTA
GT A
GAM206 MGC14697 5' GTTGAAGGACACCAGCTGCGG 2276 CTA ATCCC_
CCGCA GC CTTTCAAT
||||| || |||||
GGCGT CG GGAAGTTG
___ ACCACA
GAM206 RRN3 3' AGGTGGAAGTTGCTAGTGC 1827 ___ _
GCACTAGCA TCC CCT
||||||| ||| |||
CGTGATCGT AGG GGA
TGA T
GAM206 WDR13 5' AAGGAATGCTAGGCGG 1759 A CC
CCGC CTAGCAT CCTT
||| ||||| |||
GGCG GATCGTA GGAA
_ A_
GAM206 LOC219287 3' GAAAGAGGGATGCTACACGG 3609 CAC _
CCG TAGCATCCC CTTTC
||| ||||| |||||
GGC ATCGTAGGG GAAAG
AC_ A
GAM206 LOC221979 5' ATTGAAACTGCTAGTG 3571 TCCCC
CACTAGCA TTTCAAT
||||||| |||||
GTGATCGT AAAGTTA
C___
GAM206 LOC255328 3' TATTGAAAGGGCTGCACCATGC 3710 CTA_ TC
GCA GCA CCCTTTCAATA
||| ||| |||||
CGT CGT GGGAAAGTTAT
ACCA C_
GAM206 LOC257115 3' TATTGAAAGGAAAGTGCTATCG 3709 CAC CC_
CG TAGCAT CCTTTCAATA
|| ||||| |||||
GC ATCGTG GGAAAGTTAT
T_ AAA
GAM206 LOC51145 3' ATTGAAAGGGGAAATGTGTCA 1666 C TAGCA
C GCAC TCCCCTTTCAAT
||| |||||
A TGTG AGGGGAAAGTTA
C TAA_
GAM207 BCL11A 3' AAAC TAGAACAGGTATAT 2018 TA
ATATACCTGTTTT TTT
||||||| |||

			TATATGGACAAGA AAA		
			TC		
GAM207	C8orf1	3'	GAAACCTTGACAGGTA	1099	TA TTTA
			TGA TACCTGTT TTTC		
			ACT ATGGACAG AAAG		
			TC TTCC		
GAM207	KPNA1	3'	AAATAAAAACAGTATC	3159	TAC
			GATA CTGTTTTTATTT		
			CTAT GACAAAATAAA		
			—		
GAM207	NRXN1	3'	AAATAAAAACAAGTATCTCA	2457	T C
			TGA ATAC TGTTTTTATTT		
			ACT TATG ACAAAAATAAA		
			C A		
GAM207	NRXN1	3'	AAATAAAAACAAGTATCTCA	1158	T C
			TGA ATAC TGTTTTTATTT		
			ACT TATG ACAAAAATAAA		
			C A		
GAM207	PCDHGA8	3'	AAATAATTTTAAAGGTGTATCA	1459	GTTT__
			TGATATACCT TTATTT		
			ACTATGTGGA AATAAA		
			ATTTTT		
GAM207	SNX5	3'	GAAATATCTACAGGTATAT	1500	TTT
			ATATACCTGT TATTC		
			TATATGGACA ATAAAG		
			TCT		
GAM207	BNIP2	3'	GAAATATGCAGGTATAT	2762	TTT
			ATATACCTGT TATTC		
			TATATGGACG ATAAAG		
			T__		
GAM207	DRIL2	3'	AAATGAAAACAGATCA	1305	ATAC
			TGAT CTGTTTTTATTT		
			ACTA GACAAAAGTAAA		
			—		
GAM207	DVS27	3'	AAATAAAAGCAGAATGTATATC	2335	—
	A		TGATATAC CTGTTTTTATTT		
			ACTATATG GACGAAAATAAA		
			TAA		
GAM207	FLJ12960	3'	GAAGGGGGAGCAGGCACATCA	2074	ATA TA
			TGAT CCTGTTTT TTTC		

			ACTA GGACGAGG GAAG		
			CAC GG		
GAM207	FLJ20793	3'	GAATACTAACAGGTATTTCA 3542	T	TT
			TGA ATACCTGTT TATTT		
			ACT TATGGACAA ATAAG		
			T TC		
GAM207	KIAA0040	3'	GAAATAAAATTAAAGGTATA 1515	GT__	
			TATACCT TTTTATTT		
			ATATGGA AAAATAAAG		
			AATT		
GAM207	KIAA1349	3'	GAAATAAAAGCAGCATCA 2893	ATAC	
			TGAT CTGTTTTTATTT		
			ACTA GACGAAAATAAAG		
			C__		
GAM207	KIAA1373	3'	AAATATTAACAGGTATAT 2903	TT	
			ATATACCTGTT TATTT		
			TATATGGACAA ATAAA		
			TT		
GAM207	SCDGF-B	3'	AAGTAGAAAGGTATATCA 2147	GT	
			TGATATACCT TTTTATTT		
			ACTATATGGA AAGATGAA		
			—		
GAM207	SCDGF-B	3'	AAGTAGAAAGGTATATCA 2314	GT	
			TGATATACCT TTTTATTT		
			ACTATATGGA AAGATGAA		
			—		
GAM207	LOC121441	3'	AAATAAAACAGGAATATTA 2991	A	
			TGATAT CCTGTTTTATTT		
			ATTATA GGACAAAATAAA		
			A		
GAM207	LOC157729	3'	AAATAAAGATAGCATGTCA 3205	AC	
			TGATAT CTGTTTTTATTT		
			ACTGTA GATAGAAATAAA		
			C_		
GAM207	LOC200339	3'	GAAGTTCACAGGTATATC 3475	TTTT	
			GATATACCTGT ATTT		
			CTATATGGACA TGAAG		
			CT__		
GAM207	LOC221300	3'	AAATGGCAAACAGGTATAT 3545	_	
			ATATACCTGTTT TTATTT		

			TATATGGACAAA GGTAAG		
			C		
GAM207	LOC257235	5'	GAAACCATTCAGGTATTTCA 3728	T	TTTTA
			TGA ATACCTGT TTTC		
			ACT TATGGACG AAAG		
			T TTACC		
GAM207	LOC93333	5'	AAATGGTTAAGGGTATATCA 2932		GTTT
			TGATATACCT TTATTT		
			ACTATATGGG GGTAAG		
			AATT		
GAM208	PCDH7	3'	AAACAGTATTAATGCAGAAATG 938	A	_
			CGT TC GCATTAATACTGTTT		
			GTA AG CGTAATTATGACAAA		
			A A		
GAM208	TRC8	3'	AAACAGTATCAATGTTGA 1365	_	A
			TCG CATT ATACTGTTT		
			AGT GTAA TATGACAAA		
			T C		
GAM208	LOC145225	3'	AAACAGTATTAACCCTGC 3275	___	
			GCA TTAATACTGTTT		
			CGT AATTATGACAAA		
			CCC		
GAM209	BHMT2	3'	AGCATTATTGAAATAAATGTTT 1729	C__	TGG
	A		TAGACATTTA CA GATGCT		
			ATTTGTAAAT GT TTACGA		
			AAA TA_		
GAM209	CANX	3'	AGCATCCTGATTAAATGTCTG 3409		CCA
			TAGACATTTA TGGGATGCT		
			GTCTGTAAAT GTCCTACGA		
			TA_		
GAM209	COPG2	3'	AGCAGATCAAGCAAATGTCTA 3194		ACCA GA
			TAGACATTT TGG TGCT		
			ATCTGTAAA ACT ACGA		
			CGA_ AG		
GAM209	MS4A1	3'	CATTTACAAATGTTTAGT 711		ACCA GG
			ACTAGACATTT TG ATG		
			TGATTTGTAAA AC TAC		
			C__ TT		
GAM209	SEL1L	3'	CATGTGTATTAATGTCTA 1180	__	_
			TAGACATT TAC CATG		

			ATCTGTAA ATG GTAC	
			TT T	
GAM209	TPK1	3'	CATCCTTAAATGTCTA 1988	CCAT
			TAGACATTTA GGGATG	
			ATCTGTAAAT TCCTAC	

GAM209	CYorf14	3'	CTGTGGGCAATAAATGTCTG 1839	_____
			TAGACATTTA CCATGG	
			GTCTGTAAAT GGTGTC	
			AACG	
GAM209	HSPC228	3'	AGCATTTCATAAATGTTTAGT 1688	CCA GG
			ACTAGACATTTA TG ATGCT	
			TGATTTGTAAAT AC TACGA	
			____ TT	
GAM209	MGC1127	3'	AGCTGGGTAATAAATGTCTA 2336	____ ATGGGAT
			TAGACATT TACC GCT	
			ATCTGTAA ATGG CGA	
			ATA GT_____	
GAM209	SLC16A4	3'	AGCATTCTGAGAAATGTCTA 1144	ACCA
			TAGACATTT TGGGATGCT	
			ATCTGTAAA GTCTTACGA	
			GA__	
GAM209	LOC147180	5'	CACCTGTTTAAATGTCTG 3292	CC A
			TAGACATTTA ATGGG TG	
			GTCTGTAAAT TGTCC AC	
			T_ _	
GAM209	LOC148195	5'	GCATCCCATTTGGTGTCTAGT 3297	A ATTT _
			ACT GAC ACCA TGGGATGC	
			TGA CTG TGGT ACCCTACG	
			_ ____ T	
GAM209	LOC158572	3'	AGCATCCTTTCAATAAATGCCT 3221	A CCAT_
	G		TAG CATTTA GGGATGCT	
			GTC GTAAAT TCCTACGA	
			C AACTT	
GAM209	LOC201595	3'	AGCACTGCTGTAAATGTCTAG 3453	CATG A
			CTAGACATTTAC GG TGCT	
			GATCTGTAAATG TC ACGA	
			TCG_ _	
GAM209	LOC203427	5'	CATTTAGGAAGCAAGATGTCTA 3464	ACCATG_
	G		CTAGACATTT GGATG	

GATCTGTAGA TTTAC
 ACGAAGGA
 GAM210 PDE1A 3' ATCAGCATGAAAACATCCTA 1171 AT _ GA
 TAG TGTTTTCA GT GAT
 ||| ||||| || |||
 ATC ACAAAGT CG CTA
 CT A A_
 GAM210 ELAC1 3' AATCATCTCACCCCGAAATGCA 3506 _ A_
 TGT TTTC GTGAGATGATT
 ||| ||| |||||
 ACG AAAG CACTCTACTAA
 T CCC
 GAM210 LOC154790 5' AATCAGATCATATGAAAACAAT 3191 _ GA
 CTA TAGATTGTTTTCA GTGA TGATT
 ||||| ||| |||
 ATCTAACAAAAGT TACT ACTAA
 A AG
 GAM210 LOC158434 3' CAGTCACTAAAAACAATC 3389 C GA
 GATTGTTTT AGTGA TG
 ||||| ||| ||
 CTAACAAAA TCACT AC
 A G_
 GAM211 MAP3K5 3' TCTGAGTAGAAATGCGT 1261 A TT
 ACGCAT TTCTACTC GGA
 ||||| ||||| ||
 TGC GTA AAGATGAG TCT
 _ _
 GAM211 DKFZP564F0522 3' TAATTCCACAGTCAGAACATGC 2825 A _ CT
 GCAT TTCT ACT TGGAATTA
 ||| ||| ||| |||||
 CGTA AAGA TGA ACCTTAAT
 C C C_
 GAM211 GPCR150 3' TAATTCCAAGAAGTTTTTATAG 1496 GC TTCT _
 T AC ATA ACT CTTGGAATTA
 || ||| ||| |||||
 TG TAT TGA GAACCTTAAT
 A_ TTT_ A
 GAM211 SLC26A7 3' TAATTCAGTATAGAATATGC 2340 CT TG
 GCATATTCTA CT GAATTA
 ||||| || |||||
 CGTATAAGAT GA CTTAAT
 AT _
 GAM211 SLC6A14 3' TAATTTCAAATAGAATATG 1369 CTC
 CATATTCTA TTGGAATTA
 ||||| |||||
 GTATAAGAT AACTTTAAT
 A_
 GAM211 LOC116228 3' TAGTTCTGAATTAATAATATGC 2980 C CTC TG
 GCATATT TA T GAATTA
 ||||| || | |||||

			CGTATAA AT A CTTGAT		
			A TA_ GT		
GAM212	CCNC	3'	ATAATGTCTTCAGTGGAACAC 1192	A_____	III
			GTGTTCCA ACATTA T		
			CACAAGGT TGTAAT A		
			GACTTC III		
GAM212	MSL3L1	5'	TAATGGTTGGAACAGAA 1331	G A	
			TTC TGTTCCAA CATTA		
			III		
			AAG ACAAGGTT GTAAT		
			_ G		
GAM212	THBS1	3'	TAATGTTTGCACACTGAA 1004	_ TC	
			TTC GTGT CAAACATTA		
			III		
			AAG CACA GTTTGTAAT		
			T C_		
GAM212	CSRP3	3'	TAATGCTTGGAATGGGAG 1031	G A	
			TTC TGTTCCAA CATTA		
			III		
			GAG GTAAGGTT GTAAT		
			G C		
GAM212	FLJ11181	5'	TAATGTTCGGCAAACATGAA 1817	_ A	
			TTCGTGTT CC AACATTA		
			AAGTACAA GG TTGTAAT		
			AC C		
GAM212	FLJ23132	3'	TAATGTTTCCAACATGAA 3692	CC	
			TTCGTGTT AAACATTA		
			AAGTACAA TTTGTAAT		
			CC		
GAM212	GAB3	3'	TAATGTTTGTTACAGAA 2378	G TC	
			TTC TGT CAAACATTA		
			III		
			AAG ACA GTTTGTAAT		
			_ TT		
GAM212	MGC13033	3'	TAATGTTTGGAATGGAG 2198	G	
			TTC TGTTCCAAACATTA		
			III		
			GAG GTAAGGTTTGTAAT		
			_		
GAM212	PRO0386	5'	TAATGTTCTGTGGAACAT 1844	_	
			GTGTTCCA AACATTA		
			TACAAGGT TTGTAAT		
			GTC		
GAM212	LOC149351	5'	TAATGTGAGGAAAAACACGGA 3132	_ AA	
			TTCGTGT TCC ACATTA		

			AGGCACA AGG TGTAAT		
			AAA AG		
GAM212	LOC163590	3'	TAATGTTTGGA	2512	T T
			TTCG GT CCAAACATTA		
			AGGT CA GGTTTGTAAT		
			T _		
GAM212	LOC256307	3'	TAATGCTACATGGAACATGAA	3726	AA__
			TTCGTGTTCCA CATT		
			AAGTACAAGGT GTAAT		
			ACATC		
GAM212	LOC87769	3'	TAATGTTGAGATACGAA	2912	TC A
			TTCGTGT CAA CATT		
			AAGCATA GTT GTAAT		
			GA _		
GAM212	LOC89890	3'	TAATGTTTGAAATACGAA	2574	C
			TTCGTGT CAAACATT		
			AAGCATAA GTTTGTAAT		
			A		
GAM213	GDF8	5'	ACAAGAAAAAGATTATA	1196	CA
			TATAATCTTTT TCTTGT		
			ATATTAGAAAA AGAACA		
			—		
GAM213	REGL	3'	ACCATATAGAAAAAGATTATA	1306	ATCT A
			TATAATCTTTTTC TGTG GT		
			ATATTAGAAAAAG ATAC CA		
			AT__ _		
GAM213	DKFZP434J214	3'	ACTCAGTGTGGAAAAGA	2586	CTTG
			TCTTTTTCAT TGAGT		
			AGAAAAGGTG ACTCA		
			TG__		
GAM213	KIAA0440	5'	CTTTTAAATGAAAAAGATTA	1636	C T
			TAATCTTTTTCAT TTG GAG		
			ATTAGAAAAAGTA AAT TTC		
			_ T		
GAM213	LOC152756	3'	ACTCATGATCCAAAAAGATTA	3363	CATC TG
			TAATCTTTT T TGAGT		
			ATTAGAAAA A ACTCA		
			ACCT GT		
GAM213	LOC158428	3'	ACTCACATAGGTGAAAAA	2889	_
			TTTTTCATCT TGTGAGT		

			AAAAAGTGGA ACACTCA		
			T		
GAM214	BHLHB3	3'	TATGTAAGGGGTGAGACACAAC 2162		A A G _
			GTTGTGTCT CA CC CT ACATA		
			CAACACAGA GT GG GA TGTAT		
			_ _ G A		
GAM214	F9	3'	GCGTGTGTGTAGACACAC 709 T		_ _
			GT GTGTCTACA AC CGC		
			CA CACAGATGT TG GCG		
			_ G T		
GAM214	FLJ31737	3'	TAGCACTGTAGACACAAC 2504		ACC
			GTTGTGTCTACA GCTA		
			CAACACAGATGT CGAT		
			CA_		
GAM214	KIAA1505	5'	GCATTTAGTAGACACCACG 3638	T	_ CC
			CGT GTGTCTAC AA GC		
			GCA CACAGATG TT CG		
			C A TA		
GAM214	PHRET1	3'	GGCGCTGTAGACACAAC 1947		AC
			GTTGTGTCTACA CGCT		
			CAACACAGATGT GCGG		
			C_		
GAM214	RYD5	3'	AGCAGCCGTGGACACAACG 3103		AACC
			CGTTGTGTCTAC GCT		
			GCAACACAGGTG CGA		
			CCGA		
GAM214	LOC221337	5'	TAGTTCAAGTAAACACAATG 3556		C AACC
			CGTTGTGT TAC GCTA		
			GTAACACA ATG TGAT		
			A AACT		
GAM215	ADCY9	3'	GTGGTCATTTTCAGCCCTA 801	T	A
			TAGG GCTGAAAT ACCAC		
			ATCC CGACTTTA TGGTG		
			_ C		
GAM215	CRAT	3'	GTGGGTCATCCCAGCACCTG 1079		AA A A
			TAGGTGCTG AT ACC CAT		
			GTCCACGAC TA TGG GTG		
			CC C _		
GAM215	CRAT	3'	GTGGGTCATCCCAGCACCTG 771		AA A A
			TAGGTGCTG AT ACC CAT		

GTCCACGAC TA TGG GTG
 CC C _
 GAM215 CXCR4 3' CAGGAGTGGGTTGATTTTCAGCA 1028 AA__ AT
 CCTA TAGGTGCTGAAAT CCAC CTG
 ||||| ||| |||
 ATCCACGACTTTA GGTG GAC
 GTTG AG
 GAM215 AGMAT 3' CAGACGTGGTGTGGTGCACACC 2087 C AAATA_ A
 GGTG TG ACCAC TCTG
 ||| || |||| ||||
 CCAC AC TGGTG AGAC
 _ GTGGTG C
 GAM215 DKFZp434E0519 3' CAGATGCGGTGGCTCACACCTA 2240 C AATA A
 TAGGTG TGA ACC CATCTG
 |||| || || ||||
 ATCCAC ACT TGG GTAGAC
 _ CGG_ C
 GAM215 DKFZp762E1312 5' CAGACATGGCCTTAGTACCTA 1823 AATAA CA
 TAGGTGCTGA CCA TCTG
 ||||| || |||
 ATCCATGATT GGT AGAC
 CC__ AC
 GAM215 FLJ20619 3' CAGTGAGGTAGCATCTA 1760 GAAATA A T
 TAGGTGCT ACC CA CTG
 ||||| || |||
 ATCTACGA TGG GT GAC
 _____ A _
 GAM215 FLJ20716 3' CAGATTGCCACCCCAGCACCTA 1768 AAATAAC C
 TAGGTGCTG CA ATCTG
 ||||| || ||||
 ATCCACGAC GT TAGAC
 CCCACC_ _
 GAM215 FRAT1 3' CAGATGTGGCTACTGACATATC 1217 C AAA_ A
 TA TAGGTG TG TA CCACATCTG
 |||| || || |||||
 ATCTAT AC AT GGTGTAGAC
 _ AGTC C
 GAM215 KIAA1656 3' CAGATGTGGCCATCCCTCCCTG 2729 TGCT AATAA
 TAGG GA CCACATCTG
 ||| || |||||
 GTCC CT GGTGTAGAC
 CTCC ACC__
 GAM215 Rab11-FIP3 3' CAGATGTGGTCACCTCAGTCC 1524 T AATA
 GG GCTGA ACCACATCTG
 || ||| |||||
 CC TGA CT TGGTGTAGAC
 _ CCAC
 GAM215 TOMM34 3' AGACATGGTTGTTGCACC 1332 TGA CA
 GGTGC AATAACCA TCT
 |||| ||||| |||

		CCACG TTGTTGGT AGA		
		____ AC		
GAM215	LOC146337 3'	CAGATGCATCTGTTTCAGCCCT 3285	T	ACCA
	A	TAGG GCTGAAATA CATCTG		
		ATCC CGACTTTGT GTAGAC		
		____ CTAC		
GAM215	LOC147229 3'	AGATGCAGGCTCAGCACT 3105	AATAA A_	
		GGTGCTGA CC CATCT		
		TCACGACT GG GTAGA		
		C____ AC		
GAM215	LOC158332 3'	GGTACTAATTCAGCACCTA 3217	A ____	
		TAGGTGCTGAA TA ACC		
		ATCCACGACTT AT TGG		
		A CA		
GAM215	LOC163131 5'	AGATGTGATTACATTACT 3245	C AAA C	
		GGTG TG TAA CACATCT		
		TCAT AC ATT GTGTAGA		
		T ____ A		
GAM215	LOC221423 3'	AGATGTGGCTACAACAT 3551	C AAA A	
		GTG TG TA CCACATCT		
		TAC AC AT GGTGTAGA		
		A ____ C		
GAM215	LOC222182 5'	CAGACATGTGCCCAGCACCT 3639	AAATAAC ____	
		AGGTGCTG CACA TCTG		
		TCCACGAC GTGT AGAC		
		CC____ AC		
GAM216	B3GALT3 3'	GAAGATTACAGTTATGTA 1056	CG_	
		TACGTAAC AATCTTC		
		ATGTATTG TTAGAAG		
		ACA		
GAM216	LOC159199 5'	GAAGATCAAGAGGTTACGTG 3237	GA____	
		TACGTAACC ATCTTC		
		GTGCATTGG TAGAAG		
		AGAAC		
GAM217	ACCN2 3'	CCACCAGACACTCCTTC 1891	TCT	
		GAAGGAGTGTTT TGG		
		CTTCCTCACAGA ACC		
		CC_		
GAM217	BLAME 3'	CCAAAAAACACAAAGTGCTTC 1892	GA____ C	
	TG	TAGAAG GTGTTTT TTGG		

			GTCTTC	CACAAAA	AACC		
			GTGAAA	A			
GAM217	DLX4	3'	TTGCCACTCCCCACTCCTTCT	2432		TTTTCT	
			AGAAGGAGTG	TGGCAA			
			TCTTCCTCAC	ACCGTT			
			CCCCTC				
GAM217	DLX4	3'	TTGCCACTCCCCACTCCTTCT	870		TTTTCT	
			AGAAGGAGTG	TGGCAA			
			TCTTCCTCAC	ACCGTT			
			CCCCTC				
GAM217	IGSF6	3'	TTTGCCAAGAAAAAAATTCTA	1256		GGAGTG	
			TAGAA	TTTTCTTGGCAA			
			ATCTT	AAAAGAACCGTTT			
			AAAA__				
GAM217	ITPR2	3'	CAGGAACAAAACACTGCCT	912	-	__	
			AGG AGTGTTT	TCTTG			
			TCC TCACAAA	AGGAC			
			G	ACA			
GAM217	IVD	5'	GCTAAAAACACTCATCCTA	913	AAG	CT	
			TAG	GAGTGTTTT	TGGC		
			ATC	CTCACAAA	ATCG		
			CTA	__			
GAM217	MAP4K2	3'	TGCCAAGAGCCTGCCCT	1127	A	TT	
			AGG	GTG TTCTTGGCA			
			TCC	CGT GAGAACCGT			
			C	CC			
GAM217	POLG	3'	TGCCAAGAAGATTCCTTCTA	948		GT	
			TAGAAGGA	GTTTTCTTGGCA			
			ATCTTCCT	TAGAAGAACCGT			
			__				
GAM217	RET	3'	TTGCCAAAACCTCCTTCT	1920		GTTTTTC	
			AGAAGGAGT	TTGGCAA			
			TCTTCCTCA	AACCGTT			
			A__				
GAM217	SALL2	3'	TTGCCAAGAGGTCTCC	2672		TGT	
			GGAG	TTTCTTGGCAA			
			CCTC	GGAGAACCGTT			
			T__				
GAM217	SLC9A1	3'	CCAAGGTCTCACACTCCTCCTG	2886	A	TT__	
			TAG	AGGAGTGT	TCTTGG		

			GTC TCCTCACA GGAACC	
			C CTCT	
GAM217	ZNF132	5'	CCAAGAAAGCTAACTCCT 1020	—
			AGGAGT GTTTTCTTGG	
			TCCTCA CGAAAGAACC	
			AT	
GAM217	AD-020	3'	TTTGCCAAGAAAATCTGGGCCT 1893	AGT—
			AGG GTTTTCTTGGCAAA	
			TCC TAAAAGAACCGTTT	
			GGGTC	
GAM217	AD-020	3'	TTTGCCAAGAAAATCTGGGCCT 2524	AGT—
			AGG GTTTTCTTGGCAAA	
			TCC TAAAAGAACCGTTT	
			GGGTC	
GAM217	APOL3	3'	CCAAGAAAAACAGTCTCA 1494	A G _
			A GGA TGTTTT CTTGG	
			A TCT ACAAAA GAACC	
			C G A	
GAM217	DJ473B4	3'	TTTGCCAAAAAAGTCCCCTA 1881	AA GTG C
			TAG GGA TTTT TTGGCAAA	
			ATC CCT GAAA AACCGTTT	
			C_ _ _ A	
GAM217	KIAA0475	3'	TTTGCCAAAAGCAGTCCTTC 1571	G CT
			GAAGGA TGTTTT TGGCAAA	
			CTTCCT ACGAAA ACCGTTT	
			G _	
GAM217	KIAA1729	3'	CCAGGAACACTCCTTC 3458	TT
			GAAGGAGTGT TCTTGG	
			CTTCCTCACA AGGACC	
			—	
GAM217	PHYHIP	3'	CCACCGGGACACTCCCCCTG 1541	AA CT
			TAG GGAGTGTTTT TGG	
			GTC CCTCACAGGG ACC	
			CC CC	
GAM217	SCAMP-4	3'	TGCCAAGAGGCACCCCCTTC 2372	A_ T
			GAAGG GTGTTT CTTGGCA	
			CTTCC CACGGA GAACCGT	
			CC _	
GAM217	ST6GalNAcI	3'	TGCTGAAAAACACTCTTC 1824	G C TG
			GAAG AGTGTTTT T GCA	

CTTC TCACAAAA A CGT
 _ _GT
 GAM217 TTTY2 5' TGCCAAAAAACAGGTACTCTT 3396 G ____ C
 CTA TAGAAG AGT GTTTT TTGGCA
 ||||| ||| ||||| |||||
 ATCTTC TCA CAAAA AACCGT
 _ TGGA A
 GAM217 LOC126917 3' TTGCCAAGAAAGACCCC 3001 A G
 GG GT TTTTCTTGGCAA
 || || ||||| |||||
 CC CA GAAAGAACCGTT
 C _
 GAM217 LOC128077 3' TTGCTTCTGAAACCCCTCCT 3007 T_ CTT
 AGGAG GTTTT GGCAA
 ||||| ||||| |||||
 TCCTC CAAAG TCGTT
 CC TCT
 GAM217 LOC152485 3' TCACCCAAACACTCCTTC 3171 TCT
 GAAGGAGTGTTT TGG
 ||||| ||||| |||||
 CTTCTCACAAA ACT
 CCC
 GAM217 LOC159148 5' TGCCAAAAAACAGGTACTCTT 3397 G ____ C
 CTA TAGAAG AGT GTTTT TTGGCA
 ||||| ||| ||||| |||||
 ATCTTC TCA CAAAA AACCGT
 _ TGGA A
 GAM217 LOC159989 3' GCCAAGAAAAAAGCTCT 3238 G_
 GGAGT TTTTCTTGGC
 ||||| ||||| |||||
 TCTCG AAAAGAACCG
 AAA
 GAM217 LOC164584 5' TTGCCAAGAAAACAATCT 3250 G
 GGA TGTTTTCTTGGCAA
 ||| ||||| ||||| |||||
 TCT ACAAAGAACCGTT
 A
 GAM218 RAG1 3' CCAGTATTAAATTATCC 745 ACTACT
 GGATAATTTA ATATTGG
 ||||| ||||| |||||
 CCTATTAAAT TATGACC

 GAM218 LOC221964 3' GCCAGTAATAGTCAAATTAACC 3628 A A CTA
 GG TAATTT ACTA TATTGGC
 || ||||| ||||| |||||
 CC ATTAAA TGAT ATGACCG
 A C A_
 GAM219 ADAM12 3' TGA CTATGGATAAACTAAA 1030 AT
 TTTAGTTTATTCATA GTTA
 ||||| ||||| ||||| |||||

AAATCAAATAGGTAT CAGT

GAM219 KIAA1789 5' TAACATTATGTGATTCTAAATG 2780 TTTATT
TATTTAG CATAATGTTA
||||| |||||||
GTAAATC GTATTACAAT
TTAGT_

GAM220 NR4A2 3' AACAAACAAAACTGTTGCTAT 1276 TC__ CTA
TTC GAAATAGC GTTT TTTGTT
||||| ||| |||||
CTTTATCG CAAA AAACAA
TTGT AAC

GAM220 LOC51145 3' GCAAAAACGAGCTCTTCA 1667 AT CTAT
TGAA AGCTCGTTT TTGT
||| ||||||| |||
ACTT TCGAGCAAA AACG
C_ _

GAM221 HFE 3' GCAGGTGCTTCAGGATA 738 AC _
TATCCTGA AGCAT TGC
||||| ||||| |||
ATAGGACT TCGTG ACG
_ G

GAM221 HFE 3' GCAGGTGCTTCAGGATA 2464 AC _
TATCCTGA AGCAT TGC
||||| ||||| |||
ATAGGACT TCGTG ACG
_ G

GAM221 PKIA 3' CAATGCTGTATGATACTATTT 1334 A CTGA
AGATA TATC ACAGCATTG
||||| ||| |||||||
TTTAT ATAG TGTCGTAAC
C TA_

GAM221 PLAG1 3' GCAATGCTATCCATTGATGT 943 C_ AAC
ATATC TG AGCATTGC
||||| || |||||||
TGTAG AC TCGTAACG
TT CTA

GAM221 FLJ20371 3' GCCTATTCAGGATATTA ACT 1752 A CA_
AG TAATATCCTGAA GC
|| ||||||||| ||
TC ATTATAGGACTT CG
A ATC

GAM221 LOC202052 3' GCATCTGTT CAGGACAACATC 3485 AATA CAT
GAT TCCTGAACAG TGC
||| ||||||||| |||
CTA AGGACTTGTC ACG
CAAC T_

GAM222 EIF2C1 3' TGCCCTCAAGCTTATACTA 1413 CGTC A A
TAGTATAG GTTT AG GCA
||||| ||||| |||

			ATCATATT CGAA TC CGT	
			_____ C C	
GAM222	FMR2	3'	CTCTTAAAAAGATGCTATGC 888	G_
			GTATAGCGTC TTAAAGAG	
			CGTATCGTAG AAATTCTC	
			AA	
GAM222	FLJ13612	3'	CTCTTAAATACTGTACTA 2146	CGTC
			TAGTATAG GTTTAAGAG	
			ATCATGTC TAAATTCTC	
			A_____	
GAM223	HPS4	5'	TGTTTGAAGTGGAACTTCAA 1977	AA T
			TTGAAGTTTCCA TTT GATA	
			AACTTCAAAGGT AAG TTGT	
			C_ T	
GAM223	TEKT1	5'	GGAATTTGGAAACCTCAA 2359	A
			TTGA GTTTCCAAATTTT	
			AACT CAAAGGTTTAAGG	
			C	
GAM223	LOC145783	3'	CGGAATTTGGAAACCCCAG 3082	AA
			TTG GTTTCCAAATTTTG	
			GAC CAAAGGTTTAAGGC	
			CC	
GAM223	LOC154321	3'	TATTAGCTTTGGAACTT 3190	T T
			AAGTTTCCAAA TT GATA	
			TTCAAAGGTTT GA TTAT	
			C T	
GAM224	FEZ1	3'	AGGATATGTCCACATAAGAA 1993	_ ATTTT
			TTCTT TGT GGCATATCCT	
			AAGAA ACA CTGTATAGGA	
			T C_____	
GAM224	GOLGA4	5'	AGGATATTGAACACAAAGAA 2554	A TGGC
			TTCTTTGT TTT ATATCCT	
			AAGAAACA AAG TATAGGA	
			C T_____	
GAM224	HAS3	3'	AGGACAAATCTAAAATGCAAAG 1199	CATA_
	AA		TTCTTTGTATTTTGG TCCT	
			AAGAAACGTAAAATC AGGA	
			TAAAC	
GAM224	JUN	3'	AGGATATTTAAGAAAATACAA 914	GGC_
			TTGTATTTT ATATCCT	

			AACATAAAA	TATAGGA		
			GAATT			
GAM224	MADH9	3'	ATGTGTAAATACATAGAA	1260	T	TG
			TTCT TGTATTT GCATAT			
			AAGA ACATAAA TGTGTA			
			T	—		
GAM224	NR2C2	3'	AGGACCGTTTCACATACAAAGAA	1007		TTT ATA
			TTCTTTGTAT GGC TCCT			
			AAGAAACATA TTG AGGA			
			CAC CC_			
GAM224	AP1S3	3'	AGGACTATAGAAATGCAAAGAA	3010		GGCATA
			TTCTTTGTATTTT TCCT			
			AAGAAACGTAAAG AGGA			
			ATATC_			
GAM224	ARHE	3'	ATATGCCAAAAAATGAGAG	1190		TGTA
			TTCTT TTTTGGCATAT			
			GAGAG AAAACCGTATA			
			TAA_			
GAM224	FLJ11000	3'	AGGACACATGGGGTACAAAGA	1812		TT GCATA
			TCTTTGTATT G TCCT			
			AGAAACATGG T AGGA			
			GG ACAC_			
GAM224	FLJ11996	5'	ATAGATCTAAATACAAAGGA	2120		T CA
			TTCTTTGTATTT GG TAT			
			AGGAAACATAAA CT ATA			
			T AG			
GAM224	GADD45A	3'	AGGAACAAAAATTACAAAGAA	869		T GGCATA
			TTCTTTGTA TTT TCCT			
			AAGAAACAT AAA AGGA			
			T AACA_			
GAM224	HNRPA3	3'	AGGATATGATGGTTACAATGAA	1244	T	TTTTGG
			TTC TTGTA CATATCCT			
			AAG AACAT GTATAGGA			
			T TGGTA_			
GAM224	KIAA0179	3'	AGAATATGTCACATAAAGAA	2704	ATTT	C
			TTCTTTGT TGGCATAT CT			
			AAGAAATA ACTGTATA GA			
			C_ A			
GAM224	KIAA1831	3'	GGAAAAAATACAAAGAA	2667		GGCATA
			TTCTTTGTATTTT TCC			

			AAGAAACATAAAA	AGG	
			AA____		
GAM224	KLHL4	3'	AGGATATGTGTGCTATATAAA	1880	TTTG_
			TTTGTAT GCATATCCT		
			AAATATA TGTATAGGA		
			TCGTG		
GAM224	PANX3	3'	AGGATAGTATAAATAAAAAGAA	2350	G TG A
			TTCTTT TATTT GC TATCCT		
			AAGAAA ATAAA TG ATAGGA		
			A TA _		
GAM224	TRAF3	5'	ATATGCTAAACAAAAGAA	2541	GTAT
			TTCTTT TTTGGCATAT		
			AAGAAA AAATCGTATA		
			AC__		
GAM224	TRAF3	3'	ATATGCTAAACAAAAGAA	1008	GTAT
			TTCTTT TTTGGCATAT		
			AAGAAA AAATCGTATA		
			AC__		
GAM224	ZFD25	3'	GATTGTACAAATACAAGGAA	1672	TG T
			TTCTTTGTATTT GCA ATC		
			AAGGAACATAAA TGT TAG		
			CA _		
GAM224	ZID	3'	ATATGCCAAAAGGAA	1315	TTGTA
			TTCT TTTTGGCATAT		
			AAGG AAAACCGTATA		

GAM224	LOC151742	5'	AGGACTACGAGAAAGACAAAGA	2477	A GGCATA
	A		TTCTTTGT TTTT TCCT		
			AAGAAACA AAAG AGGA		
			G AGCATC		
GAM224	LOC152179	3'	TGCTTCAAAATCAAAGAA	3352	T _
			TTCTTTG ATTTTG GCA		
			AAGAAAC TAAAC CGT		
			_ TT		
GAM224	LOC51266	3'	GATATGTATGAATGCAAA	1691	TG
			TTTGTATTT GCATATC		
			AAACGTAAG TGTATAG		
			TA		
GAM224	LOC90317	5'	AGGATACATACTACAGAGAA	2629	TTT GCA
			TTCTTTGTA TG TATCCT		

			AAGAGACAT AC ATAGGA		
			CAT ____		
GAM224	LOC90470	3'	AGAATATGCTCAATACAAAG 2645	TT	C
			CTTTGTATT GGCATAT CT		
			GAAACATAA TCGTATA GA		
			C_ A		
GAM224	LOC90786	5'	ATATGCCAAAATTGAGA 2678	TGT	
			TCTT ATTTTGGCATAT		
			AGAG TAAAACCGTATA		
			T__		
GAM225	ATRX	3'	ATCACGTCAGTAAAATACTA 751	T A	C
			TAGTATTTT CT ACGT GGT		
			ATCATAAAA GA TGCA CTA		
			T C _		
GAM225	ATRX	3'	ATCACGTCAGTAAAATACTA 2431	T A	C
			TAGTATTTT CT ACGT GGT		
			ATCATAAAA GA TGCA CTA		
			T C _		
GAM225	D10S170	3'	ATACCATTAGAAAATACTA 1211	T	CGTC
			TAGTATTTT CTAA GGTAT		
			ATCATAAAA GATT CCATA		
			_ A__		
GAM225	RAB27A	3'	ACTGTAATTAGAAAAATAC 1128	CGT	
			GTATTTTCTAA CGGT		
			CATAAAAAGATT GTCA		
			AAT		
GAM225	CYLD	3'	AATAGTGGTCAGAAAAATACT 1616	A GT	G
			AGTATTTTCT AC CG TATT		
			TCATAAAAAGA TG GT ATAA		
			C _ G		
GAM225	LOC145945	5'	ATTTATGGTGAGAAAAATAC 3279	AA_	CG
			GTATTTTCT CGT GT		
			CATAAAAAGA GTA TA		
			GTG TT		
GAM225	LOC200273	3'	ACCGACGTCAAAAAGTCTG 2895	T	CTA
			TAG ATTTT ACGTCGGT		
			GTC TGAAAA TGCAGCCA		
			_ AC_		
GAM225	LOC220758	3'	GCGATTAGAAAAACACTA 3497	A	_
			TAGT TTTTCTAA CGT		

			ATCA AAAAAGATT GCG		
			C A		
GAM226	KNSL1	3'	TTAGTGGTTATTTCTAAAAT 1123	—	
			ATTTTAGAAATAAC ATTAG		
			TAAAATCTTTATTG TGATT		
			G		
GAM226	PLAC1	3'	TGAAGATGCTATTTCTAGAATT 1960	A	AG
			AATTTTAGAAATA CATT CG		
			TTAAGATCTTTAT GTAG GT		
			C AA		
GAM226	SCP2	3'	CTAATGTTATTTCTTAAAATT 977	—	
			AATTTTA GAAATAACATTAG		
			TTAAAAT CTTTATTGTAATC		
			T		
GAM226	STIM1	3'	GTGTTATTTTCATAAAATT 2558	—	
			AATTTTA GAAATAACAT		
			TTAAAAT CTTTATTGTG		
			A		
GAM226	CORTBP2	3'	AATGTTACTTCTAAAATT 2334	A	
			AATTTTAGAA TAACATT		
			TTAAAATCTT ATTGTAA		
			C		
GAM226	VAMP3	3'	CTACTGTTATCTCTAAAATT 1156	A	T
			AATTTTAGA ATAACA TAG		
			TTAAAATCT TATTGT ATC		
			C C		
GAM226	LOC90148	3'	TCCTTGTGTTATTTCTAAAA 2603	T	C
			TTTTAGAAATAACAT AG GA		
			AAAATCTTTATTGTG TC CT		
			T		
GAM227	AK2	3'	TGAAAAAGGAAGTTGGTTATGC 1449	TACA	— C
	CA		TGGC AACT TTTCTTTT CA		
			ACCG TTGG GAAGGAAAA GT		
			TA__ TT A		
GAM227	CRTAP	3'	GGAAAAGGAAGAAAGCCA 1291	ACAAAC	
			TGGCT TTTCTTTTCC		
			ACCGA AGAAGGAAAAGG		
			A_____		
GAM227	CXorf6	5'	TGGAAAAGTCGGCTTGTAATCA 1218	GC	A TTTC
			TG TACAA CT CTTTCCA		

			AC ATGTT GG GAAAAGGT		
			TA C CT__		
GAM227	EPHB2	3'	TGGAAAAGAAAACTGGTGCCA 1113	T AAAC C	
			TGGC AC TTTTC TTTTCCA		
			ACCG TG AAAAG AAAAGGT		
			_ GTCA _		
GAM227	FZD3	3'	TGGAAAAATTTTAATTTGTAGC 1717	CTTTTCC	
	CA		TGGCTACAAA TTTTCCA		
			ACCGATGTTT AAAAGGT		
			AATTTTA		
GAM227	HMGA2	3'	GAAAAAAAAGCTTGTGGCCA 1033	A CC	
			TGGCTACAA CTTTT TTTTC		
			ACCGGTGTT GAAAA AAAAG		
			C A_		
GAM227	SLC2A4	3'	TGGAAAAGAATCCCTGCAGCC 794	A AACTT C	
			GGCT CA TTC TTTTCCA		
			CCGA GT AAG AAAAGGT		
			C CCCT_ _		
GAM227	ATP10B	3'	AGGGAAAAGTTATAACCA 2654	C CA	
			TGG TA AACTTTTCCTT		
			ACC AT TTGAAAAGGGA		
			A A_		
GAM227	BCCIP	3'	GAAAAGGAATAGTCA 2369	CAAACCTT	
			TGGCTA TTCCTTTTC		
			ACTGAT AAGGAAAAG		

GAM227	C20orf30	3'	GGAAAAGTGTTGCCTGCCA 1478	TA_ _	
			TGGC CAA ACTTTTCC		
			ACCG GTT TGAAAAGG		
			TCC G		
GAM227	DKFZP564O043	3'	GGAAGGGAAAAATTTATAGCTA 3565	C C	
			TGGCTA AAA TTTTCCTTTTC		
			ATCGAT TTT AAAAGGGAAGG		
			A A		
GAM227	FLJ11710	3'	TGGAAAGGGGAATCTATGCCA 2097	TACAACT	
			TGGC TTTCTTTTCCA		
			ACCG AAGGGGAAAGGT		
			TATCT__		
GAM227	JDD1	3'	TGGAAAGGCAAGTTTGTACCCA 2653	C TTC	
			TGG TACAACTT CTTTCCA		

			ACC ATGTTTGAA GGAAAGGT		
			C C_		
GAM227	KIAA0265	3'	GAAAAGGAAAAGGAATAATCA 2871	GC CAAA	
			TG TA CTTTTCCTTTTC		
			AC AT GAAAAGGAAAAG		
			TA AAG_		
GAM227	KIAA0663	3'	GGAAAAGGAAGAAAGCCA 1561	ACAAAC	
			TGGCT TTTTCCTTTTCC		
			ACCGA AGAAGGAAAAGG		
			A_		
GAM227	KIAA1010	3'	TGAAAGGAGAAACTTGCAGTC 2934	A AC T	
	A		TGGCT CAA TTTTCCTTT CCA		
			ACTGA GTT AAGAGGAAA GGT		
			C CA _		
GAM227	KIAA1576	3'	GGTCAAAAGTTTGAGCCA 2734	A _	
			TGGCT CAAACTTTT CC		
			ACCGA GTTTGAAAA GG		
			_ CT		
GAM227	KIAA1634	3'	TGAAAAAGGAAAGAAAGTAACC 2658	C AAAC C	
	A		TGG TAC TTTTCCTTTT CA		
			ACC ATG GAAAGGAAAA GT		
			A AAA_ A		
GAM227	KIAA1798	3'	GAAAGTAAGTTTGTAGC 2575	TTC	
			GCTACAAACTT CTTTT		
			CGATGTTTGAA GAAAG		
			T_		
GAM227	KNSL7	3'	AAAAATAAAAGCCTGTAGCTA 1904	AA CC	
			TGGCTACA CTTTT TTTT		
			ATCGATGT GAAAA AAAA		
			CC TA		
GAM227	LALP1	3'	GAAATGAAATTTGTAGC 1916	CT CT	
			GCTACAAA TTTC TTTC		
			CGATGTTT AAAG AAAG		
			_ T_		
GAM227	MGC2488	3'	GAAAAGGAAGCATGTAGC 2044	AACT	
			GCTACA TTTCCTTTTC		
			CGATGT GAAGGAAAAG		
			AC_		
GAM227	nexilin	3'	AAAAGGAAACCAGGAGTGCCA 2484	T AAA _	
			TGGC AC CT TTTCCTTTT		

			ACCG TG GA AAAGGAAAA		
			_ AG_ CC		
GAM227	NKX2B	3'	TGGAAAAGAAAACCCTGTAGGC 934	G AAC C	
	A		TG CTACA TTTTC TTTCCA		
			AC GATGT AAAAG AAAAGGT		
			G CCC _		
GAM227	STX18	3'	TGAAAAAGGAAACAGTGCACAC 1715	CTACAA _ C	
	CA		TGG ACT TTTCTTTT CA		
			ACC TGA AAAGGAAAA GT		
			ACACG_ C A		
GAM227	ZNF271	5'	AGTAAAAGTTTTAGCCA 3670	C C	
			TGGCTA AAACCTTT CT		
			ACCGAT TTTGAAAA GA		
			_ T		
GAM227	LOC115207	3'	GAAAGTTGGAAGTTTGTACCA 2440	C CC	
			TGG TACAACTTTT TTTTC		
			ACC ATGTTTGAAGG GAAAG		
			_ TT		
GAM227	LOC133482	5'	AAAAGGAAAAAAGCCA 3014	ACAAAC	
			TGGCT TTTCTTTT		
			ACCGA AAAAGGAAAA		
			A_____		
GAM227	LOC147080	5'	TGGAAATCGCCAAATTTGTAGC 3290	CTTTTCCT	
	CA		TGGCTACAAA TTTCCA		
			ACCGATGTTT AAAGGT		
			AAACCGCT		
GAM227	LOC147990	3'	GAAAAGGAAATAAAAAAGCCA 3295	ACAAACT	
			TGGCT TTTCTTTTC		
			ACCGA AAAGGAAAAG		
			AAAAAT_		
GAM227	LOC149529	3'	AAAAGGCAAAAGTTTGCAGC 3134	A _	
			GCT CAACTTTT CCTTTT		
			CGA GTTTGAAAA GGAAAA		
			C C		
GAM227	LOC158130	3'	AAAGGAAAATTCTAGCCA 2847	C AC	
			TGGCTA AA TTTCTTTT		
			ACCGAT TT AAAAGGAAA		
			C _		
GAM227	LOC196478	5'	GAAAATGGATTTGTAGC 3413	CTTT _	
			GCTACAAA TCC TTTTC		

		CGATGTTT AGG AAAAG		
		_____ T		
GAM227	LOC219894 3'	AGAAGAAAAGTTTGAAACCA 3595	CTA	C
		TGG CAAACTTTTC TTTT		
		ACC GTTTGAAAAG AAGA		
		AAA _____		
GAM227	LOC219988 5'	GAAAGCACAAAATTTGTAGC 3535	C TC_	
		GCTACAAA TTT CTTTT		
		CGATGTTT AAA GAAAG		
		A CAC		
GAM227	LOC221272 3'	GAAAAGGAAAAGTTTACCTGC 3613	TAC_	
		GC AAACTTTTCTTTTC		
		CG TTTGAAAAGGAAAAG		
		TCCA		
GAM227	LOC221272 3'	GAAAAGGAAAGTAGCTA 3614	AAACT	
		TGGCTAC TTTCTTTTC		
		ATCGATG AAAGGAAAAG		

GAM227	LOC245771 5'	TGAAAAGGAGAGATCATCAGC 3584	ACAAAC	C
	CA	TGGCT TTTTCCTTTT CA		
		ACCGA GAGAGGAAAA GT		
		CTACTA A		
GAM227	LOC253019 3'	GGAAAAGGAAGAAAGCCA 3673	ACAAAC	
		TGGCT TTTTCCTTTTCC		
		ACCGA AGAAGGAAAAGG		
		A_____		
GAM227	LOC253975 3'	GGAAAAGGAAGAAAGCCA 3687	ACAAAC	
		TGGCT TTTTCCTTTTCC		
		ACCGA AGAAGGAAAAGG		
		A_____		
GAM227	LOC254873 3'	TGGAAGAATCCCTGCAGCC 3659	A AACTT C	
		GGCT CA TTC TTTTCCA		
		CCGA GT AAG AAAAGGT		
		C CCCT_ _		
GAM227	LOC51634 3'	AAAATGAAACCCTGTAGCCA 1655	AACT C	
		TGGCTACA TTTC TTTT		
		ACCGATGT AAAG AAAA		
		CCC_ T		
GAM228	ABCE1 3'	AAATATACAGAATGGAA 2532	GCTG	
		TTCCG TTGTATATTT		

AAGGT GACATATAAA
 AA__
 GAM228 WWP1 3' ATTTAAATACCCCAGCCAAGAA 1345 C_ TTGTA
 A TTTT GGCTG TATTTAAAT
 ||| ||| |||||
 AAAG CCGAC ATAAATTTA
 AA CCC__
 GAM229 GDF8 3' ATGAAGAATAAACTGATGCTA 1197 C GAG C
 TAGCATCG TTT ATTCT CAT
 ||||| || |||||
 ATCGTAGT AAA TAAGA GTA
 C __ A
 GAM229 DIO2 3' TGGAGAGGAAGAAACGCTA 773 ATCG GAGA
 TAGC CTTT TTCTCCA
 ||| ||| |||||
 ATCG GAAG GAGAGGT
 CAAA ____
 GAM229 DIO2 3' TGGAGAGGAAGAAACGCTA 1454 ATCG GAGA
 TAGC CTTT TTCTCCA
 ||| ||| |||||
 ATCG GAAG GAGAGGT
 CAAA ____
 GAM229 FLJ21007 5' ATGAAGAATCTCAGGCTGC 2167 TC T C
 GCA GCTT GAGATTCT CAT
 || ||| ||||| |||
 CGT CGGA CTCTAAGA GTA
 __ _ A
 GAM229 KIAA0478 3' ATGGAGAAAAAGCAGGGATGCT 1573 __ GAGA
 A TAGCATC GCTTT TTCTCCAT
 ||||| ||| |||||
 ATCGTAG CGAAA AAGAGGTA
 GGA ____
 GAM229 KIAA0513 3' GATCTCAAAACAGTGCTA 1535 CGC
 TAGCAT TTTGAGATT
 ||||| |||||
 ATCGTG AACTCTAG
 ACA
 GAM229 KIAA1323 5' ATGGAGAATGGGCTGAAGCGAT 2647 G ____
 GCT AGCATCGCTTT AG ATTCTCCAT
 ||||| || |||||
 TCGTAGCGAAG TC TAAGAGGTA
 _ GGG
 GAM229 P450RAI-2 3' GAGAATCTTGGGGATGCTG 1888 G TT
 TAGCATC CT GAGATTCTC
 ||||| || |||||
 GTCGTAG GG TTCTAAGAG
 G __
 GAM229 XYLT1 3' GAAACTCACAAAGCAATGCT 3089 C __ A
 AGCAT GCTT TGAG TTC
 |||| ||| ||||| |||

			TCGTA CGAA ACTC AAG	
			A AC A	
GAM229	LOC143282	3'	ATGGAGAATCTCTGGGATAGC 3055	_ G TT
			GC ATC CT GAGATTCTCCAT	
			CG TAG GG CTCTAAGAGGTA	
			A _ T_	
GAM229	LOC200132	3'	ATGGAGAAAATTAGCAATGCTG 3438	C TT GA
			TAGCAT GCT GA TTCTCCAT	
			GTCGTA CGA TT AAGAGGTA	
			A _ _ AA	
GAM230	FGFR1	5'	CCGCAGCGCGCGGAGGAA 759	GAGA ACA A
			TTCCTCTG TG CT CGG	
			AAGGAGGC GC GA GCC	
			_ GC_ C	
GAM230	FGFR1	5'	CCGCAGCGCGCGGAGGAA 1647	GAGA ACA A
			TTCCTCTG TG CT CGG	
			AAGGAGGC GC GA GCC	
			_ GC_ C	
GAM230	FGFR1	5'	CCGCAGCGCGCGGAGGAA 2031	GAGA ACA A
			TTCCTCTG TG CT CGG	
			AAGGAGGC GC GA GCC	
			_ GC_ C	
GAM230	FGFR1	5'	CCGCAGCGCGCGGAGGAA 2033	GAGA ACA A
			TTCCTCTG TG CT CGG	
			AAGGAGGC GC GA GCC	
			_ GC_ C	
GAM230	FGFR1	5'	CCGCAGCGCGCGGAGGAA 2035	GAGA ACA A
			TTCCTCTG TG CT CGG	
			AAGGAGGC GC GA GCC	
			_ GC_ C	
GAM230	FGFR1	5'	CCGCAGCGCGCGGAGGAA 2036	GAGA ACA A
			TTCCTCTG TG CT CGG	
			AAGGAGGC GC GA GCC	
			_ GC_ C	
GAM230	ITGB3	3'	CCTCTCATTCCAGAGGAA 718	A CACTAC
			TTCCTCTGGAG TGA GG	
			AAGGAGACCTT ACT CC	
			_ CT_	
GAM230	PCSK2	3'	GCCATGCAATTCATCCCAGAGG 940	A CACTAC_
	AA		TTCCTCTGG GATGA GGC	

AAGGAGACC CTACT CCG
 _ TAACGTA
 GAM230 STK24 3' CCATAGTGCACATATTCCAGG 1038 _ A_ C
 TCTGGAG ATG CACTA GG
 ||||| || ||||| ||
 GGACCTT TAC GTGAT CC
 A AC A
 GAM230 TIMP3 5' CCTGCTCTCTCCAGAG 733 T _ CTAC
 CTCTGGAGA GA CA GG
 ||||| || || ||
 GAGACCTCT CT GT CC
 _ C _
 GAM230 AF038169 3' GCCAGGGGGCATCTCCAAAGGA 1440 C ACA AC
 A TTCCT TGGAGATG CT GGC
 ||||| || || ||
 AAGGA ACCTCTAC GG CCG
 A GG_ GA
 GAM230 CRTAM 3' GCCGCAGTGTACCTCAGTGGA 1883 T G A A
 TCC CTG AG TGACACT CGGC
 || || || ||||| ||||
 AGG GAC TC ACTGTGA GCCG
 T _ C C
 GAM230 DKFZP564J0863 3' GCCACAGGTTTCATATCCAGAGG 2815 G CA AC
 AA TTCCTCTGGA ATGA CT GGC
 ||||| || || ||
 AAGGAGACCT TACT GA CCG
 A TG CA
 GAM230 FLJ14297 5' GCCATAGAATTCTCTCCAGAAG 2108 C T CA_ C
 AG TTC TCTGGAGA GA CTA GGC
 || ||||| || || ||
 GAG AGACCTCT CT GAT CCG
 A _ TAA A
 GAM230 FLJ20508 3' GCTGTTACCATCTCAGAGGAA 1757 G ACACT
 TTCCTCTG AGATG ACGGC
 ||||| || || ||
 AAGGAGAC TCTAC TGTCTG
 _ CAT_
 GAM230 FLJ23462 3' GCTTCTGTCTATCTCCAGAG 2096 CTAC
 CTCTGGAGATGACA GGC
 ||||| || ||
 GAGACCTCTACTGT TCG
 CT_
 GAM230 LOC126167 3' CCAAGAATTTATCTCCAAAGGA 2998 C CACTAC
 A TTCCT TGGAGATGA GG
 ||||| || || ||
 AAGGA ACCTCTATT CC
 A TAAGAA
 GAM230 LOC157247 5' CCACAGTGTCTATCCCACAG 3200 C A AC
 CT TGG GATGACACT GG
 || || ||||| || ||

			GA ACC CTACTGTGA CC		
			C _ CA		
GAM230	LOC161357	5'	CCGTAGTGGCTCCAAAG 3240	C	ATGA
			CT TGGAG CACTACGG		
			GA ACCTC GTGATGCC		
			A G__		
GAM230	LOC201965	3'	CCGTAAATTACTTCAGAG 3455	A	CAC
			CTCTGGAG TGA TACGG		
			GAGACTTC ATT ATGCC		
			_ AA_		
GAM230	LOC253758	5'	GCCGTCTCACCTCCAAAGG 3723	C	A CACT
			CCT TGGAG TGA ACGGC		
			GGA ACCTC ACT TGCCG		
			A C C__		
GAM230	LOC91661	3'	CCACTGCATCTCAGAGGAA 2438	G	A CTAC
			TTCTCTG AGATG CA GG		
			AAGGAGAC TCTAC GT CC		
			_ _ CA__		
GAM231	SPG4	3'	AATCTACAGACATTAAACAAT 1595	C	TA
			ATTGTTTAAT GTTT TAGATT		
			TAACAAATTA CAGA ATCTAA		
			_ C_		
GAM231	KIAA0672	3'	AATCTATAAAACAAAACAA 1569	AATC	
			TTGTTT GTTTTATAGATT		
			AACAAA CAAAATATCTAA		
			A__		
GAM231	MGC32104	3'	AATCTATAAAGAACTCAAACAA 2495	AATCG	
			TTGTTT TTTTATAGATT		
			AACAAA GAAATATCTAA		
			CTCAA		
GAM231	PRO0082	3'	AATCTATGGCTTGATTA AAAAAT 1851	G	TT
	A		TATT TTTAATCG TTATAGATT		
			ATAA AAATTAGT GGTATCTAA		
			_ TC		
GAM232	TRAP1	3'	GATGACAGCCCCACCTCC 1678	A	A_
			GGAGGTGG GT TCGTC		
			CCTCCACC CG AGTAG		
			C AC		
GAM232	ASAH	3'	TGGTGA ACTCCACCTCC 1098	A	GT
			GGAGGTGGAGT TC CA		

			CCTCCACCTCA AG GT		
			— TG		
GAM232	CNNM1	3'	ATTATTGACTTCACCACACCCC 1913	A	GA ATC
			GG GGTG GT GTCAATAAT		
			CC CCAC CA CAGTTATTA		
			— AC CTT		
GAM232	Rab11-FIP2	3'	ATTATGCATTACTCCACATCC 1582	G	TC CA
			GGA GTGGAGTA GT ATAAT		
			CCT CACCTCAT CG TATTA		
			A TA —		
GAM232	RNF38	3'	ATTGAATACTCCATCCC 2009	A	CG
			GG GGTGGAGTAT TCAAT		
			CC CTACCTCATA AGTTA		
			— —		
GAM232	LOC152283	3'	TGGTCGACATCCCACCTCC 3357	AG A	—
			GGAGGTGG T TCG TCA		
			CCTCCACC A AGC GGT		
			CT C T		
GAM232	LOC160484	5'	TATTGGCCTGACAGTCCACCTC 3239	—	ATC
	C		GGAGGTGGA GT GTCAATA		
			CCTCCACCT CA CGGTTAT		
			GA GTC		
GAM232	LOC90119	3'	ATTATTGACAACACCAT 2600	A	ATC
			GTGG GT GTCAATAAT		
			TACC CA CAGTTATTA		
			A A—		
GAM233	MTMR2	3'	GATCAAAATCATTTGATA 1664	T	
			TATCAGATGATTTTG ATT		
			ATAGTTTACTAAAAC TAG		
			—		
GAM233	PCDHGA8	5'	GATCTAATCTGATCATTTAATA 2227	C	TTGT
			TAT AGATGATT ATTAGATC		
			ATA TTTACTAG TAATCTAG		
			A TC—		
GAM233	PCDHGA8	5'	GATCTAATCTGATCATTTAATA 1460	C	TTGT
			TAT AGATGATT ATTAGATC		
			ATA TTTACTAG TAATCTAG		
			A TC—		
GAM233	PTGES	3'	CTAATGATCATCTGA 1162	TTGT	
			TCAGATGATT ATTAG		

AGTCTACTAG TAATC

GAM233 SOX11 3' AATCATAATCATCTGATA 991 T T
TATCAGATGATT TG ATT
||||||| || |||
ATAGTCTACTAA AC TAA
T _

GAM234 C6 5' TGGGAGGACAAAGGCAGT 3656 A A_
ACT CCTTTGTC CCCA
||| ||||| |||
TGA GGAAACAG GGGT
C GA

GAM234 CGB 5' ATAAAGCCAGGTACACGAGGCA 770 A _ C CAA
G CT CCTT TGT ACC CTTTAT
|| ||| ||| ||| |||||
GA GGAG ACA TGG GAAATA
C C _ ACC

GAM234 CUL3 3' AGTTGGGTAACAAAAATGG 1040 CC C
CTA TTTGT ACCCAACT
||| ||||| |||||
GGT AAACA TGGGTTGA
AA A

GAM234 GRINL1A 3' ATAAAGTTACACAAAGGTAGT 2863 CACCC
ACTACCTTTGT AACTTTAT
||||||| |||||
TGATGGAAACA TTGAAATA
CA__

GAM234 PRKG1 3' AGTTGAGAGACAAAGGTA 1283 ACC
TACCTTTGTC CAACT
||||||| |||||
ATGGAAACAG GTTGA
AGA

GAM234 WHSC1 3' AAAGTTGGGTTGATAGG 2409 TT _
CCT GTCA CCCAACTTT
||| ||| |||||
GGA TAGT GGGTTGAAA
_ T

GAM234 CGB5 5' ATAAAGCCAGGTACACGAGGCA 2311 A _ C CAA
G CT CCTT TGT ACC CTTTAT
|| ||| ||| ||| |||||
GA GGAG ACA TGG GAAATA
C C _ ACC

GAM234 DDX33 3' ATAAAATTGGGTTTCATAAAG 1895 C_ C
CTTTGT ACCCAA TTTAT
||||| ||||| |||||
GAAATA TGGGTT AAATA
CT A

GAM234 FLJ20296 5' TAAAGCTGGTTAAGGTGGT 1749 TGTCAC A
ACTACCTT CCA CTTTA
||||||| ||| |||||

			TGGTGGAA	GGT GAAAT		
			TT____	C		
GAM234	IRO039700	5'	GTGGGGCAGACAAAGGCAG	1858	A	A_ A
			CT CCTTTGTC	CCC AC		
			GA GGAAACAG	GGG TG		
			C	AC G		
GAM234	KIAA0594	3'	ATAAAATTAGGTGACAAGGGT	2706		C C
			ACCTTTGTCACC	AA TTTAT		
			TGGGAACAGTGG	TT AAATA		
			A	A		
GAM234	MAL2	3'	AGTTGAATGACAAAGCAGT	2343	AC	CC
			ACT CTTTGTCA	CAACT		
			TGA GAAACAGT	GTTGA		
			C_	AA		
GAM234	LOC145622	3'	AAAGTTGTGTAAAGTGACGAA	3080		C_____
			TTTGTCAC	CAACTTT		
			AAGCAGTG	GTTGAAA		
			AAATGT			
GAM234	LOC152982	3'	ATAAAGTTACACAAAGGTAGT	3176		CACCC
			ACTACCTTTGT	AACTTTAT		
			TGATGGAAACA	TTGAAATA		
			CA__			
GAM234	LOC256174	5'	ATAAAGTTGGATGGAAAGG	3742	G	C
			CCTTT TCA	CCAACCTTAT		
			GGAAA GGT	GGTTGAAATA		
			_	A		
GAM235	CALCR	3'	GAGGGGAAAAAATTA	ACTGCTC	854	A A _ G
	CA		TG AGTA	TTAATTTT	CT CCTC	
			AC TCGT	AATTAAAAA	GG GGAG	
			C	C	A _	
GAM235	IL1F9	3'	GAAGAAGCAATTACTTCA	1886	AA	
			TGAAGTAATT	TTTTTC		
			ACTTCATTAA	AAGAAG		
			CG			
GAM235	LTA	3'	AGGCAAAAAAATTA	AATTATTT	757	_ C
			AAGTAATT	AATTTT	TGCCT	
			TTTATTAA	TTAAAAA	ACGGA	
			A	A		
GAM235	PPP1R12B	3'	AGGCAGGGTCTAACCCTTCA	2229	TAA	ATTT
			TGAAG	TTA	TTCTGCCT	

			ACTTC AAT GGGACGGA		
			CC_ CT__		
GAM235	TFF3	3'	GCAGAAAAAATACATTTC	2661	AAT A
			TGAAGT TA TTTTCTGC		
			ACTTTA AT AAAAAGACG		
			C__ A		
GAM235	ZHX1	3'	AGGAGAATCAATTCTTCA	1366	T A
			TGAAG AATT ATTTTCT		
			ACTTC TTAA TAAGAGGA		
			_ C		
GAM235	DKFZP434C1715	3'	AGGCAGAAGGATCACTT	3371	AATTA
			AAGT ATTTTCTGCCT		
			TTCA TAGGAAGACGGA		
			C__		
GAM235	FLJ21075	3'	GAGGCAGAAAATTCCACTT	2130	AATTAAT
			AAGT TTTTCTGCCTC		
			TTCA AAAAGACGGAG		
			CCTT__		
GAM235	FLJ23556	3'	AGGCAGAAGGATCACTT	2101	AATTA
			AAGT ATTTTCTGCCT		
			TTCA TAGGAAGACGGA		
			C__		
GAM235	HSD17B7	3'	AGGCAGAAGGATCACTT	1682	AATTA
			AAGT ATTTTCTGCCT		
			TTCA TAGGAAGACGGA		
			C__		
GAM235	IDN3	3'	AGGCAGAAAACTTGAAATAC	2415	A_ _
			GTA TTAA TTTTCTGCCT		
			CAT AGTT AAAAAGACGGA		
			AA C		
GAM235	KIAA1456	3'	AGGCAGAAGGATCACTT	2772	AATTA
			AAGT ATTTTCTGCCT		
			TTCA TAGGAAGACGGA		
			C__		
GAM235	NXPH3	3'	AGACAGAAATGTTACTTC	2727	TAATT C
			GAAGTAAT TTTCTG CT		
			CTTCATTG AAAGAC GA		
			T__ A		
GAM235	PNPASE	3'	GAGGCAGAAGAATCACTTCA	2901	AATTA
			TGAAGT ATTTTCTGCCTC		

			ACTTCA	TAAGAAGACGGAG		
			C_____			
GAM235	SPRY4	3'	AGGCAGAAGAATCACTT	2176	AATTA	
			AAGT	ATTTTTCTGCCT		
			TTCA	TAAGAAGACGGA		
			C_____			
GAM235	ZNF33A	3'	AGGCAGAAGAATCACTT	3519	AATTA	
			AAGT	ATTTTTCTGCCT		
			TTCA	TAAGAAGACGGA		
			C_____			
GAM235	LOC126282	3'	AGGCAGGATAATCACTT	2999	A	ATTT
			AAGT	ATTA TTCTGCCT		
			TTCA	TAAT AGGACGGA		
			C _____			
GAM235	LOC144583	3'	AGGCAGGATAATCACTT	3068	A	ATTT
			AAGT	ATTA TTCTGCCT		
			TTCA	TAAT AGGACGGA		
			C _____			
GAM235	LOC145231	3'	AGGCAGGCGAATTACTTCA	3273		AATTTT
			TGAAGTAATT	TCTGCCT		
			ACTTCATTAA	GGACGGA		
			GC_____			
GAM235	LOC147837	3'	AGGCAGGATAATCACTT	3113	A	ATTT
			AAGT	ATTA TTCTGCCT		
			TTCA	TAAT AGGACGGA		
			C _____			
GAM235	LOC149910	3'	GAGACAGAATCTTTAGTTACTT	3141	TTT	C
	CA		TGAAGTAATTAA	TTCTG CTC		
			ACTTCATTGATT	AAGAC GAG		
			TCT	A		
GAM235	LOC158160	3'	AGGCAGAAGGATCACTT	2967	AATTA	
			AAGT	ATTTTTCTGCCT		
			TTCA	TAGGAAGACGGA		
			C_____			
GAM235	LOC158292	5'	AGGCAGAAGAATCACTT	3385	AATTA	
			AAGT	ATTTTTCTGCCT		
			TTCA	TAAGAAGACGGA		
			C_____			
GAM235	LOC162333	5'	GAAGCAGAAGATACTACTTTA	3401	ATTAAT	C
			TGAAGTA	TTTTCTGC TC		

			ATTTCAT	AGAAGACG AG		
			CAT__	A		
GAM235	LOC200057	5'	GAAGCAGAAAGAGGTTACTT	3437	AA	C
			AAGTAATT TTTTCTGC TC			
			TTCATTGG AGAAAGACG AG			
			__	A		
GAM235	LOC202018	3'	GCTTTAAACTAATTACTTCA	3460	A	TCT
			TGAAGTAATTA TTTT GC			
			ACTTCATTAAT AAAA CG			
			C TTT			
GAM235	LOC219392	5'	GCAGAGGGAACCAGCTTCA	3511	AATTAA	
			TGAAGT TTTTCTGC			
			ACTTCG AGGGAGACG			
			ACCA__			
GAM236	TACC1	3'	TAATTGGTAGCCATCTCATG	1285	C	_
			CGTGA GTGGT ATCAATTA			
			GTACT TACCG TGGTTAAT			
			C A			
GAM237	EIF4G2	3'	AAGCAGAGGCAGTCTATTG	827	T	GTAAG
			CAAT AGAC TTCTGCTT			
			GTTA TCTG GAGACGAA			
			_ ACG__			
GAM237	PEX12	3'	AAGCAAAATACTAATCTAATTG	727	CGTAA	C
	TG		TACAATTAGA GTT TGCTT			
			GTGTTAATCT TAA ACGAA			
			AATCA A			
GAM237	LOC130162	3'	AAGCAGAACAGATACCTAATT	3009	AC	AA
			AATTAG GT GTTCTGCTT			
			TTAATC TA CAAGACGAA			
			CA GA			
GAM237	LOC152573	3'	AAGCAAAGAAAAATACCTAATT	3172	AC	AG_ _
	GTA		TACAATTAG GTA TTCT GCTT			
			ATGTTAATC CAT AAGA CGAA			
			_ AAA AA			
GAM238	FACL2	3'	AGAGTACATGTATTATAT	1942	TTT	A
			ATGTAATACA TG ACTCT			
			TATATTATGT AC TGAGA			
			_ A			
GAM238	PTER	3'	AGTCAAAATATATTACAT	2154	C	A
			ATGTAATA ATTTTGA CT			

			TACATTAT TAAAACT GA		
			A _		
GAM238	ATP6V1G1	3'	AGAATTCAAGAACTTGTTACAT 1163	CA_	C
			GTA TACATGTAATA TTTTGAA TCT		
			ATGTACATTGT AGAACTT AGA		
			TCA A		
GAM238	GFR	3'	AGATGCAAATGTATTACTGTA 1423	T	T AAC
			TACA GTAATACATTT G TCT		
			ATGT CATTATGTAAA C AGA		
			_ _GT_		
GAM238	KIAA0349	3'	TTTGGAATGTATCATATGTA 3562	A	TG
			TACATGT ATACATTT AA		
			ATGTATA TATGTAAG TT		
			C GT		
GAM238	RGS20	3'	AAGATGTGACCACTACATGTA 1049	A_____	
			TACATGTA TACATTTT		
			ATGTACAT GTGTAGAA		
			CACCA		
GAM238	LOC253573	3'	GAGTTCAAAAGTACCACA 3725	AA A	
			TGT TAC TTTTGAACTC		
			ACA ATG AAAACTTGAG		
			CC _		
GAM238	LOC83690	3'	AGATGAACTAATGTATTACATT 2203	C	TTGAAC
			A A ATGTAATACATT TCT		
			A TACATTATGTAA AGA		
			T TCAAGT		
GAM239	RBM8A	3'	AATGTTCCATTTTGTTC 1186	A_	
			GAAAACAAAAAT GATATT		
			CTTTTGTTCCTTA TTGTAA		
			CC		
GAM239	SLC7A6	3'	GTCTGTTTTTGTTCCTGA 1078	AA	
			TCG AACAAAAATAGAT		
			AGC TTGTTTTGTCTG		
			CC		
GAM239	SEMA3E	3'	AGTGTTTATTTTCAAGTTTC 1432	AA	
			GAAAAC AAATAGATATT		
			CTTTTG TTTATTTGTGA		
			AC		
GAM239	LOC151201	3'	AATGTCATTTTGTTC 3339	A	
			GAAAACAAAAAT GATATT		

TTTTTGTTTTTA CTGTAA

GAM239 LOC90979 3' AATAATATTTTTTTTGT TTTT 2692 T
—
AAAACAAAAA AGATATTATT
||||||| |||||||
TTTTGTTTTT TTTATAATAA

GAM240 ZIC1 3' CGAATCAAACAACCCCCACAC 1017 ATAGA AC
A
TGT GG GTTTTGATTG
||| || |||||||
ACA CC CAAACTAAGC
CACCC AA

GAM240 KIAA1550 3' CAGGACGTCCTCTACACA 2752 A
TGT TAGAGGACGTTTTG
||| |||||||
ACA ATCTCCTGCAGGAC
C

GAM240 LOC143720 3' TCAAAGCTCCCCTATACA 2568 A C
TGTATAG GGA GTTTTGA
||||| ||| |||||
ACATATC CCT CGAACT
C _

GAM240 LOC150848 5' TCAAATCCCTTTTGTCTCTATA 3335 G TTTT_ C
CA
TGTATAGAG ACG GATT GA
||||||| ||| ||| ||
ACATATCTC TGT CTAA CT
_ TTTCC A

GAM241 MAIL 3' AGTCTTTGTAGATAAA 2194 AC
TTTATCTACAG AGACT
||||||| |||||
AAATAGATGTT TCTGA

GAM241 LOC151414 3' ATTATTCTTAGATCTGTAGATA 3157 C__ C
TATCTACAGA AGA TAAT
||||||| ||| |||||
ATAGATGTCT TCT ATTA
AGAT T

GAM241 LOC155038 3' AGCTATTTGTAGATAAA 3197 C A
TTTATCTACAGA AG CT
||||||| ||| ||
AAATAGATGTTT TC GA
A _

GAM242 CRH 3' TTAGCTAGCATGCACAAA 772 A GA
TTTGT CA CTAAGTAA
||||| || |||||||
AAACA GT GATTCATT
C AC

GAM242 C1orf24 3' AAGAATTTTCTGTACA 2351 CTAAGT
TGTACAGA AATTCTT
||||||| |||||||

			ACATGTCT	TTAAGAA	
			T_____		
GAM242	C21orf67	5'	AAAGATACTCACCTGTACAAA	2367	ACTA AT
			TTTGTACAG AGTA TCTTT		
			AAACATGTC TCAT AGAAA		
			CAC_ _		
GAM242	KIAA0940	3'	AAGAAATGTCTGTACAAA	1585	TAAGTAA
			TTTGTACAGAC TTCTT		
			AAACATGTCTG AAGAA		
			TA_____		
GAM242	LOC158722	3'	AAAGAATTATATTGCTGACAAA	3225	A ACTAA
			TTTGT CAG GTAATTCTTT		
			AAACA GTC TATTAAGAAA		
			_ GTTA_		
GAM242	LOC220705	3'	AATGTCTTAGTTGTACAAA	3514	A TA
			TTTGTACAG CTAAG ATT		
			AAACATGTT GATTC TAA		
			_ TG		
GAM243	ACVR1	3'	AAGCAAAGATTTTCAGTAGA	800	_ A
			TCT TTGAAATCTTT CTT		
			AGA GACTTTAGAAA GAA		
			T C		
GAM243	CELSR1	3'	AAGTAAATGCAAAGATGT	1486	AAATC
			ACATCTTTG TTTACTT		
			TGTAGAAAC AAATGAA		
			GTA_		
GAM243	GJA1	3'	AAGTAGTGGATTCAAAGA	715	A T
			TCTTTGAA TC TTA		
			AGAAACTT GG GATGAA		
			A T		
GAM243	PLN	3'	AAGTAATTTTTTCAAAGA	945	TCT
			TCTTTGAAA TTA		
			AGAAACTTT AATGAA		
			TTT		
GAM243	CNOT7	3'	AAGTAAAGATATAATTAGAGAT	2363	A_
			ATCTTTGA ATCTTTACTT		
			TAGAGATT TAGAAATGAA		
			AATA		
GAM243	Groc9	3'	AAGTAAAAATAGTAAGAGATGT	2268	GAA_ C
		T	AACATCTTT AT TTTACTT		

			TTGTAGAGA TA AAATGAA	
			ATGA A	
GAM243	KIAA1287	3'	AAGTAGAAATCTCAAAGAT 3106	A C
			ATCTTTGA AT TTTACTT	
			TAGAAACT TA AGATGAA	
			C A	
GAM243	KIAA1673	3'	AAGTGTTTGATTGAGAGATGT 2894	A TT_
			ACATCTTTGAA TC TACTT	
			TGTAGAGACTT AG GTGAA	
			_ TTT	
GAM243	LHFP	3'	AAGCAAGGTACCCCCAAAGATG 1248	AAAT__ A
	TT		AACATCTTTG CTTT CTT	
			TTGTAGAAAC GGAA GAA	
			CCCCAT C	
GAM243	PDE10A	3'	AAGTAGCAGTTCAAAAGATGT 1320	GA CT
			ACATCTTT AAT TTACTT	
			TGTAGAAA TTG GATGAA	
			AC AC	
GAM243	TBDN100	3'	AAGTAAAGATTTATCTGAT 2135	TTTG
			ATC AAATCTTTACTT	
			TAG TTTAGAAATGAA	
			TCTA	
GAM243	LOC149448	3'	GTAATTTTCAAAGATG 3310	TCT
			CATCTTTGAAA TTAC	
			GTAGAAACTTT AATG	
			T__	
GAM243	LOC155434	3'	AGTGGCGATTCAAAGATG 3375	A T
			CATCTTTGAA TC TTACT	
			GTAGAAACTT AG GGTGA	
			_ C	
GAM243	LOC221583	3'	AAGTATACTACTCTCAAAGGTG 3557	AATCTT__
	T		ACATCTTTGA TACTT	
			TGTGGAAACT ATGAA	
			CTCATCAT	
GAM243	LOC54466	3'	AAGTGGCAACTGTCAAAGATG 1871	AATCT_
			CATCTTTGA TTACTT	
			GTAGAAACT GGTGAA	
			GTCAAC	
GAM244	MECP2	3'	CCAGAGACAAATATTTCTAGA 1167	C C AA_
			TC AGAGATAT TTGT TGG	

			AG TCTTTATA AACA ACC		
			A _ GAG		
GAM244	ATP10B	3'	CCAGGCAATATCTCAGGATA 2655	A	CT AA
			TATCC GAGATAT TGT TGG		
			ATAGG CTCTATA ACG ACC		
			A _ G_		
GAM244	BDG-29	3'	CCATTACAGTGGCCTGGATA 2943	AGA	CT
			TATCCAG TAT TGTAATGG		
			ATAGGTC GTG ACATTACC		
			CG_ _		
GAM244	GW112	3'	CCACTTACTTAGATATCTGCAG 1298	CAG	T_ _
	ATA		TATC AGATATCT GTAA TGG		
			ATAG TCTATAGA CATT ACC		
			ACG TT C		
GAM244	HSPB7	3'	CCATTACAACAGCTCCAGGA 1498	A_	ATATC
			TCC GAG TTGTAATGG		
			AGG CTC AACATTACC		
			AC GAC_		
GAM244	KIAA1464	3'	CCAGTATTTATCTCTGGA 2813	TCTT	A
			TCCAGAGATA GTA TGG		
			AGGTCTCTAT TAT ACC		
			T_ G		
GAM244	KIAA1634	3'	CCACCAACTATTTCTGGATA 2656	TC	TAA
			TATCCAGAGATA TTG TGG		
			ATAGGTCTTTAT AAC ACC		
			C_ C_		
GAM244	NETO1	3'	CCATCATCTCATCTCTGGATG 2463	ATCT	TA
			TATCCAGAGAT TG ATGG		
			GTAGGTCTCTA AC TACC		
			CTCT _		
GAM244	PRO2533	3'	CCATTACAAAATGTAATGG 1854	GAG	C
			CCA ATAT TTGTAATGG		
			GGT TGTA AACATTACC		
			AA_ A		
GAM244	LOC151201	3'	TGTAATAACCTCTGGATA 3343	A	C
			TATCCAGAG TAT TTGTA		
			ATAGGTCTC ATA AATGT		
			C A		
GAM245	FLJ14124	3'	CAAAACGAGTAAAGAGCAG 2099	T	TAAAG
			CT CTT TACTCGTTTTG		

		GA GAG ATGAGCAAAAC		
		C AA__		
GAM245	FLJ20039 3'	TGGGATAACTACTTTAAAGAA 1735		_____
		TTCTTTAAAGTA CTCG		
		AAGAAATTCAT GGGT		
		CAATA		
GAM245	FLJ21369 5'	CAAAACCTGAACTTTAAAGGA 2090		ACTC_
		TTCTTTAAAGT GTTTTG		
		AGGAAATTTCA CAAAC		
		AAGTC		
GAM245	KIAA1577 5'	ATGGGTACCCCAGAGAAG 2690		AAA
		CTTCTTT GTACTCGT		
		GAAGAGA CATGGGTA		
		CCC		
GAM245	LOC144524 3'	CAAAACAAGGCATAAAGAAGT 3269		AAGTA C
		ACTTCTTTA CT GTTTTG		
		TGAAGAAAT GA CAAAC		
		ACG_ A		
GAM245	LOC150170 5'	CAAAATGGAACCTTTAAACAGT 3143	TC	A T
	A	TACT TTTAAAGT C CGTTTG		
		ATGA AAATTTCA G GTAAAC		
		CA A_		
GAM245	LOC150175 5'	CAAAATGGAACCTTTAAACAGT 3144	TC	A T
	A	TACT TTTAAAGT C CGTTTG		
		ATGA AAATTTCA G GTAAAC		
		CA A_		
GAM245	LOC150215 5'	CAAAATGGAACCTTTAAACAGT 3145	TC	A T
	A	TACT TTTAAAGT C CGTTTG		
		ATGA AAATTTCA G GTAAAC		
		CA A_		
GAM245	LOC150218 5'	CAAAATGGAACCTTTAAACAGT 3146	TC	A T
	A	TACT TTTAAAGT C CGTTTG		
		ATGA AAATTTCA G GTAAAC		
		CA A_		
GAM246	CCRL1 3'	TGTAACCTCCTGTGAATTTA 1697	G	A C
		TAAATTCG CAGGAA GT ACA		
		ATTTAAGT GTCCTT CA TGT		
		_ _ A		
GAM246	PAFAH1B1 3'	TGTGACTTCCAAGTAGAATTTA 741	G A_ A	
		TAAATTC GC GGAA GTCACA		

			ATTTAAG TG CCTT CAGTGT	
			A AA _	
GAM246	PSMB9	3'	TGACTTTCTTCTCAAACCTGGA 956	AA C C
			TCTA TT GG AGGAAAGTCA	
			AGGT AA CT TTCTTTCAGT	
			CC A C	
GAM246	SLC4A4	3'	TGTGACTTTTTATGGAATTAAGA 1055	A GG G
			TCT AATTC CA GAAAGTCACA	
			AGA TTAAG GT TTTTCAGTGT	
			A _ A	
GAM246	TNFAIP1	3'	TGACTTTCCACAGAGACTGGA 1944	AA GGCA
			TCTA TTC GGAAAGTCA	
			AGGT GAG CCTTTCAGT	
			CA ACAC	
GAM246	CAT56	3'	GTGACTTCCCAGCACTAGA 2149	AATT CG A A
			TCTA GC GG AAGTCAC	
			AGAT CG CC TTCAGTG	
			CA_ A C	
GAM246	FLJ10520	3'	TGTGACTTTCTGGACCTTAGA 1785	ATTC CA_
			TCTAA GG GGAAAGTCACA	
			AGATT CC TCTTTCAGTGT	
			_ AGG	
GAM246	FLJ14001	5'	TGCGACCCCCCTGCCCGAAT 2081	_ AAA A
			ATTC GGCAGG GTC CA	
			TAAG CCGTCC CAG GT	
			CC CCC C	
GAM246	FLJ14917	3'	TGTGACTTTCCTGGTGCATCCA 2290	AA T G
	GG		TCT AT CG CAGGAAAGTCACA	
			GGA TA GT GTCCTTTCAGTGT	
			CC C G	
GAM246	KIAA0618	3'	TGTGACTTTGCCCAAATTTG 1564	C CA _
			TAAATT GG GG AAAGTCACA	
			GTTTAA CC CC TTTTCAGTGT	
			A _ G	
GAM246	KIAA1750	3'	GACTTTCCCATTTTAG 2812	TTC CA
			CTAAA GG GGAAAGTC	
			GATTT CC CCTTTCAG	
			TA_ _	
GAM246	MAGEF1	3'	GTGACTTTAAGGATTTAGA 2555	GGCAGG
			TCTAAATTC AAAGTCAC	

			AGATTTAGG	TTTCAGTG	
			AA__		
GAM246	LOC253017	5'	TGACTTTACCAATTTA	3685	C CAG
			TAAATT GG GAAAGTCA		
			ATTTAA CC CTTTCAGT		
			_ A_		
GAM246	LOC51705	3'	TGACTTTCCTTAATGTTTA	1674	TCGGC
			TAAAT AGGAAAGTCA		
			ATTTG TCCTTTCAGT		
			TAAT_		
GAM247	BCL11B	3'	AATGGTGGGTCTATAAATTTGT	2019	AT TT
			ATAAATTTATA G CGCCATT		
			TGTTTAAATAT T GTGGTAA		
			C_ GG		
GAM247	FGFR4	3'	AATGGCGTTTTATAAATT	2022	TGTT
			AATTTATAA CGCCATT		
			TTAAATATT GCGGTAA		
			TT_		
GAM247	FGFR4	3'	AATGGCGTTTTATAAATT	887	TGTT
			AATTTATAA CGCCATT		
			TTAAATATT GCGGTAA		
			TT_		
GAM247	FLJ22833	3'	AATGGCCGGGGACTTATAAAT	2015	T ____
			ATTTATAA GTTC GCCATT		
			TAAATATT CAGG CGGTAA		
			_ GGC		
GAM247	SSH2	3'	AATGGCCGGCTCTGCAAATTTA	2625	A AT TC
	T		ATAAATTT TA GT GCCATT		
			TATTTAAA GT CG CGGTAA		
			C CT GC		
GAM248	RARB	3'	TTCACAAGCCATTAGGGA	792	AA C
			TCCCTAAT CTT GTGAA		
			AGGGATTA GAA CACTT		
			CC _		
GAM248	RARB	3'	TTCACAAGCCATTAGGGA	1663	AA C
			TCCCTAAT CTT GTGAA		
			AGGGATTA GAA CACTT		
			CC _		
GAM248	BTN2A2	3'	CACTTAGAAGTTATTGAGGA	1344	C ____
			TCC TAATAACTTC GTG		

			AGG GTTATTGAAG CAC		
			A ATT		
GAM248	ZNF337	3'	TTACCTGGGCTATTGGGGA 2806	A_ TC	
			TCCCTAATA CT GTGA		
			AGGGGTTAT GG CATT		
			CG TC		
GAM248	LOC139231	3'	TCACTTGAGAAGTTGTTAGG 3021	_____	
			CCTAATAACTTC GTGA		
			GGATTGTTGAAG CACT		
			AGTT		
GAM248	LOC221399	5'	CACTCAAGTCATTAGGGA 3622	A C_	
			TCCCTAAT ACTT GTG		
			AGGGATTA TGAA CAC		
			C CT		
GAM249	DKFZp762E1511	3'	AGGTTGGAAATGCACTGAA 2530	C AT	
			TTCAG GTG TTTCCAACCT		
			AAGTC CGT AAAGGTTGGA		
			A _		
GAM249	LOC123591	5'	AGGTTGGAAAAGGCTCCGC 3032	T _	
			GCG GA TTTTCCAACCT		
			CGC CT AAAAGGTTGGA		
			_ CGG		
GAM250	EFNB2	3'	GTTGAAAAGCCAAAGGT 1085	C TTA	
			GCCT TGGCTTT TCAGC		
			TGGA ACCGAAA AGTTG		
			A _		
GAM250	FACL4	5'	AGGCTTTCAAAAGCCAAAG 2025	C TATC	
			CT TGGCTTTT AGCCT		
			GA ACCGAAAA TCGGA		
			A CTT_		
GAM250	GATA2	3'	AGGCTGGGCTGAGCCAAAGC 892	CTC TTTA	
			GC TGGCTT TCAGCCT		
			CG ACCGAG GGTCGGA		
			AA_ TCG_		
GAM250	IRS2	3'	CTGATAAAAAGAGGC 2540	GGCT	
			GCCTCT TTTTATCAG		
			CGGAGA AAAATAGTC		

GAM250	PAH	5'	AGGCCCTAAAAAGCCAGAG 725	TCA	
			CTCTGGCTTTTTA GCCT		

GAGACCGAAAAAT CGGA
 CC_
 GAM250 PODXL 3' GCTGCACAGGAGGCCAGA 1207 AT_
 TCTGGCTTTT CAGC
 ||||| |||
 AGACCGGAGGA GTCG
 CAC
 GAM250 RPL15 3' GCTGGTGAGCCAGTGGC 973 T TTT
 GCC CTGGCTT ATCAGC
 || ||||| |||||
 CGG GACCGAG TGGTCG
 T _
 GAM250 SERPINE1 3' AGGCTGGTGACAGGCCAAAGGC 758 C T
 GCCT TGGCTT TTATCAGCCT
 ||| ||||| |||||
 CGGA ACCGGA AGTGGTCGGA
 A C
 GAM250 ABIN-2 3' GCTTAAGCCAGAGCTA 2057 C TTTATC
 TAGC TCTGGCTT AGC
 ||| ||||| |||
 ATCG AGACCGAA TCG
 _ T____
 GAM250 C20orf48 5' GGCCGAGGGACAAAGGCTA 2118 C G TTTA A
 TAGCCT TG CTT TC GCC
 ||||| || ||| |||
 ATCGGA AC GGG AG CGG
 A A _ C
 GAM250 C9orf7 3' AGACTGGCTTAAGCCAGGAGC 1724 CT TTTA C
 GC CTGGCTT TCAG CT
 || ||||| ||| ||
 CG GACCGAA GGTC GA
 AG TTC_ A
 GAM250 DUSP10 3' CTGACAAATTAAGGAGGTTA 1364 GGCTT A
 TAGCCTCT TTT TCAG
 ||||| ||| |||
 ATTGGAGG AAA AGTC
 AATT_ C
 GAM250 DUSP10 3' CTGACAAATTAAGGAGGTTA 2501 GGCTT A
 TAGCCTCT TTT TCAG
 ||||| ||| |||
 ATTGGAGG AAA AGTC
 AATT_ C
 GAM250 ERMAP 3' GCTGATGGTCCTGTCCAAAGGC 1838 C _ TTT_
 TA TAGCCT TGG C TTATCAGC
 ||||| ||| | |||||
 ATCGGA ACC G GGTAGTCG
 A T TCCT
 GAM250 FLJ12892 3' GCTGATAAAGAAGTGCTA 2802 CT GGC C
 TAGC CT TTTTATCAG C
 ||| || ||||| |||

			ATCG GA AGAAATAGTC G		
			T_ ____ A		
GAM250	FLJ22059	5'	GA CTGGAGAGCCAGAGGC 2003		_
			GCCTCTGGCTTTTTTA TC		
			CGGAGACCGAGAGGT AG		
			C		
GAM250	HEMK	3'	GGCCAAAGCCAGAGACT 1669 C		TTATCA
			AG CTCTGGCTTT GCC		
			TC GAGACCGAAA CGG		
			A C_____		
GAM250	KIAA0227	3'	GGGCCCCAAAAGACCAGAGGC 2578		_ TATCA
			GCCTCTGG CTTT GCCT		
			CGGAGACC GAAAA CGGG		
			A CCC__		
GAM250	KIAA0527	3'	GAATAAAAGCCAGAGACTG 3684 C		TA
			TAG CTCTGGCTTT TC		
			GTC GAGACCGAAAA AG		
			A TA		
GAM250	KIAA1244	3'	AGGCTTCAGTAAAGCAGAGGCT 2930		G TTATC
	A		TAGCCTCTG CTTT AGCCT		
			ATCGGAGAC GAAA TCGGA		
			_ TGA CT		
GAM250	KIAA1649	3'	TGAAAAAAACCAGAGACT 2771 C		C A
			AG CTCTGG TTTT TCA		
			TC GAGACC AAAAA AGT		
			A _ A		
GAM250	KIAA1981	3'	AGGCCACGGGAGCCGAGGC 3431		T TATCA
			GCCTC GGCTTT GCCT		
			CGGAG CCGAGGG CGGA		
			_ CAC__		
GAM250	MGC2306	3'	AGGCTGGGCTGAGCCAAAGC 2266		CTC TTTA
			GC TGGCTT TCAGCCT		
			CG ACCGAG GGTCGGA		
			AA_ TCG_		
GAM250	RPL39L	5'	GTGGGAAAAAAGCAGAGGC 2352		G A A
			GCCTCTG CTTTTT TC GC		
			CGGAGAC GAAAAA GG TG		
			_ A G		
GAM250	SNPH	3'	CTGAAAAAGCCAGAGGC 1531		TA
			GCCTCTGGCTTT TCAG		

CGGAGACCGAAAA AGTC

GAM250 TMG3 3' GCCCCCGGGAAGAGCCAAAGGC 2053 C ATCA__
GCCT TGGCTTTTT GC
||||| ||
CGGA ACCGAGAAG CG
A GGCCCC

GAM250 LOC145240 3' GCTCGAAAAGGCAAAGGCTA 3076 C G ATC
TAGCCT TG CTTTTT AGC
||||| || |||
ATCGGA AC GAAAAG TCG
A G C__

GAM250 LOC146287 5' AGGCTGAACAGCAAACCCAGAG 3284 C TTA__
GC GCCTCTGG TTT TCAGCCT
||||| || |||
CGGAGACC AAA AGTCGGA
C CGACA

GAM250 LOC148696 5' AGACTGTACAGGAAACCTAAGG 3301 CT C AT_ C
C GCCT GG TTTTT CAG CT
||| || ||| |||
CGGA CC AAGGA GTC GA
AT A CAT A

GAM250 LOC150577 3' AGGCCGACAACCACCAGAAGCT 3330 C CTTTTTA A
G TAGC TCTGG TC GCCT
||||| || |||
GTCG AGACC AG CGGA
A ACCAAC_ C

GAM250 LOC151521 3' TGTTTAAAAACCCAAAGGC 3347 C C T_
GCCT TGG TTTTCA CA
||||| ||| ||
CGGA ACC AAAAAT GT
A C TT

GAM250 LOC157273 5' AGGCTGGATGAAGCCAGGGGCT 3379 TTA
A TAGCCTCTGGCTTT TCAGCCT
||||| |||
ATCGGGGACCGAAG GGTCGGA
TA_

GAM250 LOC163682 5' GAGCCAAAAGCCAGAGCCTA 3398 C TA_
TAG CTCTGGCTTTT TC
||| ||| ||| ||
ATC GAGACCGAAAA AG
C CCG

GAM250 LOC221749 3' GCTGAGGTCACAGCCGGAGGC 3549 TTTTA_
GCCTCTGGCT TCAGC
||||| |||
CGGAGGCCGA AGTCG
CACTGG

GAM250 LOC222234 3' AGGCTGATGCCCCAAAAGGC 3646 C_ CTTTT
GCCT TGG TATCAGCCT
||| ||| ||| |||

CGGA ACC GTAGTCGGA
AA CC___

GAM251 ADAMTSL1 3' AACCATTAGAGGTGCAATCTAC 2479 _ CA_ TTA
A TG AGAT ACT TCTAATGGTT
|| ||| ||| |||||
AC TCTA TGG AGATTACCAA
A ACG ___

GAM251 KIAA1862 3' AACCACCAGCCGTTCTGATCT 2834 ACTTTAT AA
CA TGAGATCA CT TGGTT
||||| || |||
ACTCTAGT GA ACCAA
CCTTGCC CC

GAM251 LOC153951 5' AACCATGAAAGACAGAGTTGAT 3184 A A_
CTCA TGAGATCAACTTT TCT ATGGTT
||||||| ||| |||
ACTCTAGTTGAGA AGA TACCAA
C AAG

GAM251 LOC221596 3' AACCATTAGACAAAACCTCTTCT 3548 TCAAC A
AGA TTT TCTAATGGTT
||| ||| |||||
TCT AAA AGATTACCAA
TCTCA C

GAM252 ESAM 3' CTTTACTGTGGGAAAACCATCT 2461 GA A AC
CA TG AT GTTTTTT TAGTAAAG
|| || ||||| |||||
AC TA CAAAAGG GTCATTTT
TC C GT

GAM252 KIAA0379 3' ACTAAGAAAACCTATTTC 2809 AC
TGGAATAGTTTTTT TAGT
||||||| |||
ACTTTATCAAAAGA ATCA

GAM252 LOC161784 3' CTTTAATTTTAAAAAACGTATT 3241 _ CTAG
CCA TGGAATA GTTTTTTA TAAAG
||||| ||||| |||
ACCTTAT CAAAAAAT ATTTC
G TTTA

GAM252 LOC255229 3' CTTTAATTTTAAAAAACGTATT 3676 _ CTAG
CCA TGGAATA GTTTTTTA TAAAG
||||| ||||| |||
ACCTTAT CAAAAAAT ATTTC
G TTTA

GAM253 HIP2 3' TGTTTTTAACATGGATC 1201 G
GAT CCATGTTAAAAATG
||| |||||
CTA GGTACAATTTTGT

GAM253 ITK 3' TATTTTAAACATGAATC 1224 GC
GAT CATGTTAAAAATG
||| |||||

CTA GTACAATTTTAT
A_
GAM253 ONECUT1 3' GCGGACATCTTTTAAGAT 2622 G _
AT TTA AAA ATGTCCGC
|| ||||| |||||
TA AATTTT TACAGGCG
G C
GAM253 BTN3A2 5' GACATTTTTGGCAGAGCAT 1354 CA
ATGC TGT TAAAAATGTC
|||| |||||
TACG ACGGTTTTTACAG
AG
GAM253 BTN3A3 5' GACATTTTTGGCAGAGCAT 1343 CA
ATGC TGT TAAAAATGTC
|||| |||||
TACG ACGGTTTTTACAG
AG
GAM253 IDN3 3' GGCAAACATTTTTGTGG 2416 GTT CC
CCAT AAAAATGT GCC
|||| ||||| ||
GGTG TTTTACA CGG
_ AA
GAM253 KIAA1635 3' CGGACATTTATTTGCATC 2803 CAT TAA
GATGC GT AAATGTCCG
|||| || |||||
CTACG TA TTTACAGGC
TT_ _
GAM253 LOC130106 3' GGCAAACACCTGACATGGCA 3008 AAAA CC
TGCCATGTTA TGT GCC
||||||| ||| ||
ACGGTACAGT ACA CGG
CC_ AA
GAM253 LOC151031 3' GGCATCTTAACATGGCATT 3403 AA
GATGCCATGT TAA ATGTC
||||||| ||||
TTACGGTACAATT TACGG
C_
GAM253 LOC162545 3' GGCATCTACATGGCATC 3402 TAAAA
GATGCCATGT ATGTC
||||||| ||||
CTACGGTACA TACGG
TC_
GAM253 LOC165666 5' GGCAGGGTTTTTAAATAGCATC 3257 CATG GT _
GATGC TTA AAAAAT CC GCC
|||| ||||| ||| ||
CTACG AATTTTGT GG CGG
ATA_ _ A
GAM254 MEN1 5' AATGACTTGGGGATGATGC 3599 A
GCATCATCTTTAG TCATT
||||||| ||||

			CGTAGTAGGGGTT AGTAA		
			C		
GAM254	SRD5A2	5'	AATTAATGATGAGGTTACATGC 2525	C__	TAG
		T	AGCAT ATCTT ATCATTAATT		
			TCGTA TGGAG TAGTAATTAA		
			CAT _		
GAM254	DKFZP564O043	3'	TGATGTCTGAAGATAATGCT 3566	C	T
			AGCAT ATCTTTAGA CATTA		
			TCGTA TAGAAGTCT GTAGT		
			A _		
GAM254	FLJ22794	5'	AATTAATGACAGCTTTGAAGAT 3533	__	
			ATCTTTAGA TCATTAATT		
			TAGAAGTTT AGTAATTAA		
			CGAC		
GAM254	HTMP10	3'	AATTGTTATCTAAAGATGATTC 2322	C	CAT
		T	AG ATCATCTTTAGAT TAATT		
			TC TAGTAGAAATCTA GTTAA		
			T TT_		
GAM254	SEC24B	3'	AATTAATGGTAACGATGATGCT 1288		TTTAG
			AGCATCATC ATCATTAATT		
			TCGTAGTAG TGGTAATTAA		
			CAA_		
GAM254	LOC196812	5'	AATGATCTAGTCAGAAGCT 3466	A	ATCT
			AGC TC TTAGATCATT		
			TCG AG GATCTAGTAA		
			A ACT_		
GAM255	ATRN	3'	TAAGGGAGGTCTGTGCATTTTA 2480	A	AAT A
			TAAAAT CA GAC TTCCCTTA		
			ATTTTA GT CTG GAGGGAAT		
			C GT_ _		
GAM255	CD59	3'	AATGACATTTGTATTTTA 760	A	
			TAAAATACAAATG CATT		
			ATTTTATGTTTAC GTAA		
			A		
GAM255	CENTD1	3'	GGATCATTTGTATTTTG 1615		CAT
			TAAAATACAAATGA TCC		
			GTTTTATGTTTACT AGG		
			__		
GAM255	CENTD1	3'	GGATCATTTGTATTTTG 2474		CAT
			TAAAATACAAATGA TCC		

GTTTTATGTTTACT AGG

GAM255 CLNS1A 3' GAGGGTATTTGTAGTTTA 816 A ACATT
TAAA TACAAATG CCCTT
||||| |||||
ATTT ATGTTTAT GGGAG
G

GAM255 NDUFA5 3' AGTGTCATTTTATTTTA 1169 C
TAAAATA AAATGACATT
||||| |||||
ATTTTAT TTTACTGTGA

GAM255 PBX3 3' GGAATCATAATCATTTGTATTT 1279 C____
AAATACAAATGA ATTCC
||||| |||||
TTTATGTTTACT TAAGG
AATAC

GAM255 SCD 3' TAAGGGAAGATCACTGTAGTTT 1178 A AA CA
A TAAA TACA TGA TTCCCTTA
||||| |||||
ATTT ATGT ACT AAGGGAAT
G C_ AG

GAM255 SLC2A2 3' TAAGGGAACCGTCTGTTTTTA 731 T AAT A_
TAAAA ACA GAC TTCCCTTA
||||| |||||
ATTTT TGT CTG AAGGGAAT
_ _ CC

GAM255 TCF7 3' TAAGGGAATCCCTTGTA 998 AT CA
TACAA GA TTCCCTTA
||||| |||||
ATGTT CT AAGGGAAT
CC _

GAM255 DKFZP586B0923 3' AAGACATGTGATTTGTATTTTA 3589 G TCC
TAAAATACAAAT ACAT CTT
||||| |||||
ATTTTATGTTTA TGTA GAA
G CA_

GAM255 DKFZp761K1824 3' TAAGAGAATGTTGTGTATTT 1726 AA C
AAATACA TGACATTC CTTA
||||| |||||
TTTATGT GTTGTAAG GAAT

GAM255 FLJ14624 3' TAAGGAAATATTTATTTGTATT 2913 C_ C
TT AAAATACAAATGA ATT CCTTA
||||| |||||
TTTTATGTTTATT TAA GGAAT
TA A

GAM255 GRO3 3' TAAGGGAATGTATGTA 2636 AATG
TACA ACATTCCCTTA
||||| |||||

		ATGT TGTAAGGGAAT	
		A__	
GAM255	KIAA0907 3'	AAGAAAGTTTTATTGTATTTT 1596	C CC
	A	TAAATACAAATGA ATT CTT	
		ATTTTATGTTTATT TGA GAA	
		T AA	
GAM255	MGC14289 3'	AAGGATACTGTCATTTGCATTT 2382	A TTC_
	T	AAAAT CAAATGACA CCTT	
		TTTTA GTTTACTGT GGAA	
		C CATA	
GAM255	NLP_1 3'	AAGGGAATTTTTTTGT 1395	T C
		TACAAA GA ATTCCCTT	
		ATGTTT TT TAAGGGAA	
		T _	
GAM255	PARVA 3'	GAGTGCTCCTTTTGTATTTTA 1802	T_ _
		TAAAATACAAA GA CATTC	
		ATTTTATGTTT CT GTGAG	
		TC C	
GAM255	PRO2176 3'	AAGGGCTGCATTGTATTTTA 1833	A A TT
		TAAAATACAA TG CA CCCTT	
		ATTTTATGTT AC GT GGGAA	
		_ _ C_	
GAM255	TIMM22 3'	AAGGTTGGTTTATTTGTATTTT 3104	_ ATTG
	A	TAAATACAAATGA C CCTT	
		ATTTTATGTTTATT G GGAA	
		T GTT_	
GAM255	LOC143914 5'	GAGGGAGTCATTTTATT 3061	C AT
		AATA AAATGAC TCCCTT	
		TTAT TTTACTG AGGGAG	
		- -	
GAM255	LOC154862 3'	AAGGGTGAAATTTGTGTTTTTA 3193	GA TT
		TAAAATACAAAT CA CCCTT	
		ATTTTGTGTTTA GT GGGAA	
		AA _	
GAM255	LOC158314 3'	AAGGGAATGTTTAAGCCATTT 3386	ACAAAT
		AAAT GACATTCCCTT	
		TTTA TTGTAAGGGAA	
		CCGAAT	
GAM255	LOC221405 3'	AAGGGACTATTTGTATT 3623	ACAT
		AATACAAATG TCCCTT	

			TTATGTTTAT AGGGAA		
			C___		
GAM256	YES1	3'	ATGATGAATTTATCAGCGT 1209	A	CCG
			AC CTGATAAA CATTAT		
			TG GACTATTT GTAGTA		
			C AA_		
GAM256	ACTR3	3'	GATGGGATTTATCAGTGT 1238		_ G
			ACACTGATAAA CC CATT		
			TGTGACTATTT GG GTAG		
			A _		
GAM256	GENX-3414	3'	CAGATAATGCTTCCAGTG 1073		ATAAACC
			CACTG GCATTATCTG		
			GTGAC CGTAATAGAC		
			CTT___		
GAM256	HT007	3'	ACAGATAATAAATATCCAGTGT 1832		_ AACCGC
			ACACTG ATA ATTATCTGT		
			TGTGAC TAT TAATAGACA		
			C AAA___		
GAM256	SPRY4	3'	ACAGACAATGCAGGGGCAG 2175	ATAAA _	A
			CTG CC GCATT TCTGT		
			GAC GG CGTAA AGACA		
			GG___ A C		
GAM257	POF1B	3'	GAACCATGCTGCTACCCAA 2114		_ TG A
			TTGGGTAGT GT ATG TTC		
			AACCCATCG CG TAC AAG		
			T _ C		
GAM257	RODH-4	5'	CATGGGTAGCTACCCAATAAG 1050		GT_ G
			TTTATTGGGTAGT T ATG		
			GAATAACCCATCG G TAC		
			ATG G		
GAM257	SFRS12	3'	GAATCATTGGGACTACCCA 2472		G TG
			TGGGTAGT T ATGATTC		
			ACCCATCA G TACTAAG		
			G GT		
GAM257	TCBAP0758	3'	GAATCCCCAACACCCAATAAA 2181		AGT AT
			TTTATTGGGT GTTG GATTC		
			AAATAACCCA CAAC CTAAG		
			_ CC		
GAM258	HYOU1	3'	CTCTGTTTTCCCCATTCA 2537	T TA	
			C AGTG GAAAACAGAG		

			A TTAC CTTTTGTCTC		
			C CC		
GAM258	ITGB1	3'	ATCTTGTTTCACACTAGT 910	A A G	
			ACTAGTGT GAAA CA AGAT		
			TGATCACA CTTT GT TCTA		
			- - -		
GAM258	MAGEA4	3'	TATCTCTGTTTCCTTTTACA 922	___	
			TGTAGAA AACAGAGATA		
			ACATTTT TTGTCTCTAT		
			CCT		
GAM258	PTTG1IP	3'	ATCTCTGTTTCTAGATTTAGT 1100	_ G A	
			ACTAG T TAGAAA CAGAGAT		
			TGATT A ATCTTT GTCTCTA		
			T G _		
GAM258	RAB27A	3'	ATCTCTGTCTTTACCAGC 1129	___ AA	
			GT GTAGA ACAGAGAT		
			CG CATT TGTCTCTA		
			AC C_		
GAM258	SALL2	5'	ATCTCTGCTTCACAGT 2671	A T AAAA	
			ACT GTG AG CAGAGAT		
			TGA CAC TC GTCTCTA		
			_ T ____		
GAM258	SFRS7	3'	TGCTTTCTACATTAGTTA 2529	A	
			TAAGTAGTGTAGAAA CA		
			ATTGATTACATCTTT GT		
			C		
GAM258	SLC19A2	3'	GTCTTTCTACATAGTTA 2836	G AAACA	
			TAAGTA TGTAGA GAGAT		
			ATTGAT ACATCT TTCTG		
			- - -		
GAM258	C20orf97	3'	ATCTCTGTCCTCTTGATTA 1946	GT AA	
			TAGT AGA ACAGAGAT		
			ATTA TCT TGTCTCTA		
			GT CC		
GAM258	CYB5-M	3'	TCTGTTTTTCTACCCTAG 2150	T _	
			CTAG GTAGAAA ACAGA		
			GATC CATCTTT TGTCT		
			C TT		
GAM258	CYB5-M	3'	TCTGTTTTTCTACCCTAG 3658	T _	
			CTAG GTAGAAA ACAGA		

			GATC CATCTTT TGTCT		
			C TT		
GAM258	FAM8A1	3'	TATCCCTGGGTTACACTA 1675	AAAA	A
			TAGTGTAG CAG GATA		
			ATCACATT GTC CTAT		
			GG__ C		
GAM258	FLJ10853	5'	TCTGCCTACACTATTTA 1804	C	AAAA
			TAA TAGTGTAG CAGA		
			ATT ATCACATC GTCT		
			T C__		
GAM258	FLJ14327	3'	ATCTCTGTCTACAAACTAG 2111	__	AAA
			CTAGT GTAGA CAGAGAT		
			GATCA CATCT GTCTCTA		
			AAA __		
GAM258	FLJ14681	5'	TATCTCTGCCTTCCAGGCAT 2285	A__	AA
			GTGT GAA CAGAGATA		
			TACG CTT GTCTCTAT		
			GAC CC		
GAM258	HNRPA3	3'	ATCTCTATTCTACATTTA 1245	T	AAC
			C AGTGTAGAA AGAGAT		
			A TTACATCTT TCTCTA		
			T A__		
GAM258	KIAA0426	3'	TATCTCTGTTTTGGGAGACAGG 1532	A	GTAG__
	T		ACT GT AAAACAGAGATA		
			TGG CA TTTTGTCTCTAT		
			A GAGGG		
GAM258	KIAA0594	3'	TATCTCTAAGTTATACTAATTA 2707	C	AAAAC
			TAA TAGTGTAG AGAGATA		
			ATT ATCATATT TCTCTAT		
			A GAA__		
GAM258	KIAA0635	5'	ATCTCAATTTTACACTAG 1513		AAACA
			CTAGTGTAGA GAGAT		
			GATCACATTT CTCTA		
			AA__		
GAM258	PDZD2	5'	ATCCCTGTTTTCGGGGACTA 3181	GTA__	A
			TAGT GAAAACAG GAT		
			ATCA CTTTTGTC CTA		
			GGGG C		
GAM258	PP1628	5'	ATCTCTGTTCCCATCCCCAGT 2145	A__	TA AA
			ACT GTG GA ACAGAGAT		

			TGA TAC CT TGTCTCTA		
			CCCC CC _		
GAM258	TIP120A	3'	TATCCCTGTTGCGCACACTA	1829	AGAA A
			TAGTGT AACAG GATA		
			ATCACA TTGTC CTAT		
			CGCG C		
GAM258	LOC220988	3'	ATCTCTATTCTACATTTA	3501	T AAC
			C AGTGTAGAA AGAGAT		
			A TTACATCTT TCTCTA		
			T A_		
GAM258	LOC221337	5'	ATCTCTGTTCTCTAAGCAC	3555	_ A
			GTGT AGA AACAGAGAT		
			CACG TCT TTGTCTCTA		
			AA C		
GAM258	LOC257017	5'	TATCTCTGTTTTGGCAT	3737	AG
			GTGT AAAACAGAGATA		
			TACG TTTTGTCTCTAT		
			G_		
GAM258	LOC90829	5'	TATCTCTGTTTTGGTACCAGT	2680	A AG
			ACT GTGT AAAACAGAGATA		
			TGA CATG TTTTGTCTCTAT		
			C G_		
GAM259	KIAA0268	3'	ACAAAACAATGCTGAAGTTAAT	2874	T A T
	AT		ATATTA CT CG CATTGTTTTGT		
			TATAAT GA GT GTAACAAAACA		
			T A C		
GAM259	KIAA1255	3'	ACAAAACAACCTCTGAGATGA	2783	A TCA
			TTATCT CG TTGTTTTGT		
			AGTAGA GT AACAAAACA		
			_ CTC		
GAM259	MGC5370	3'	CAAAACATCAGATAATAT	2275	ACGTCAT
			ATATTATCT TGTTTTG		
			TATAATAGA ACAAAC		
			CT_		
GAM259	UK114	3'	ACAAAATGTTATATAGATAATA	1255	CG CAT
	T		ATATTATCTA T TGTTTTGT		
			TATAATAGAT A GTAAAACA		
			AT TT_		
GAM260	OSBPL8	3'	CTACATATGAGTATAATA	1927	CC
			TATTATACTCATG TAG		

		ATAATATGAGTAT ATC	
		AC	
GAM260	LOC147463 3'	CTATTACTATTGCAGGAATATA 3109	C A C_
	A	TTATA TC TGC TAGTAATAG	
		AATAT AG ACG ATCATTATC	
		A G TT	
GAM260	LOC151201 5'	ATTAGTAGCATGAGTATAA 3340	C G
		TTATACTCATGC TA TAAT	
		AATATGAGTACG AT ATTA	
		_ G	
GAM261	JJAZ1 3'	AGCACTGTGGTTGAGTAACATC 1621	_ TT_
		GATGTTAC CAATCG TGCT	
		CTACAATG GTTGGT ACGA	
		A GTC	
GAM261	SIAT1 3'	AGGGGATTGGAAACATCGT 986	A G
		ACGATGTT CCAATC TTT	
		TGCTACAA GGTTAG GGA	
		A G	
GAM261	ATP6V0A1 3'	AGGGGACACTGGTAACAT 1191	ATC G
		ATGTTACCA GTTT CT	
		TACAATGGT CAGG GA	
		CA_ G	
GAM261	FLJ21313 3'	AGCGAATTGGTTACATCGTT 2038	T ATC
		AACGATGT ACCA GTTTGCT	
		TTGCTACA TGGT TAAGCGA	
		T _	
GAM261	FLJ23548 3'	AGCAAATTTGGCTCGATAATAT 2068	_____ TC
	CG	CGATGTTA CCAA GTTTGCT	
		GCTATAAT GGTT TAAACGA	
		AGCTC _	
GAM261	LOC196510 3'	GCAAAAGGCAACATTGTT 3414	A AATCG
		AACGATGTT CC TTTGC	
		TTGTTACAA GG AAACG	
		C A_____	
GAM261	LOC200220 3'	GCAAAAGGCAACATTGTT 3443	A AATCG
		AACGATGTT CC TTTGC	
		TTGTTACAA GG AAACG	
		C A_____	
GAM261	LOC222234 3'	AGCAAGATGGGTAACATC 3645	A GT
		GATGTTACC ATC TTGCT	

CTACAATGG TAG AACGA
G _
GAM262 CDKN1B 3' GACAAAATTTTCTCATTTTCTT 1082 TGT____ C
TTCAC TGTAAAAGAA AAA TTTGTC
||||||| ||| |||||
CACTTTTCTT TTT AAACAG
TTACTCT A
GAM262 CSPG3 3' ACAAAGGTCTTCTTTTCCT 1107 T TGTA
AG GAAAAGAA CTTTGT
|| ||||| |||||
TC CTTTCTT GAAACA
_ CTG_
GAM262 ITSN1 3' ACAAAGTTTACATTTTCACT 981 AAAA
AGTG GAATGTAACTTTGT
||| |||||
TCAT TTTACATTTGAAACA
AC_
GAM262 MBNL 5' GACATGCAACAGTCTTTTCACT 1937 A AAACCTT
AGTGAAAAGA TGT TGTC
||||||| ||| |||||
TCACTTTTCT ACA ACAG
G ACGT_
GAM262 MEFV 3' GACAAAGTTTTGCTCTTGTCAC 719 A ATGT
GTGA AAGA AAACCTTGTC
||| ||| |||||
CACT TTCT TTTGAAACAG
G CGT_
GAM262 NR3C1 3' GACAAAGTAATTCCTCTCACT 716 AAA GTAA
AGTGA GAAT ACTTTGTC
|||| ||| |||||
TCACT CTTA TGAAACAG
CTC A_
GAM262 TIF1 3' ACAAAGACATTCTTCCCACT 2564 AA AAA
AGTG AAGAATGT CTTTGT
||| ||||| |||||
TCAC TTCTTACA GAAACA
CC _
GAM262 BZW1 3' ACAAATGGGTATTCTTTTCAT 1516 AAAC
GTGAAAAGAATGT TTTGT
||||||| |||
TACTTTTCTTATG AAACA
GGT_
GAM262 FLJ10998 3' GACAAAGTCTCGCTCTGTCAC 1811 AA A TAA
GTGA AGA TG ACTTTGTC
||| ||| |||||
CACT TCT GC TGAAACAG
G_ C TC_
GAM262 FLJ12409 3' GACAAAGTGATGTTTCTTCCC 2137 AA TG A_
AT GTG AAGAA TA ACTTTGTC
||| ||||| || |||||

			TAC TTCTT GT TGAAACAG		
			CC TT AG		
GAM262	FLJ32356	3'	ACAAAGCTTGATGTTTTCACT 2492	GAATG	A
			AGTGAAAA TAA CTTTGT		
			TCACTTTT GTT GAAACA		
			GTA__ C		
GAM262	GRP3	3'	GTTTACATCCTTCCCACT 1624	AA	A
			AGTG AAG ATGTAAAC		
			TCAC TTC TACATTTG		
			CC C		
GAM262	KIAA0210	3'	GACACTGTTTACGTCCCTCCCA 1538	AAA A_	TT
		CT	AGTG AG ATGTAAAC TGTC		
			TCAC TC TGCATTTG ACAG		
			CC_ CC TC		
GAM262	MGC2477	3'	GACAAAAGCAAGGCCCTTTTC 2054	AAT AAAC_	
		ACT	AGTGAAAAG GT TTTGTC		
			TCACTTTTC CG AAACAG		
			CC_ GAACGA		
GAM262	MGC2742	5'	ACAAAAGGGTATTTCTTTTCTC 2039	T T AA _	
		T	AG GAAAAGAA GTA CTTT GT		
			TC CTTTCTT TAT GAAA CA		
			T _ GG A		
GAM262	MRF2	3'	GTTCTCATTCTTTTCACT 3056	TA	
			AGTGAAAAGAATG AAC		
			TCACTTTTCTTAC TTG		
			TC		
GAM262	P2RXL1	3'	GAGGGCCACACTCTTTTCAC 1213	A AAA	
			GTGAAAAGA TGT CTTT		
			CACTTTTCT ACA GGAG		
			C CCG		
GAM262	STK38L	3'	GACAAAGTTTAACACCTTCACT 2844	AAGAATG	
			AGTGAA TAACTTTGTC		
			TCACTT ATTTGAAACAG		
			CCACA_		
GAM262	LOC151579	3'	ACAAATGGGTATTCTTTTCAT 2859	AAAC	
			GTGAAAAGAATGT TTTGT		
			TACTTTTCTTATG AAACA		
			GGT_		
GAM262	LOC51312	5'	GACAAAATTCATTTTTTCA 1849	TAAAC	
			TGAAAAGAATG TTTGTC		

			ACTTTTTTTAC	AAACAG	
			TTA__		
GAM262	LOC91574	3'	GACAAAGTTCTGTTTCTTCAC	2751	AA TGTA
			GTGA AGAA AACTTTGTC		
			CACT TCTT TTGAAACAG		
			__ TGTC		
GAM263	MAB21L2	5'	CACTACAAACAAACAAACC	1301	CA_ C
			GGTTTGTT TTGT GTG		
			CCAAACAA AACA CAC		
			ACA T		
GAM263	LOC220672	3'	CACGAATAAACAAACTTAA	2565	CATTG
			TTAGGTTTGTT TCGTG		
			AATTCAAACAA AGCAC		
			ATA__		
GAM264	FLRT2	3'	AACTTCACTCTACACTATA	1437	ACAC A C
			TATAGTGTA GA TG AGTT		
			ATATCACAT CT AC TCAA		
			__ C T		
GAM264	KDEL2	3'	AACTTGCAATCCCACTATA	1335	TAACAC _
			TATAGTG GAATGCA GTT		
			ATATCAC CTTACGT CAA		
			__ T		
GAM264	SMT3H2	3'	AAACTGCAATTTGGTTCCAC	1341	T A _
			GTG AAC CGAAT GCAGTTT		
			CAC TTG GTTTA CGTCAAA		
			C _ A		
GAM264	LOC158997	3'	AAACTGCAATTTGGTTCCAC	3230	T A _
			GTG AAC CGAAT GCAGTTT		
			CAC TTG GTTTA CGTCAAA		
			C _ A		
GAM265	APOC4	3'	GTTTCATACTTCTCCAATAAATA	841	C AT T
	AA		TTTAT TATTG GG GTATGAAC		
			AAATA ATAAC CT CATACTTG		
			A CT T		
GAM265	DKFZP434P0721	3'	TTCATACATATATAGATA	2664	TGATG
			TATCTAT GTGTATGAA		
			ATAGATA TACATACTT		
			TA__		
GAM265	FLJ14082	3'	TCATACACACAGATAAA	2129	ATTGATG
			TTTATCT GTGTATGA		

			AAATAGA CACATACT	
			CA_____	
GAM266	LMO7	3'	AATAAACTTGCTGATGCATTT 1202	TAAT T
			AAATGC G CAAGTTTATT	
			TTTACG C GTTCAAATAA	
			TAGT_	
GAM266	LMO7	3'	AATAAACTTGCTGATGCATTT 1643	TAAT T
			AAATGC G CAAGTTTATT	
			TTTACG C GTTCAAATAA	
			TAGT_	
GAM266	CDV-1	3'	AATAAACTTGGTACGTATTT 1466	TAA GT
			AAATGC T CAAGTTTATT	
			TTTATG A GTTCAAATAA	
			C__TG	
GAM266	KIAA1671	3'	TTTGACATCAGCATTTTA 2726	A _
			TAAAATGCT ATGT CAAG	
			ATTTTACGA TACA GTTT	
			C C	
GAM266	SEMA5A	3'	AAACCTTTGAAATTAGCATT 1075	G _
			AATGCTAAT TCAA GTTT	
			TTACGATTA AGTT CAAA	
			A TC	
GAM266	LOC127133	3'	AATAAATGGGAGTTAGCATTTT 3004	G AA
	A		TAAAATGCTAAT TC GTTTATT	
			ATTTTACGATTG AG TAAATAA	
			_ GG	
GAM266	LOC143154	3'	AATTTGACATCACATTTTA 3052	CTA
			TAAAATG ATGTCAAGTT	
			ATTTTAC TACAGTTTAA	
			AC_	
GAM266	LOC219294	3'	AATTTGACATCACATTTTA 3587	CTA
			TAAAATG ATGTCAAGTT	
			ATTTTAC TACAGTTTAA	
			AC_	
GAM267	GARP	3'	TGGAGTTTGAGACTATGGAA 1221	_ TGGA
			TTCCGTAGTC CA TCCA	
			AAGGTATCAG GT AGGT	
			A TTG_	
GAM267	FLJ30213	3'	GATCATGGACCACAGAA 2507	C A G
			TTC GT GTCCATG ATC	

			AAG CA CAGGTAC TAG		
			A C _		
GAM267	LOC196510	3'	GGTCCATGAACTAGGAA	3415	G C
			TTCC TAGT CATGGATC		
			AAGG ATCA GTACCTGG		
			_ A		
GAM267	LOC200220	3'	GGTCCATGAACTAGGAA	3444	G C
			TTCC TAGT CATGGATC		
			AAGG ATCA GTACCTGG		
			_ A		
GAM267	LOC220930	3'	GGTCATAGACTATGGAA	3591	C AT
			TTCCGTAGTC ATGG CC		
			AAGGTATCAG TACT GG		
			A _		
GAM268	ZNF161	3'	ACTAGCAGAACTCTT	1359	TAGT T
			AAGAGTTT TG CTAGT		
			TTCTCAAG AC GATCA		
			_ _		
GAM268	DKFZP566D193	3'	ACTGAATAACTAAAATCTC	3353	_ C
			GAG TTTTAGTTGT TAGT		
			CTC AAAATCAATA GTCA		
			T A		
GAM268	LOC200574	3'	GCTGACTACTAAACTC	3450	T T
			GAGTTTTAGT GTC AGT		
			CTCAAATCA CAG TCG		
			T _		
GAM269	RAD50	3'	TGTTGATAAATCCATCA	1240	A T
			TGA TGGATTTATCA CA		
			ACT ACCTAAATAGT GT		
			_ T		
GAM269	RAD50	3'	TGTTGATAAATCCATCA	2420	A T
			TGA TGGATTTATCA CA		
			ACT ACCTAAATAGT GT		
			_ T		
GAM269	SMURF1	3'	ATGATGTAAATCCACCCA	3564	AA T
			TG TGGATTTA CATCAT		
			AC ACCTAAAT GTAGTA		
			CC _		
GAM269	TRIM9	3'	ATGAATGAAAAATCCATCCA	1611	A A _
			TG ATGGATTT TCAT CAT		

AC TACCTAAA AGTA GTA
 C A A
 GAM269 FLJ13902 3' AACGATGATGATGAACACA 2076 GA
 TG TTTATCATCATCGTT
 || |||||
 AC AAGTAGTAGTAGCAA
 AC
 GAM269 KIAA0650 3' AAACGATGATGATGTTAACC 3427 ATT_
 GG TATCATCATCGTTT
 || |||||
 CC GTAGTAGTAGCAAA
 AATT
 GAM269 MGC16075 3' AAACGATGATGCAGGCTATTCA 2277 ATTTAT
 TGAATGG CATCATCGTTT
 ||||| |||||
 ACTTATC GTAGTAGCAAA
 GGAC__
 GAM270 PAIP2 3' ACTGAAAATAGAATTGG 1687 TATA
 CCA TTTATTTTCAGT
 ||| |||||
 GGT AGATAAAAGTCA
 TA__
 GAM270 PIN4 3' CTGAAAATATTGGGCATC 1282 A ATATATT
 GATG CC TATTTTCAG
 ||| || |||||
 CTAC GG ATAAAAGTC
 _ GTT____
 GAM271 HLA-G 3' TCCTTCCCAATCACCTT 900 AAT
 AAGGTGATTGG GGGA
 ||||| |||
 TTCCACTAACC TCCT
 CCT
 GAM271 HRH2 5' TTCATTCCCAACACCTTA 1984 ATT
 TAAGGTG GGAATGGG
 ||||| |||||
 ATTCCAC CCTTACTT
 AAC
 GAM271 KCNJ15 3' ATTTATTTAACCAATGACCTTA 916 G AATG
 TAAGGT ATTGG GGATAAAT
 ||||| ||||| |||||
 ATTCCA TAACC TTTATTTA
 G AA__
 GAM271 C1orf8 5' ATCTCAGTCTCAATCACC 1161 _ A
 GGTGATTG GA TGGGAT
 ||||| || |||||
 CCACTAAC CT ACTCTA
 T G
 GAM271 FLJ10738 3' ATCCCATCTGGGTCACTT 1798 _TG A
 AGGTGA T GA TGGGAT
 ||||| | |||||

TTCACT G CT ACCCTA
 G GT _
 GAM271 FLJ23511 3' ATCCACAATCCAATTACC 2239 A _
 GGTGATTGGA TG GGAT
 ||||| || ||||
 CCATTAACCT AC CCTA
 A A
 GAM271 GAB3 3' ATTCAGGGTTTCCAATCACC 2377 ____ GG
 GGTGATTGGAA TG AT
 ||||| || ||
 CCACTAACCTT AC TA
 TGGG TT
 GAM271 ITPK1 3' CTCACCCCATCACCTTG 1484 T AA
 TAAGGTGAT GG TGGG
 ||||| || ||||
 GTTCCACTA CC ACTC
 _ CC
 GAM271 TRIP-Br2 3' TCCCCCCCCATCACCTTA 1539 T AAT
 TAAGGTGAT GG GGA
 ||||| || ||||
 ATTCCACTA CC CCCT
 C CC_
 GAM271 LOC152313 3' ATCCCCCTGATCCAATCACCT 3355 AT____
 AGGTGATTGGA GGGAT
 ||||| ||||
 TCCACTAACCT CCCTA
 AGTCC
 GAM271 LOC256642 3' TTTAGGCCCAATACCTTA 3701 A AAT GA
 TAAGGTG TTGG GG TAAA
 ||||| |||| || ||||
 ATTCCAT AACC CC ATTT
 _ ____ GG
 GAM272 C22orf2 3' TTTTATTATTAACGATGT 3655 A
 ACGTC TTTAATAAAAAA
 |||| |||||
 TGTAG AAATTATTTTTT
 C
 GAM272 LOC153277 3' ATACTTAATAAATGACGT 3369 A AAAAA
 ACGTCATTTA TA AGTAT
 ||||| || ||||
 TGCAGTAAAT AT TCATA
 A ____
 GAM273 SH3BP4 3' CAGTGTGCAATTAGTCATTGAC 1506 G A AG
 A TG CAAT ACTAATTG ATATTG
 || |||| ||||| |||||
 AC GTTA TGATTAAC TGTGAC
 A C G_
 GAM273 UFD1L 3' CAACATCTTGGCTTTTAGTTAC 2973 G A ____ TG A
 TGGCA TG CA TAACTAA T AGAT TTG
 || || ||||| | |||||

AC GT ATTGATT G TCTA AAC
 G C TTC GT C
 GAM273 FLJ20081 3' CAATACTCTCAATTATTAACCA 1736 CAA C _
 TGG TAA TAATTGAGA TATTG
 ||| ||| ||||| |||||
 ACC ATT ATTA ACTCT ATAAC
 A _ _ C
 GAM273 KIAA1635 3' GTCCA ACTATTTATTGCCA 2804 C A A
 TGGCAATAA TA TTG GAT
 ||||| || ||| |||
 ACCGTTATT AT AAC CTG
 T C _
 GAM273 PRO1257 5' CAATATCTCATAAGACTACTGC 1848 A ACTAAT
 GCA TA TGAGATATTG
 ||| || ||||| |||
 CGT AT ACTCTATAAC
 C CAGAAT
 GAM273 LOC153020 3' CTCAATCAGTATTGCCA 3177 A A
 TGGCAATA CT ATTGAG
 ||||| || |||||
 ACCGTTAT GA TAACTC
 _ C
 GAM274 BNC 3' TGTTTCTGTTTCATATC 851 T
 GATATGA AACAGGAATA
 ||||| ||||| |||||
 CTATACT TTGTCTTTGT
 _
 GAM274 PROS1 5' TGTCCTTGTTATCACTTC 3407 TA A
 GA TGATAACAGG ATA
 || ||||| |||
 CT ACTATTGTTT TGT
 TC C
 GAM274 FLJ20147 3' ATGTTGTAATTGTCATATC 1738 CAGGA
 GATATGATAA ATAACAT
 ||||| |||||
 CTATACTGTT TGTTGTA
 AA _
 GAM274 KIAA0737 3' ATGTTATTCCCCATTATCA 1562 CA_
 TGATAA GGAATAACAT
 |||| ||||| |||||
 ACTATT CCTTATTGTA
 ACC
 GAM275 CA4 3' AGGCATGATTA AAAATATGGAC 769 T TGAG
 GTCCATATTTTA TC GCCT
 ||||| || |||
 CAGGTATA AAAAT AG CGGA
 T TA _
 GAM275 LU 3' AGGCCCCAGAATAGCTCCTGGA 1227 TATT A
 C GTCCA TTATTCTG GGCCT
 |||| ||||| |||||

			CAGGT GATAAGAC CCGGA		
			CCTC C		
GAM275	FNBP3	5'	AGGAGTTACAAAATATGGAC 3155	ATTC	GG
			GTCCATATTTT TGA CCT		
			CAGGTATAAAA ATT GGA		
			C__ GA		
GAM275	SAP18	3'	AGCCCTTCTGTAAAATATG 1258	TCT	C
			CATATTTTAT GAGG CT		
			GTATAAAATG TTCC GA		
			TC_ C		
GAM275	SCYA4	3'	CTTTAAAATAAAATGCAGAC 978	CA	C
			GTC TATTTTATT TGAGG		
			CAG GTAAAATAA ATTTC		
			AC A		
GAM275	SLC6A14	3'	CGTGATAAATATATGGAC 1368	_	C
			GTCCATAT TTTATT TG		
			CAGGTATA AAATAG GC		
			T T		
GAM275	LOC158629	5'	CCCAGGAAAACATGGAT 3393	A TA	A
			GTCCAT TTT TTCTG GG		
			TAGGTA AAA AGGAC CC		
			C _ _		
GAM275	LOC163115	5'	AGGCCTCAGTTTATATTGAC 3243	C	TTTATT
			GTC ATAT CTGAGGCCT		
			CAG TATA GACTCCGGA		
			T TTT__		
GAM275	LOC200339	3'	TCTTAGAAGAAAACATAGACG 3476	C A	A
			CGTC AT TTTT TTCTGAGG		
			GCAG TA AAAA AAGATTCT		
			A C G		
GAM275	LOC200953	5'	AGGCCTCAGAGGGCCCTAGGGA 3481	ATATTTTA	
			C GTCC TTCTGAGGCCT		
			CAGG GAGACTCCGGA		
			GATCCCGG		
GAM275	LOC255527	5'	AGGCCACATAAAATACCAAC 3718	CCA	TC A
			GT TATTTTAT TG GGCCT		
			CA ATAAAATA AC CCGGA		
			ACC C_ _		
GAM275	LOC51334	3'	CCTCAGAATGATGAAAAATATG 1706	C	_____
			AATG CGT CATATT TTATTCTGAGG		

			GTA GTATAA AGTAAGACTCC	
			A AAAGT	
GAM275	LOC92710	3'	AGGCCTCAAAACAATGAAA 2884	C___
			TTTTATT TGAGGCCT	
			AAAGTAA ACTCCGGA	
			CAAA	
GAM276	TSN	3'	TACACTTGGGGAGATTTGCCA 1136	GCAA C_
			TGGCAAATCT TCA TGTA	
			ACCGTTTAGA GGT ACAT	
			GG__ TC	
GAM276	FLJ20039	3'	TACAGTGATAGCAACTTTCCA 1734	C TC A
			TGG AAA TGC ATCACTGTA	
			ACC TTT ACG TAGTGACAT	
			_ CA A	
GAM276	KIAA1204	3'	ACAGGGCCAGCTTGCCATA 2849	AT CAA A
			TATGGCAA CTG TC CTGT	
			ATACCGTT GAC GG GACA	
			C_ C_ _	
GAM276	OR2C3	3'	TACAGTGAGGCGAGATTCACCA 3023	CA _ AA
	T		ATGG AATCT GC TCACTGTA	
			TACC TTAGA CG AGTGACAT	
			AC G G_	
GAM276	QKI	3'	TACCTTGATGCAAATTTGCCA 2722	C A CT
			TGGCAAAT TGCA TCA GTA	
			ACCGTTTA ACGT AGT CAT	
			A _ TC	
GAM276	TIP120A	3'	ACAGTAACAATTTGCCA 1828	C CAATC
			TGGCAAAT TG ACTGT	
			ACCGTTTA AC TGACA	
			_ AA__	
GAM276	LOC90750	3'	CAGTGGTCCAGACTTGCCA 2673	A CA
			TGGCAA TCTG ATCACTG	
			ACCGTT AGAC TGGTGAC	
			C C_	
GAM276	LOC92912	3'	ACAGTAATTTTTGCCATG 2898	TCTGC C
			TATGGCAAA AAT ACTGT	
			GTACCGTTT TTA TGACA	
			_____ A	
GAM277	BACH2	3'	ATTTCTGGTGAGTCAGTCCAC 1962	AA TA_
			GT ATT TCACCAGAAAT	

			CA TGA AGTGGTCTTTA		
			CC CTG		
GAM277	DUSP11	3'	TTTGCTGATAAATTTGCAGT 1039	C	C
			AC GTAAATTTATCA CAGA		
			TG CGTTTAAATAGT GTTT		
			A C		
GAM277	EPS8	3'	ATTTCTGGTAATAAGAAGC 1114	AAA	C
			GT TTTAT ACCAGAAAT		
			CG GAATA TGGTCTTTA		
			AA_ A		
GAM277	TK1	3'	TCTGGTGATGGTTTCCACAGG 1005	_	AAAT_
			CC GT TTATCACCAGA		
			GG CA GGTAGTGGTCT		
			A CCTTT		
GAM277	TRPC6	3'	ATTTCTGGGAGCATTTAC 1134	TTA	A
			GTAAAT TC CCAGAAAT		
			CATTTA AG GGTCTTTA		
			CG_ _		
GAM277	KIAA0924	3'	TTCTGAATAAATTTACAGT 1577	C	CAC
			AC GTAAATTTAT CAGAA		
			TG CATTTAATA GTCTT		
			A A_		
GAM277	KIAA1946	3'	ATTTTGGGTGATGAATTTACA 3247	C	_
	GT		AC GTAAATTTATCACC AGAAAT		
			TG CATTTAAGTAGTGG TTTTTA		
			A G		
GAM277	OSBPL3	3'	ATTTCTGGTGAATTAC 1635	ATTTA	
			GTAA TCACCAGAAAT		
			CATT AGTGGTCTTTA		
			A_		
GAM277	PSKH1	3'	TCTGGTGGAGGGCCATGG 2810	AAA	A
			CCGT TTT TCACCAGA		
			GGTA GGA GGTGGTCT		
			CCG _		
GAM277	URB	5'	ATTTCTGGGACTGAATCCAGG 3162	GTAA	_ A
			CC ATTTA TC CCAGAAAT		
			GG TAAGT AG GGTCTTTA		
			ACC_ C _		
GAM278	PLS3	3'	TAGAAGAAAAATGTACCTTA 1174	_	CA
			TAAGGTAC TTTTCT TA		

		ATTCCATG AAAAAGA AT	
		T AG	
GAM278	LOC121227 3'	TTATGCAAAAAAGTATCTTA 2989	CT
		TAAGGTACTTTTT CATAA	
		ATTCTATGAAAAA GTATT	
		AC	
GAM278	LOC145786 3'	ATTATGAGAAAGGCC 3277	ACT
		GGT TTTTCTCATAAT	
		CCG GAAAGAGTATTA	
		—	
GAM278	LOC149650 3'	TTAAGAGAAAAAAGTACC 3136	_ A
		GGTACTTTTT CTC TAA	
		CCATGAAAAA GAG ATT	
		A A	
GAM278	LOC222223 3'	TTATCACATGGTCAAGTACCTT 3641	TT TCATA
	G	TAAGGTACTT TC ATAA	
		GTTCCATGAA GG TATT	
		CT TACAC	
GAM279	OGT 5'	GGTAATTTATAGAACAAA 1042	C C
		TTTGTTCCTAT AA TACC	
		AAACAAGATA TT ATGG	
		T A	
GAM279	TNFRSF10B 3'	TTTATAGGTAGTTGTTTACA 1065	TCTAT
		TGT CAACTACCTATAAA	
		ACA GTTGATGGATATTT	
		TTT_	
GAM279	BA108L7.2 3'	TTATAGACACTAGTAGGACAAA 2180	CAACTAC
		TTTGTTCCTAT CTATAA	
		AAACAGGATG GATATT	
		ATCACA_	
GAM279	FLJ12598 5'	TTTACAGGTACCATGCAGAGAA 2086	AT_ AC_ A
	CAAA	TTTGTTCCT CA TACCT TAAA	
		AAACAAGA GT ATGGA ATTT	
		GAC ACC C	
GAM279	FLJ23071 3'	GGTAATTTATAGAACAAA 2144	C C
		TTTGTTCCTAT AA TACC	
		AAACAAGATA TT ATGG	
		T A	
GAM279	LOC91266 5'	TATAGGTTAGGAACAAA 2720	ATCAACT
		TTTGTTCCT ACCTATA	

			AAACAAGG	TGGATAT		
			AT_____			
GAM280	CDH11	5'	CCGCTGACTTGTGAATGGGA	2339	A TG	AAAA
			TCC ATT TAA TCAGCGG			
			AGG TAA GTT AGTCGCC			
			G GT C____			
GAM280	IGF1	3'	CCTGATGCAAATTGGA	761	AAAAA	C
			TCCAATTTGT ATCAG G			
			AGGTAAACG TAGTC C			
			_____ A			
GAM280	FKBP9	3'	CCGCTAATTTTTGTATTTTTGG	3632	TTTGTA	C
			CCAA AAAAAT AGCGG			
			GGTT TTTTTCGCGC			
			TTTATG A			
GAM280	FLJ23045	3'	TGCTTGACAAATTGGAT	2082	AAAAAATC	
			ATCCAATTTGT AGCG			
			TAGGTAAACA TCGT			
			GT_____			
GAM280	FLJ30567	3'	CCTGATTTGAATTGG	2510	GTAAA	C
			CCAATTT AAATCAG G			
			GGTTAAG TTTAGTC C			
			_____ A			
GAM280	FLJ30678	5'	CCGCTGATTCCTTTCGTAA	2490	TA	__
			TTG AAA AATCAGCGG			
			AAT TTT TTAGTCGCC			
			GC CC			
GAM280	KIAA1676	3'	CCACTGTGGGAACCAAATTGGA	3590	TAAAAAAT	C
	T		ATCCAATTTG CAG GG			
			TAGGTAAAC GTC CC			
			CAAGGGT_ A			
GAM280	KLF3	3'	CCGCCAATTTTTTACAAAT	1693	CA	
			ATTTGTAAAAAAT GCGG			
			TAAACATTTTTTA CGCC			
			AC			
GAM280	LOC146952	5'	CCACTGATTTTTTTTTCTGGA	3286	ATTTGT	C
			TCCA AAAAATCAG GG			
			AGGT TTTTTTAGTC CC			
			CTTTT_ A			
GAM280	LOC81569	3'	CCACTGATTTTTCATTGG	2616	TTGTA	C
			CCAAT AAAAATCAG GG			

			GGTTA	TTTTTAGTC	CC		
			C_____	A			
GAM280	LOC83690	3'	CCACTGATTTTTTTTAAAT	2204	T_	C	
			ATTTG	AAAAAATCAG	GG		
			TAAAT	TTTTTTAGTC	CC		
			TT	A			
GAM281	ASPH	3'	AAAAAAGCATGGAAAATG	1896	C	A	
			CATTT	CCATGT	TTTTT		
			GTAAA	GGTACG	AAAAA		
			A	A			
GAM281	ASPH	3'	AAAAAAGCATGGAAAATG	2252	C	A	
			CATTT	CCATGT	TTTTT		
			GTAAA	GGTACG	AAAAA		
			A	A			
GAM281	CABC1	3'	ATAAAAATGCTCATGGGAAGTG	1908		TATTT	
	A		TCATTTCCCATG	TTTTTAT			
			AGTGAAGGGTAC	AAAAATA			
			TCGT_				
GAM281	SLC6A12	5'	ATAAAAAGGGACATGAAAATGA	987	CC	A	
			TCATTT	CATGT	TTTTTTTTAT		
			AGTAAA	GTACA	GGGAAAAATA		
			A_	_			
GAM281	CSAD	3'	AAAATACATAGGAAAAGA	1654	A	C	
			TC	TTTCC	ATGTATTTT		
			AG	AAAGG	TACATAAAA		
			A	A			
GAM281	DICER1	3'	AAAAAAAATTAAGGGGAAA	2151	ATGT		
			TTTCCC	ATTTTTTTT			
			AAAGGG	TAAAAAAA			
			GAAT				
GAM281	KIAA1025	3'	AAAAAAAGGGGAAATGG	2675	ATGTA		
			TCATTTCCC	TTTTTTTTT			
			GGTAAAGGG	GAAAAAAA			

GAM281	KLF12	3'	AAAAAAAATACATGGGAA	1372			
			TTCCCATGTATTTTTTTT				
			AAGGGTACATAAAAAAAA				
GAM281	NFAT5	3'	AAAAAGTGTCAAAGGAAATGA	2451	CA	_	
			TCATTTCC	TG	TATTTTTT		

			AGTAAAGG AC GTGAAAAA	
			AA T	
GAM281	LOC170261	3'	ATAAAAAAGGTACAAAAAGTGA 3256	CCCA
			TCATTT TGTATTTTTTTTAT	
			AGTGAA ACATGGAAAAAATA	
			AA__	
GAM281	LOC222602	3'	ATAAAAAACAAAAATGGAAAT 3583	CATGTAT
			GA TCATTTC TTTTTTAT	
			AGTAAAGG AAAAAAATA	
			TAAAAAC	
GAM281	LOC257051	3'	ATAAAAAAGGTACAAAAAGTGA 3703	CCCA
			TCATTT TGTATTTTTTTTAT	
			AGTGAA ACATGGAAAAAATA	
			AA__	
GAM282	FGF7	3'	TATAAGAACCCAGTTCCA 886	C C
			TGGAATTGGG TC TTATA	
			ACCTTGACCC AG AATAT	
			A A	
GAM282	MTNR1B	3'	TGGGGCAGAAGAGCCCAACTCC 1262	A C ATA_
			GGA TTGGGCTC TT CCA	
			CCT AACCCGAG AG GGT	
			C A ACGG	
GAM282	SEPX1	3'	TGTGAGGCCCAATTCCA 1681	TC
			TGGAATTGGGC CTTATA	
			ACCTTAACCCG GAGTGT	
			—	
GAM282	PPFIA4	3'	TGGCATAAGCTGAATCCCA 2883	A G CCT A
			TGG ATT GGCT TAT CCA	
			ACC TAA TCGA ATA GGT	
			C G _ C	
GAM282	LOC145231	3'	CTTGACACGAGACTAGTCCCAA 3274	_ C_ ATAC
			TTCCA TGGAATTGGG CT CTT CAAG	
			ACCTTAACCC GA GAG GTTC	
			T TCA CACA	
GAM283	CAV3	3'	AATGCCCAGTACTGCCATTTGA 2329	ATCC
			TCAAATG TGTTGGGCATT	
			AGTTTAC ATGACCCGTAA	
			CGTC	
GAM283	HOXC4	5'	AATGACGTCAGAATCATTTG 1509	C T GG
			CAAATGAT CTG TG CATT	

			GTTTACTA GAC GC GTAA	
			A T A_	
GAM283	MYCL1	3'	CTTTTACACGACCATTGATA 1203	A C T_
			TATCAAATG TC TGT GGG	
			ATAGTTTAC AG ACA TTC	
			C C TT	
GAM283	FLJ20666	5'	AACAGGAGAATCACTTGATG 1762	A ____
			TATCAA TGA TCCTGTT	
			GTAGTT ACT AGGACAA	
			C AAG	
GAM283	KIAA1001	3'	AATGCCTGGCAAATTACCTGA 1599	AA CC TG
			TCA TGAT TGT GGCATT	
			AGT ATTA ACG CCGTAA	
			CC A_ GT	
GAM283	PGRMC2	3'	AACAGAAAGATCATTTGA 1286	____
			TCAAATGATC CTGTT	
			AGTTTACTAG GACAA	
			AAA	
GAM283	LOC152286	3'	AATGCAGGGAGACATTTGATA 3354	A_ GTTGG
			TATCAAATG TCCT GCATT	
			ATAGTTTAC AGGG CGTAA	
			AG A____	
GAM283	LOC158549	3'	AATGCTTAGGAATCATTTTATA 3392	C _ TTG
			TAT AAATGAT CCTG GGCATT	
			ATA TTTACTA GGAT TCGTAA	
			T A ____	
GAM284	DKFZp761G0313	3'	AAGATAAGCTATTATTAA 2731	TA
			TTAATAAT CTTATCTT	
			AATTATTA GAATAGAA	
			TC	
GAM285	NRCAM	3'	CAGCATGCCAACAGTAATA 1170	A T__
			TATTATT TTGGC CTG	
			ATAATGA AACCG GAC	
			C TAC	
GAM285	C22orf23	3'	TGATTAAGTGGCCAATAA 2259	C__
			TTATTGGCT TGATCA	
			AATAACCGG ATTAGT	
			TCA	
GAM285	SARM	3'	GACAGCGCCAATAACAATA 1609	A T A
			TATT TTATTGGC CTG TC	

			ATAA AATAACCG GAC AG		
			C C _		
GAM285	LOC219918	3'	CGGTGGTTAAACAACAATAAT 3529	A	GCTC
	A		TATTATT TTG TGATCACCG		
			ATAATAA AAC ATTGGTGGC		
			C AAA_		
GAM286	FABP5	3'	TTTATCATAAACATTTTACA 828	T	C
			TGTAAAAT TTTGT GATAAA		
			ACATTTTA AAATA CTATTT		
			C _		
GAM286	ZHX1	3'	TTGACCAAAAATTTTACA 1367	_	
			TGTAAAATTTTTCG		
			ACATTTTAAAAAC AGTT		
			C		
GAM286	KIAA0981	3'	TTTGTGGCAAAAATTTTCA 2599	T	G
			TG AAAATTTTGTG ATAAA		
			AC TTTTAAAAACGG TGTTT		
			_ _		
GAM286	KIAA1615	3'	ATTTTATAAGAAAATTTTAC 2829		GTCG
			GTAAAATTTT ATAAAAAT		
			CATTTTAAAAG TATTTTA		
			AA_		
GAM286	SGP28	3'	TTTTTATCTGCATAAATTTTAC 1271	T	C
	A		TGTAAAATTT TGT GATAAAAA		
			ACATTTTAAA ACG CTATTTT		
			T T		
GAM286	LOC201973	3'	TTTTTTGAGAAAAATTTTGCA 3456	G	T
			TGTAAAATTTTTCG AAA		
			ACGTTTAAAAA AGTT TTT		
			G T		
GAM287	LOC146237	3'	CGCACGCTCAGCAGGCATGA 3283	A	CACCGA
			TCGT CC GAGCGTGTG		
			AGTA GG CTCGCACGC		
			C ACGA_		
GAM287	LOC255146	5'	CACACGCTCCCGCCAGCGA 3679	ACCCAC	A
			TCGT CG GAGCGTGTG		
			AGCG GC CTCGCACAC		
			ACC_ C		
GAM288	ATBF1	5'	CGTACTGGGTGCAATGAA 1336	A	
			TTCGTTGTAT TAGTACG		

			AAGTAACGTG GTCATGC		
			G		
GAM289	FMR2	3'	GCATCAGTGTTTTTCAACTCC 889	ATT _ C	
			GGAG AAAAATA TGA GC		
			CCTC TTTTGT ACT CG		
			AAC G A		
GAM289	SF1	3'	GCGTGGGGTTTTTAATCTCTG 1138	TATG_	
			CGGAGATTAAAAA ACGC		
			GTCTCTAATTTT TGCG		
			TGGGG		
GAM289	BAL	3'	GCAGTTGTTCTTTAATCTCC 2201	AAT TG _	
			GGAGATTAAA A AC GC		
			CCTCTAATTT T TG CG		
			CT_ GT A		
GAM289	BTN3A1	3'	ATATTTTAAATCCCGTTA 1355	A	
			TAACGG GATTAAAAATAT		
			ATTGCC CTAATTTTATA		
			—		
GAM289	PDE4DIP	3'	CGTCATATTCTCAACAGTTTCT 1512	AAA__	
			GGAGATT AATATGACG		
			TCTTTGA TTATACTGC		
			CAACTC		
GAM289	LOC200251	3'	GCGAGTGCCTGTAATCTCCG 3447	AAAA GA	
			CGGAGATTA TAT CGC		
			GCCTCTAAT GTG GCG		
			GTCC A_		
GAM290	CDK10	3'	CGGAAGCAGCCCTACAACAAC 2354	TTGCGA	
			GTTGTTGT CTGCTTCCG		
			CAACAACA GACGAAGGC		
			TCCC__		
GAM290	COL1A1	3'	CGGAAACAGACAAGCAAC 704	CGA C	
			GTTGTTTG CTG TTCCG		
			CAACGAAC GAC AAGGC		
			A__ A		
GAM290	ESPN	3'	AAGCTGCTGACGCAAACAACAA 2210	ACT__	
	C		GTTGTTGTTTGCG GCTT		
			CAACAACAAACGC CGAA		
			AGTCGT		
GAM290	GRIA1	3'	CAGTGCCAAAAACAACAAC 779	__ G	
			GTTGTTGTTT GC ACTG		

			CAACAACAAA	CG TGAC	
			AAC _		
GAM290	PLAG1	3'	AAGCAGAAAACAAAAACAAC	942	G CGA_
			GTTGTT TTTG CTGCTT		
			CAACAA AAAC GACGAA		
			_ AAAA		
GAM290	SORCS1	3'	TCAGAAGTTCCAAACAGCAAC	2345	C CT C
			GTTGTTGTTTG GA GCTTC GA		
			CAACGACAAAC CT TGAAG CT		
			_ _ A		
GAM290	BM046	3'	AAGCAAGACAACAAC	1830	GCGAC
			GTTGTTGTTT TGCTT		
			CAACAACAGA ACGAA		

GAM290	KLF12	3'	AAGCAGTTGAGTAACAGCAAC	1373	TG_
			GTTGTTGTT CGACTGCTT		
			CAACGACAA GTTGACGAA		
			TGA		
GAM290	PSMA6	5'	CGGAAGCAGTCGCTGCAAC	2880	TT
			GTTGT GCGACTGCTTCCG		
			CAACG CGCTGACGAAGGC		
			T_		
GAM290	LOC157292	5'	CAGCTCAAAAACAACAAC	3377	GC _
			GTTGTTGTTT GA CTG		
			CAACAACAAA CT GAC		
			AA C		
GAM291	CELSR3	3'	TCCCCAGTGGTGGGTG	825	T T A
			CACCCAT CA CTGG GA		
			GTGGGTG GT GACC CT		
			_ _ C		
GAM291	CMAR	5'	CTCCTTGGGAATGGGTACCAC	1195	AC ATC_
	A		TGTG ACCCATTC TGGAG		
			ACAC TGGGTAAG ACCTC		
			CA GTTC		
GAM291	FCER2	3'	TCTCCAGATGAGAGTACAC	881	_ ACCCA
			GTG AC TTCATCTGGAGA		
			CAC TG GAGTAGACCTCT		
			A A_____		
GAM291	FCER2	3'	TCTCCAGATGAGAGTACAC	882	_ ACCCA
			GTG AC TTCATCTGGAGA		

			CAC TG	GAGTAGACCTCT		
			A A	_____		
GAM291	FCER2	3'	TCTCCAGATGAGAGTACAC	883	_	ACCCA
			GTG AC	TTCATCTGGAGA		
			CAC TG	GAGTAGACCTCT		
			A A	_____		
GAM291	MEN1	3'	CTCCAGAGTGGGTGTCCA	3601	T	TCA
			TG GACACCCAT	TCTGGAG		
			AC CTGTGGGTG	AGACCTC		
			—	—		
GAM291	NCSTN	3'	TTCTCCAGGCCCTCAGATGGCA	2979	ACAC	CA_____
	CA		GTG CCATT	TCTGGAGAA		
			CAC GGTAG	GGACCTCTT		
			—	ACTCCC		
GAM291	RBM10	3'	TTCTCCACATGTTGGGTGTCCA	1235	T	TT C
			TG GACACCCA	CAT TGGAGAA		
			AC CTGTGGGT	GTA ACCTCTT		
			—	T_ C		
GAM291	TNFSF8	3'	GGATGAATGGATGTCCCA	812	T	C
			TG GACA CCATTCATCT			
			AC CTGT GGTAAGTAGG			
			C	A		
GAM291	YES1	3'	TCCTTATGGGGATGGGTGCCAC	1210	A	ATCT__
	A		TGTG CACCCATTC	GGA		
			ACAC GTGGGTAGG	CCT		
			C	GGTATT		
GAM291	ZNF256	5'	TTCTCCACAGCGGGTGTGACA	1247		ATTCATC
			TGTGACACCC	TGGAGAA		
			ACACTGTGGG	ACCTCTT		
			CGAC	_____		
GAM291	BAT8	3'	TCCCCAGCATGGATGGCCACA	1325	ACAC	_ A
			TGTG CCATTCAT	CTGG GA		
			ACAC GGTAGGTA	GACC CT		
			C_____	C C		
GAM291	CPLX1	3'	TCTCCGGATGGAATCACA	1318		CACCCA
			TGTGA	TTCATCTGGAGA		
			ACACT	AGGTAGGCCTCT		
			A	_____		
GAM291	DKFZP566K0524	3'	TTCCAGTGAAACAGATGTTACA	2855		CCCA_ T
			TGTGACA	TTCA CTGGAG		

			ACATTGT AAGT GACCTT	
			AGACA _	
GAM291	FLJ12891	3'	TCTCCAGGGCCACAAC TGTGACA TCTGGAGA	CCCATTCA
	A			
			ACACTGT GGACCTCT	
			CAACACCG	
GAM291	GR6	3'	CCTGAATGAATGGGTGTCAC 1396	_T
			GTGACACCCATTCAT C GG	
			CACTGTGGGTAAGTA G CC	
			A T	
GAM291	KIAA0455	3'	CAGATGAATAGTATCACA 2947	C CC
			TGTGA AC ATTCATCTG	
			ACACT TG TAAGTAGAC	
			A A_	
GAM291	KIAA0513	3'	TTCCCTGCAATGGGTGCACA 1536	A _ TCT
			TGTG CACCCATT CA GGAG	
			ACAC GTGGGTAA GT CCTT	
			_ C C__	
GAM291	KIAA1655	5'	CTCTGAGAAGAGTGTGACA 2753	CCA A T
			TGTGACAC TTC TC GGAG	
			ACACTGTG AAG AG TCTC	
			AG_ _ _	
GAM291	SCAND2	3'	TTCCCCAGCCAGATGGGGTGCAC 2338	A CAT A
	A		TGTGAC CCCATT CTGG GAA	
			ACACTG GGGTAG GACC CTT	
			_ ACC C	
GAM291	WDR5B	3'	TCTCCACGTCCAGGTGTACACA 1878	_ CATT C
			TGTG ACACC AT TGGAGA	
			ACAC TGTGG TG ACCTCT	
			A ACC_ C	
GAM291	LOC146330	5'	TCTCCAAGAAGGGTGTCA 3088	A ATC
			TGACACCC TTC TGGAGA	
			ACTGTGGG AAG ACCTCT	
			_ A_	
GAM291	LOC148181	5'	CTCCAGACCCAGATGGTGTCTC 3117	T C CA_
	A		TG GACACC ATT TCTGGAG	
			AC CTGTGG TAG AGACCTC	
			T _ ACCC	
GAM291	LOC150271	5'	TCTCCAGACTGGTGACACA 3326	A CATTCA
			TGTG CACC TCTGGAGA	

		ACAC GTGG AGACCTCT	
		A TC_____	
GAM291	LOC150605 5'	TCTCCGGTGGAACCAGTGTAC 3331	CCA_ T
	A	TGTGACAC TTCA CTGGAGA	
		ACACTGTG AGGT GGCCTCT	
		ACCA _	
GAM291	LOC153277 3'	AGATAAATGTGTGTCACA 3368	C C
		TGTGACAC CATT ATCT	
		ACACTGTG GTAA TAGA	
		T A	
GAM291	LOC154990 5'	CTCCAGACCCAGATGGTGTCTC 3196	T C CA__
	A	TG GACACC ATT TCTGGAG	
		AC CTGTGG TAG AGACCTC	
		T _ ACCC	
GAM291	LOC158014 5'	TTCTCCAGATAAGAAAATCACA 3209	CACCCA C
		TGTGA TT ATCTGGAGAA	
		ACACT AA TAGACCTCTT	
		AAAAG_ _	
GAM291	LOC158056 5'	TCTCCAGGCCCCAGGTGCCAGC 3210	GA_ CATTCA
	A	TGT CACC TCTGGAGA	
		ACG GTGG GGACCTCT	
		ACC ACCC_	
GAM291	LOC202908 3'	CTCCAGACCCAGATGGTGTCTC 3462	T C CA__
	A	TG GACACC ATT TCTGGAG	
		AC CTGTGG TAG AGACCTC	
		T _ ACCC	
GAM291	LOC220143 5'	CTCCCGAGATGGTGTGTCACA 3610	CAT A T
		TGTGACACC TC TC GGAG	
		ACACTGTGG AG AG CCTC	
		T_ _ C	
GAM291	LOC220143 5'	CTCCCGAGATGGTGTGTCACA 3611	CAT A T
		TGTGACACC TC TC GGAG	
		ACACTGTGG AG AG CCTC	
		T_ _ C	
GAM291	LOC222057 3'	CTCCAGACCCAGATGGTGTCTC 3576	T C CA__
	A	TG GACACC ATT TCTGGAG	
		AC CTGTGG TAG AGACCTC	
		T _ ACCC	
GAM291	LOC255096 3'	CTCATGGATGAGTACCACA 3744	AC C CTG
		TGTG AC CATT CAT GAG	

			ACAC TG GTAGGTA CTC		
			CA A ____		
GAM291	LOC255975 5'		CTCCAGACCCAGATGGTGTCTC 3686	T	C CA__
	A		TG GACACC ATT TCTGGAG		
			AC CTGTGG TAG AGACCTC		
			T _ ACCC		
GAM291	LOC256878 3'		CTCCAGACCCAGATGGTGTCTC 3720	T	C CA__
	A		TG GACACC ATT TCTGGAG		
			AC CTGTGG TAG AGACCTC		
			T _ ACCC		
GAM291	LOC51333 3'		TTCTCCAGGCTCAGGTGCCA 1705	A	CATTCA
			TG CACC TCTGGAGAA		
			AC GTGG GGACCTCTT		
			C ACTC__		
GAM291	LOC89919 3'		TCAGAACAGATGGATGTCACA 2580	C	CA_
			TGTGACA CCATT TCTGG		
			ACACTGT GGTAG AGACT		
			A ACA		
GAM292	IL2RA 3'		TCCACCCTATATGTAGTATAAA 739	_	CA CAA
	GA		TCTTT TAC ACA AGGGTGGA		
			AGAAA ATG TGT TCCCACCT		
			T A_ ATA		
GAM292	INPP5D 3'		CCATCGTGCTGGTAGAAGA 3263	A	AAAG
			TCTTTTACCA CAC GGTGG		
			AGAAGATGGT GTG CTACC		
			C ____		
GAM292	PLXNA1 3'		TCCACCCTTGCCCTCAGCAAGA 2941		ACCAACACA
	GA		TCTTTT AAGGGTGGA		
			AGAGAA TTCCCACCT		
			C GACTCCCG		
GAM292	PRKCN 3'		TCTTTAAGTCGTGTTTGTA AAA 1253	C	AAAGGGT
	GA		TCTTTTAC AACAC GGA		
			AGAAAATG TTGTG TCT		
			T CTGAATT		
GAM292	BHMT 3'		CCACTTTTCTACCAGTAAAAGA 849		CAACACA
			TCTTTTAC AAGGGTGG		
			AGAAAATG TTTTCACC		
			ACCATC_		
GAM292	DKFZP434B044 3'		CCACCCCTTTAAGGAGTTGGTA 2211	AC__	_
	AAA		TTTTACCAAC AAAGGG TGG		

			AAAATGGTTG TTTCCC ACC	
			AGGAA C	
GAM292	FLJ10458	3'	CCCCGTGTTGGTAAGAGA 1777	AAA
			TCTTTTACCAACAC GGG	
			AGAGAATGGTTGTG CCC	
			C__	
GAM292	FLJ20272	3'	CACCTGCTGGTAAAAGA 1744	ACACAAA
			TCTTTTACCA GGGTG	
			AGAAAATGGT TCCAC	
			CG_____	
GAM292	FLJ23598	3'	TCCACCCTGGGTAATAAAAGA 3665	CCAAC AA
			TCTTTTA AC AGGGTGGA	
			AGAAAAT TG TCCCACCT	
			AA__ GG	
GAM292	KIAA1755	3'	CCACCCTTCATACTGGCCAGAG 2595	TA ACACA
			CTTT CCA AAGGGTGG	
			GAGA GGT TTCCCACC	
			CC CATA C	
GAM292	MGC21621	3'	CCCTAGGCTGGTTGGTAAAAGA 2508	A A__
			TCTTTTACCAAC CA AGGG	
			AGAAAATGGTTG GT TCCC	
			_ CGGA	
GAM292	MGC3077	3'	TCCTTGCTCTGGTAAAAGA 2048	ACACA
			TCTTTTACCA AAGGG	
			AGAAAATGGT TTCCT	
			CTCG_	
GAM292	MGC4707	3'	CCCTCATGTCTGGTAAAA 2055	_ CAA
			TTTTACCA ACA AGGG	
			AAAATGGT TGT TCCC	
			C AC_	
GAM292	MGC5149	3'	TCCTCATTGGTAAAAGA 2940	CACAA
			TCTTTTACCAA AGGG	
			AGAAAATGGTT TCCT	
			AC__	
GAM292	RAB3IL1	3'	CAGGCTTTGTTGGTAAAA 1448	CA GG
			TTTTACCAACA AAG TG	
			AAAATGGTTGT TTC AC	
			_ GG	
GAM292	LOC119369	5'	TCCACCCTATTTCTGGAAAAA 3026	A ACACAA
			TTTT CCA AGGGTGGA	

		AAAA GGT TCCCACCT		
		A CTTTA_		
GAM292	LOC150035 5'	TTGTAGTACTGGTAAAAGA 3321	—	—
		TCTTTTACCA AC ACAA		
		AGAAAATGGT TG TGTT		
		CA A		
GAM292	LOC219649 5'	TCCACCCTTTGTGCTTTGGT 3586	—	
		ACCAA CACAAAGGGTGGA		
		TGGTT GTGTTTCCCACCT		
		TC		
GAM292	LOC221688 5'	TCCAACCACATTGGTAAAA 3617	CACAAA	G
		TTTTACCAA GG TGGA		
		AAAATGGTT CC ACCT		
		ACA__ A		
GAM293	RLBP1 5'	CAGGTACCAGGTAGCCCCA 729	A	CGACA G
		TG GGCTACCT TAC TG		
		AC CCGATGGA ATG AC		
		C CC__ G		
GAM293	MGC23280 3'	GCTGGTATCGAGGTGCCCA 2493	A T	CA GT
		TG GGC ACCTCGA TAC GT		
		AC CCG TGGAGCT ATG CG		
		C _ _ GT		
GAM293	LOC113523 3'	TATGCCGAAATAGCTTCA 2966	CC	A
		TGAGGCTA TCG CATA		
		ACTTCGAT AGC GTAT		
		AA C		
GAM293	LOC150157 3'	CACACGTATGCCATGGCC 3325	CCTCGA	
		GGCTA CACACGTGTG		
		CCGGT GTATGCACAC		
		ACC__		
GAM293	LOC196890 3'	CACACGTATGCCATGGCC 3468	CCTCGA	
		GGCTA CACACGTGTG		
		CCGGT GTATGCACAC		
		ACC__		
GAM294	ARHGAP6 3'	TGTATTCTGTAACAGATTA 807	CA	
		TAA TGTTACAGAATATA		
		ATT ACAATGTCTTATGT		
		AG		
GAM294	ARHGAP6 3'	TGTATTCTGTAACAGATTA 1450	CA	
		TAA TGTTACAGAATATA		

			ATT ACAATGTCTTATGT		
			AG		
GAM294	ATP11B	3'	TAATTTGAATCTGAACATGTTA 3158	A	ATA
			TAACATGTT CAGA TAAATTA		
			ATTGTACAA GTCT GTTTAAT		
			_ AA_		
GAM294	BNC	3'	TAATTCTTGTCTGTAACATG 850	TA	
			CATGTTACAGAATA AATTA		
			GTACAATGTCTTGT TTAAT		
			TC		
GAM294	CREBL2	3'	TAATTTATATTCTTTCCATGT 817	TTAC	
			ACATG AGAATATAAATTA		
			TGTAC TCTTATATTTAAT		
			CTT_		
GAM294	GCNT1	3'	TAATTTATATTCTGCTCTAATA 830	___	
			TGTTA CAGAATATAAATTA		
			ATAAT GTCTTATATTTAAT		
			CTC		
GAM294	MBNL	3'	TATACTGTATAACATGTTA 1938	___	A
			TAACATGT TACAG ATA		
			ATTGTACA ATGTC TAT		
			AT A		
GAM294	AFAP	3'	TAATTTATATCTGTACATATTA 1952	C T	A
			TAA ATGT ACAGA TATAAATTA		
			ATT TACA TGTCT ATATTTAAT		
			A _ _		
GAM294	LOC148195	3'	TAATTTATCTGTTAACATGTT 3299	_	ATA
			AACATGTTA CAGA TAAATTA		
			TTGTACAAT GTCT ATTTAAT		
			T _		
GAM295	ATP6V1A1	3'	GAGGTTTCTCAGAATATCT 847	CGCT	
			AGATATTCTGAG AACCTT		
			TCTATAAGACTC TTGGAG		
			T_		
GAM295	DAP	3'	AGGTTAGGAGAAAACCTCA 2954	ATA	GAGCG
			TGAG TTCT CTAACCT		
			ACTC AAGA GATTGGA		
			CAA G_		
GAM295	LIFR	3'	AAGTATAGTGACTCAGAATCCT 919	AT	_ AC
	CA		TGAG ATTCTGAG CGCTA CTT		

			ACTC TAAGACTC GTGAT GAA		
			C_ A AT		
GAM295	RECK	3'	AGCTTTCAGAATATGTCA 1941	G	C
			TGA ATATTCTGAG GCT		
			ACT TATAAGACTT CGA		
			G T		
GAM295	SLC13A3	3'	AAGGCCAGGGTAAAATGTCTCA 2570		CTGA G AA
			TGAGATATT GC CT CCTT		
			ACTCTGTAA TG GA GGAA		
			AA_ G CC		
GAM295	TEM8	3'	GGGGCCAGAATATCTCA 2236	A	G
			TGAGATATTCTG GC CT		
			ACTCTATAAGAC CG GG		
			_ G		
GAM295	DKFZp5471224	3'	GTTAGCAAGGATATCCA 1903	A	GAGC
			TG GATATTCT GCTAAC		
			AC CTATAGGA CGATTG		
			_ A_		
GAM295	OLFM3	3'	AGCATCATCCTCAAATATCTCA 3232	C	C_
			TGAGATATT TGAG GCT		
			ACTCTATAA ACTC CGA		
			_ C TACTA		
GAM295	TSARG1	3'	AGATGTTTCAGAATATCTCA 2470		_
			TGAGATATTCTGAGCG CT		
			ACTCTATAAGACTTGT GA		
			A		
GAM295	LOC114987	3'	AGGCCAAAAATATCTCA 2517	C_	A G
			TGAGATATT TG GC CT		
			ACTCTATAA AC CG GA		
			AA _ _		
GAM295	LOC152445	5'	AGGCTCCGCAAATATCTCA 3360		CT_ G
			TGAGATATT GAGC CT		
			ACTCTATAA CTCG GA		
			ACGC _		
GAM296	FLJ20139	5'	ACCATATCAATCCATATA 1737	CAA	
			TGTA ATTGATATGGT		
			ATAT TAACTATACCA		
			ACC		
GAM296	LOC91796	3'	ACGTTTTACAATCAATTTGTAC 2785	A	GTCGT
	A		TGTACAAATTGAT TG CGT		

ACATGTTTAACTA AC GCA
 _ ATTTT
 GAM297 CMAR 3' CCCCATCGCCTACTCCATG 1194 A AGA
 CATGGAGTAG TGAT GGGG
 ||||| ||| |||
 GTACCTCATC GCTA CCCC
 C ____
 GAM297 CRHR1 3' TTCCCCTCACTTAACCACCCCA 1105 A AGA TA
 T ATGG GT TGA GAGGGGAA
 ||| || ||| |||||
 TACC CA ATT CTCCCCTT
 C CCA CA
 GAM297 DTR 3' TTCCCCTCCACCAAACCCCA 874 A AGA ATA
 TGG GT TG GAGGGGAA
 ||| || ||| |||||
 ACC CA AC CTCCCCTT
 C A__ CAC
 GAM297 FGF5 3' TCCCCTCTCCACCCACCCCA 1117 A AGA AT
 TGG GT TG AGAGGGGA
 ||| || ||| |||||
 ACC CA AC TCTCCCCT
 C CCC C_
 GAM297 FGF5 3' TCCCCTCTCCACCCACCCCA 2315 A AGA AT
 TGG GT TG AGAGGGGA
 ||| || ||| |||||
 ACC CA AC TCTCCCCT
 C CCC C_
 GAM297 GAA 3' CCCCTCCATCTGTTCC 713 ATA
 GGAGTAGATG GAGGGG
 ||||| |||||
 CCTTGTCTAC CTCCCC

 GAM297 GNL1 3' TCCCCTCTGCCACCCCA 3550 A AGAT A
 TGG GT G TAGAGGGGA
 ||| || | |||||
 ACC CA C GTCTCCCCT
 C ____ C
 GAM297 GNL1 3' TCCCCTCTGCCACCCCA 3748 A AGAT A
 TGG GT G TAGAGGGGA
 ||| || | |||||
 ACC CA C GTCTCCCCT
 C ____ C
 GAM297 KCNA6 3' TCCCCTCCCTACCTCATG 915 GA ATGATA
 CATG GTAG GAGGGGA
 ||| ||| |||||
 GTAC CATC CTCCCCT
 TC C____
 GAM297 LDHB 5' CCCCATACACCATCTATTCCAT 918 ATAGA_
 ATGGAGTAGATG GGGG
 ||||| |||

TACCTTATCTAC CCCC
 CACATA
 GAM297 LTBP2 3' TTCCCCTCCACTCAGAAACCCC 740 A AGA TA_
 GG GT TGA GAGGGGAA
 || || || |||||
 CC CA ACT CTCCCCTT
 C AAG CAC
 GAM297 MARK1 5' CCCCTCCTCTTACTCCG 1856 AT TA
 TGGAGTAG GA GAGGGG
 ||||| || |||||
 GCCTCATT CT CTCCCC
 _ C_
 GAM297 PLAT 3' TTCCCCTTTCCCCACTCCCTG 2306 T AGAT TA
 CA GGAGT GA GAGGGGAA
 || |||| || |||||
 GT CCTCA CT TTCCCCTT
 C CCC_ _
 GAM297 PLAT 3' TTCCCCTTTCCCCACTCCCTG 788 T AGAT TA
 CA GGAGT GA GAGGGGAA
 || |||| || |||||
 GT CCTCA CT TTCCCCTT
 C CCC_ _
 GAM297 PTGIR 3' CCCCTCTACCAAGCCACTCCA 791 AGA_ A
 TGGAGT TG TAGAGGGG
 |||| || |||||
 ACCTCA AC ATCTCCCC
 CCGA C
 GAM297 PXN 3' CCCCTCTTTCACTTCAT 965 AGAT T
 ATGGAGT GA AGAGGGG
 |||| || |||||
 TACTTCA CT TCTCCCC
 _ T
 GAM297 RNH 5' TCCCCTCTACCAAGGGTTCC 2536 AGA A
 GGAGT TG TAGAGGGGA
 |||| || |||||
 CCTTG AC ATCTCCCCT
 GGA C
 GAM297 SCN4A 3' TCCCTTCTCATCTCCCCA 730 AGT TA
 TGG AGATGA GAGGGGA
 || |||| |||||
 ACC TCTACT CTTCCCT
 CC_ _
 GAM297 SH3GL1 3' TCCCTTCCCCACTCCATG 982 AGATGATA
 CATGGAGT GAGGGGA
 ||||| |||||
 GTACCTCA CTTCCCT
 CCC____
 GAM297 ZNF261 3' TTCCCCTCTATTGTTCCCC 1184 AGTA TG
 GG GA ATAGAGGGGAA
 || || |||||

CC TT TATCTCCCCTT
 CC__ GT
 GAM297 AKAP3 3' CCCCTCTATATCCTC 1300 TA A
 GAG GATG TAGAGGGG
 ||| ||| |||||
 CTC CTAT ATCTCCCC

— —
 GAM297 C3F 3' TCCCCTCTGATTCCCCCATG 1246 AGTA TGA
 CATGG GA TAGAGGGGA
 |||| || |||||
 GTACC CT GTCTCCCCT
 CC__ TA_

GAM297 CL24751 5' CTCCTTCATCTACTCC 2698 TAG
 GGAGTAGATGA AGGGG
 ||||| |||
 CCTCATCTACT TCCTC

—
 GAM297 DIS3 3' TTCCCCTAAGTTCTATTCCAT 1597 TGATAG
 ATGGAGTAGA AGGGGAA
 ||||| |||||
 TACCTTATCT TCCCCTT
 TGAA__

GAM297 FLJ10700 3' CCTTCATCCACTCCATG 1794 A TAG
 CATGGAGT GATGA AGG
 ||||| ||| ||
 GTACCTCA CTA CT TCC
 C —

GAM297 FLJ13102 3' TCCCCTCTACCAATCCCTG 2104 T GTAGA A
 CA GGA TG TAGAGGGGA
 || ||| || |||||
 GT CCT AC ATCTCCCCT
 C A__ C

GAM297 FLJ32978 3' TCCCATTGGTCACCTTACTCCA 2488 A_ AGAG
 TGGAGTAG TGAT GGGA
 ||||| ||| |||
 ACCTCATT ACTG CCCT
 CC GTTA

GAM297 HSPB7 3' TTCCCCTCTACCAGCCTCCA 1499 TAGA A
 TGGAG TG TAGAGGGGAA
 |||| || |||||
 ACCTC AC ATCTCCCCTT
 CG__ C

GAM297 HTCD37 3' TTCCCCTTTTTCCTACCCCA 2796 A AT T
 TGG GTAG GA AGAGGGGAA
 ||| ||| || |||||
 ACC CATC CT TTTCCCCTT
 C __ T

GAM297 KIAA0280 3' TTCCCCTCCATCTGATCC 3537 G ATA
 GGA TAGATG GAGGGGAA
 ||| ||||| |||||

CCT GTCTAC CTCCCCTT
 A ____
 GAM297 KIAA0450 5' TCCCCTCTACTACCCC 1511 A ATGA
 GG GTAG TAGAGGGGA
 || ||| |||||
 CC CATC ATCTCCCCT
 C ____
 GAM297 KIAA0731 3' CCCCTCCTCTCTCCATG 2767 T TGATA
 CATGGAG AGA GAGGGG
 ||||| || |||||
 GTACCTC TCT CTCCCC
 _ C ____
 GAM297 KIAA1462 3' TCCCCTCTGTGTCTCCATG 3523 TAGATG
 CATGGAG ATAGAGGGGA
 ||||| |||||
 GTACCTC TGTCTCCCCT
 TG ____
 GAM297 LIMK2 3' CCCCTTTCTACTCCA 1710 TGATA
 TGGAGTAGA GAGGGG
 ||||| |||||
 ACCTCATCT TTCCCC

 GAM297 LIMK2 3' CCCCTTTCTACTCCA 1225 TGATA
 TGGAGTAGA GAGGGG
 ||||| |||||
 ACCTCATCT TTCCCC

 GAM297 MGC2541 5' TCCCCTTCCTAGCTCCATG 2385 _ ATGATA
 CATGGAGT AG GAGGGGA
 ||||| || |||||
 GTACCTCG TC TTCCCCT
 A C ____
 GAM297 MGC3101 3' CCCTTCTTCTACTCCA 2046 TGAT
 TGGAGTAGA AGAGGGG
 ||||| |||||
 ACCTCATCT TCTTCCC

 GAM297 NCOA2 3' TTCCCCTCTCTCATTCCCCAT 1307 AGTA T
 ATGG GATGA AGAGGGGAA
 ||| ||| |||||
 TACC TTACT TCTCCCCTT
 CC__ C
 GAM297 RBM14 3' TTCCCCTCTACCCTGCCTCC 1289 _ ATGA
 GGAG TAG TAGAGGGGAA
 ||| ||| |||||
 CCTC GTC ATCTCCCCTT
 C CC__
 GAM297 SCYA5 3' TTCCCCTCACTATCCTACCCCA 979 A AT ____
 TGG GTAG GATA GAGGGGAA
 ||| ||| ||| |||||

			ACC CATC CTAT CTCCCCTT	
			C _ CA	
GAM297	U5-116KD	3'	CCCCTTGCTCCCACTCCATG 1095	AGAT TA
			CATGGAGT GA GAGGGG	
			GTACCTCA CT TTCCCC	
			CC_ CG	
GAM297	WSB1	3'	TCCCCCACCTACTCCA 2429	A ATAGA
			TGGAGTAG TG GGGGA	
			ACCTCATC AC CCCCT	
			C _	
GAM297	LOC144501	3'	TCCCCTTCCTCCCTCCATG 3268	TAGAT TA
			CATGGAG GA GAGGGGA	
			GTACCTC CT TTCCCCT	
			C_ CC	
GAM297	LOC146940	3'	TCCCTTCCCCACTCCATG 3101	AGATGATA
			CATGGAGT GAGGGGA	
			GTACCTCA CTTCCCT	
			CCC_	
GAM297	LOC197003	3'	TCCCCTTCTCCACTCC 3418	A T TAG
			GGAGT GA GA AGGGGA	
			CCTCA CT CT TCCCCT	
			C _	
GAM297	LOC200953	5'	CCCCTCCACCTGCTCCA 3482	A ATA
			TGGAGTAG TG GAGGGG	
			ACCTCGTC AC CTCCCC	
			C _	
GAM297	LOC257541	3'	TCCCCTCTGCCACCCCA 3746	A AGAT A
			TGG GT G TAGAGGGGA	
			ACC CA C GTCTCCCCT	
			C _ C	
GAM298	G2	5'	TGGGACAGCCGACTT 2756	ATCTTA
			AAGTTGGCTGTC CCA	
			TTCAGCCGACAG GGT	
GAM298	REM	5'	ATTGGCTGACAGCCAATT 1462	TCTTA
			AGTTGGCTGTCA CCAAT	
			TTAACCGACAGT GGTTA	
			C_	
GAM298	LOC90321	3'	GTAAGATGACAGGGCTGACTT 2631	TG _
			AAGT GCT GTCATCTTAC	

			TTCA CGG CAGTAGAATG		
			GT GA		
GAM298	LOC91650	5'	ATTGGTAAACAACCAAT 2766	C	CATC
			GTTGG TGT TTACCAAT		
			TAACC ACA AATGGTTA		
			A ____		
GAM299	CD28	3'	ATAATTAATGGTACTCCTATAA 1274	ATAC	
	TT		AATTATAG GCTATTAATTAT		
			TTAATATC TGGTAATTAATA		
			CTCA		
GAM299	ABCA6	3'	ATAATTAATAGTATGTTTA 2374	CG	
			TAGATA CTATTAATTAT		
			ATTTGT GATAATTAATA		
			AT		
GAM299	FLJ21302	3'	GTAGCACAATCTATAATT 2021	AC_	
			AATTATAGAT GCTAT		
			TTAATATCTA CGATG		
			ACA		
GAM299	SLC7A11	3'	TAATAGTCCCATATCTGTAAT 1492	C__	
			ATTATAGATA GCTATTA		
			TAATGTCTAT TGATAAT		
			ACCC		
GAM300	AP2B1	3'	AGTGTTACACTGTTTGA 814	TCC	
			TTAGATA GTAACACT		
			AGTTTGT CATTGTGA		
			CA_		
GAM300	GOT1	3'	TGGTAAGAAGGATATTTAA 897	GTAACAC	
			TTAGATATCC TACCA		
			AATTTATAGG ATGGT		
			AAGA__		
GAM300	ZNF14	3'	TGGTAGTGCATGCCTCTAA 1934	TATC AA	
			TTAGA CGT CACTACCA		
			AATCT GTA GTGATGGT		
			CC_ C_		
GAM300	FLJ11827	3'	TAGTGTTTAGAATATCTAA 2136	CCGT	
			TTAGATAT AACACTA		
			AATCTATA TTGTGAT		
			AGAT		
GAM300	HEYL	3'	TGGGTTGTTGCGGACATC 1507	A	CTA
			GAT TCCGTAACA CCA		

		CTA AGGCGTTGT GGT		
		C TG_		
GAM300	LOC158722 5'	TGGTAGTGCAGCTCATCTGA 3226	ATCC	AA
		TTAGAT GT CACTACCA		
		AGTCTA CG GTGATGGT		
		CT__ AC		
GAM301	ADAMTS5 3'	AAAATTCATAGTAATCCTGCCA 1350	A	GCTC
		TGGTA GATTACTG GTTTT		
		ACCGT CTAATGAT TAAAA		
		C ACT_		
GAM301	SLC38A4 3'	GACGTTTACCAGTAATATCACC 1774	AAG	CT__
	A	TGGT ATTACTGG CGTT		
		ACCA TAATGACC GCAG		
		CTA ATTT		
GAM302	SLC19A2 3'	ATGGAATGTGGTACAAATTGTT 2835	G	A AAAT
		AA AATTT TAT CATTCCAT		
		TT TTAAG ATG GTAAGGTA		
		G C GT__		
GAM302	COLEC12 3'	ATGGACTGAATCACATAGATTC 2165	ATAAA	T
	T	AGAATTTAT TCA TCCAT		
		TCTTAGATA AGT AGGTA		
		CACTA C		
GAM302	COLEC12 3'	ATGGACTGAATCACATAGATTC 2395	ATAAA	T
	T	AGAATTTAT TCA TCCAT		
		TCTTAGATA AGT AGGTA		
		CACTA C		
GAM302	SH3BGRL 3'	ATGGAATGATATATCCAAGTTC 2615	AT	A
		GAATTT ATA ATCATTCCAT		
		CTTGAA TAT TAGTAAGGTA		
		CC A		
GAM302	LOC150848 5'	GAATGATTTGGAGTTCTT 3334	ATA	
		AAGAATTT TAAATCATTC		
		TTCTTGAG GTTTAGTAAG		
		—		
GAM302	LOC219846 3'	ATGAAATGATTTTATAATTCT 3504	T T	C
		AGAATT ATA AAATCATT CAT		
		TCTTAA TAT TTTAGTAA GTA		
		_ T A		
GAM303	DRD1 3'	ATTAACCTCCGTTTCCAAATACA 774	GCTCCT	
		TGTAT AGCGGAGTTAAT		

			ACATA	TTGCCTCAATTA		
			AACCT_			
GAM303	KIAA0182	3'	AAGTCCTAGGAGCACACA	2931	A	GC G
			TGT TGCTCCTA	GGA TT		
			ACA ACGAGGAT	CCT AA		
			C	_ G		
GAM303	SSH2	3'	AGCCCCAGGAGCATACA	2626		AGC A
			TGTATGCTCCT	GG GTT		
			ACATACGAGGA	CC CGA		
			C	_ _		
GAM303	LOC90918	5'	ATTAAATCCAGGAACATATA	2687	C	AGC G
			TGTATG TCCT	GGA TTAAT		
			ATATAC AGGA	CCT AATTA		
			A	_ A		
GAM304	PAFAH1B2	3'	ACATTCATTGAATTATTATCAC	937	A	_
			TG	CAGT ATAATAATTCAGT AATGT		
			GTCA TATTATTAAGTTA	TTACA		
			C	C		
GAM305	GL004	3'	CGACAGAATAAGGTACAAATGT	2736	A	G C_ A
			AG	CTACATTT TAT TT TCT TCG		
			GATGTAAA ATG AA	AGA AGC		
			C	G TA C		
GAM305	KIAA1336	3'	CGATTTTCATATAAATGTATGA	2942	_	TTCTCT
			TC TACATTTATATG	ATCG		
			AG ATGTAAATATAC	TAGC		
			T	TTT_		
GAM305	LOC147711	3'	GAGAAAAACCATATAAATG	3112	_	
			CATTTATATG	TTCTC		
			GTAAATATAC	AAGAG		
			CAAA			
GAM306	B3GALT3	3'	TACTACACTGCCAGTTGTA	1058		ATA
			TACAA GCAGTGTAGTG			
			ATGTT CGTCACATCAT			
			GAC			
GAM306	CSNK1G3	3'	TACTGATGGTACTGTTATT	1106		TA G
			AATAGCAGTG	GT CAGTA		
			TTATTGTCAT	TA GTCAT		
			GG	_		
GAM306	DSC3	3'	TACTGCACTACCAAATTCATTT	2061		AGCAGT_
			G	CAAAT GTAGTGCAGTA		

			GTTTA CATCACGTCAT	
			CTTAAAC	
GAM306	DSC3	3'	TACTGCACTACCAAATTCATTT 872	AGCAGT_
	G		CAAAT GTAGTGCAGTA	
			GTTTA CATCACGTCAT	
			CTTAAAC	
GAM306	STK24	3'	CAGAACA CTCTATTTGTA 1037	C AG
			TACAAATAG AGTGT TG	
			ATGTTTATC TCACA AC	
			C AG	
GAM306	SUV39H2	3'	TACTCACTGTACTTGTA 2080	ATA T
			TACAA GCAGTG AGTG	
			ATGTT TGTCAC TCAT	
			CA_ _	
GAM306	TAC1	3'	TATTACACTGTATTTGTA 1456	G
			TACAAATA CAGTGTAGTG	
			ATGTTTAT GTCACATTAT	
			—	
GAM306	TAC1	3'	TATTACACTGTATTTGTA 1457	G
			TACAAATA CAGTGTAGTG	
			ATGTTTAT GTCACATTAT	
			—	
GAM306	TAC1	3'	TATTACACTGTATTTGTA 1458	G
			TACAAATA CAGTGTAGTG	
			ATGTTTAT GTCACATTAT	
			—	
GAM306	TAC1	3'	TATTACACTGTATTTGTA 996	G
			TACAAATA CAGTGTAGTG	
			ATGTTTAT GTCACATTAT	
			—	
GAM306	UBQLN1	3'	TACTGCATGCATCACTTCTG 1452	C TA__
			TAG AGTG GTGCAGTA	
			GTC TCAC TACGTCAT	
			T TACG	
GAM306	ZNF207	3'	GCTTACATTGCTATTTGTA 1023	T
			TACAAATAGCAGTGTAG GC	
			ATGTTTATCGTTACATT CG	
			—	
GAM306	AKAP12	3'	TACTACATGCTTTTTGTA 1185	T G
			TACAAA AGCA TGTAGTG	

			ATGTTT TCGT ACATCAT		
			T _		
GAM306	AKAP12	3'	TACTACATGCTTTTGTGTA 2481	T G	
			TACAAA AGCA TGTAGTG		
			ATGTTT TCGT ACATCAT		
			T _		
GAM306	FLJ10352	3'	CACTACAATTATGCTTTTGTGTA 2232	T G__	
			TACAAA AGCA TGTAGTG		
			ATGTTT TCGT ACATCAC		
			_ ATTA		
GAM306	FLJ11222	3'	CACTACAGAGCACTGTTTG 1819	_ AG	
			CAAATA GC TGTAGTG		
			GTTTGT CG ACATCAC		
			CA AG		
GAM306	FLJ14641	3'	TACTGCCTGTGCTGCTA 2284	TG T	
			TAGCAG TAG GCAGTA		
			ATCGTC GTC CGTCAT		
			GT _		
GAM306	FLJ23537	3'	ACTGCAGTACTGTTTGTA 2105	GCAGT G	
			TACAAATA GTA TGCAGT		
			ATGTTTGT CAT ACGTCA		
			_____ G		
GAM306	KIAA1161	5'	ACTGCACTAACCCATTTGTG 3212	AGCA G	
			TACAAAT GT TAGTGCAGT		
			GTGTTTA CA ATCACGTCA		
			CC__ _		
GAM306	MGC10646	3'	CACTACGCTGCCATTTTA 2270	C A	
			A AAAT GCAGTGTAGTG		
			A TTTA CGTCGCATCAC		
			T C		
GAM306	MLL5	3'	TACAGTCTCACACTGCTATCGT 3644	AA _ T A	
	A		TAC ATAGCAGTGT AG GC GTA		
			ATG TATCGTCACA TC TG CAT		
			C_ C _ A		
GAM306	ZAK	3'	ACTGCACATATTGCTTTTG 2426	T A	
			CAAA AGCAGTGT GTGCAGT		
			GTTT TCGTTATA CACGTCA		
			_ _		
GAM306	ZNF387	3'	ACTGTTATTACTGTTACCTG 1520	AA TAGT	
			CA TAGCAGTG GCAGT		

		GT ATTGTCAT TGTCA		
		CC TAT_		
GAM306	LOC126661 3'	ACTGCAGCCTCCGCTTCCTGT 3000	C_ T _	
		ATAG AGTG AG TGCAGT		
		TGTC TCGC TC ACGTCA		
		CT C CG		
GAM306	LOC139770 3'	CACTACCGCTGTATCTGTA 3022	A G _	
		TACA ATA CAGTG TAGTG		
		ATGT TAT GTCGC ATCAC		
		C _ C		
GAM306	LOC150577 3'	ACCGCATTGCTGCTATCTGTG 3329	A T A	
		TACA ATAGCAGTG AGTGC GT		
		GTGT TATCGTCGT TTACG CA		
		C _ C		
GAM306	LOC89919 5'	TACTACACACATTGCTATTTG 2579	A C	
		CAAATAGCAGTGT GTG AGTA		
		GTTTATCGTTACA CAC TCAT		
		_ A		
GAM306	LOC92573 5'	ACCGCAGGCTATGCTCTTTGTA 2869	T GT AG A	
		TACAAA AGCA GT TGC GT		
		ATGTTT TCGT CG ACG CA		
		C AT G_ C		
GAM307	NTRK2 3'	GATGGCTTCCGTGAGACA 1275	C GA	
		TGTC CACGGAAGT ATC		
		ACAG GTGCCTTCG TAG		
		A G_		
GAM307	ING3 3'	AGGATTACATAGACAAT 1879	CCACGGAA	
		ATTGTC GTGAATCCT		
		TAACAG CATTAGGA		
		ATA_____		
GAM307	KIAA1164 5'	AAGGAACGCTTCCCGGGACAAT 2861	AC AA	
		ATTGTCCC GGAAGTG TCCTT		
		TAACAGGG CCTTCGC AGGAA		
		C_ A_		
GAM307	LOC150577 5'	AAGGAATTATTTCCACGAGACA 3328	CCAC A	
	A	TTGTC GGAAGTGA TCCTT		
		AACAG CCTTTATT AGGAA		
		AGCA A		
GAM307	LOC199936 3'	AAGGGGCCCCCATGGGACAA 3474	C AA GAA	
		TTGTCCCA GG GT TCCTT		

AACAGGGT CC CG GGGAA
A CC ____
GAM307 LOC257235 3' AAGGATTTTCAGTATTCATGGGA 3727 C AG_ _
CAA TTGTCCCA GGA TGAA TCCTT
||||||| ||| ||| |||||
AACAGGGT CTT ACTT AGGAA
A ATG T
GAM308 COL19A1 3' ATCCACATGGTACAAGCCTTTC 863 ACCA G _
TCA TGAGAAAG GTA TAT TGGAT
||||||| ||| ||| |||||
ACTCTTTC CAT GTA ACCTA
CGAA G C
GAM308 EFEMP1 3' ATCCACTAAACTGGTCTTCTTC 1089 GA AG T
A TGA AAGACCAGT TA TGGAT
||| ||||||| || |||||
ACT TTCTGGTCA AT ACCTA
TC A_ C
GAM308 EFEMP1 3' ATCCACTAAACTGGTCTTCTTC 1864 GA AG T
A TGA AAGACCAGT TA TGGAT
||| ||||||| || |||||
ACT TTCTGGTCA AT ACCTA
TC A_ C
GAM308 FACL2 3' ATCCCTGCTACTGTCCCTTCTC 1943 A_ C TT
A TGAGAA GAC AGTAGTA GGAT
||||| ||| ||||||| |||||
ACTCTT CTG TCATCGT CCTA
CC _ C_
GAM308 HDGF 3' CCTCTTCCTACTGGTCTCTCT 1120 A TATT_
AGA AGACCAGTAG GG
||| ||||||| ||
TCT TCTGGTCATC CC
C CTTCT
GAM308 HGF 3' ATCCAAGTAGTTGCTGGTCTCT 3642 GAA _ _
ATCA TGA AGACCAGTAG TA TTGGAT
||| ||||||| || |||||||
ACT TCTGGTCGTT AT AACCTA
ATC G C
GAM308 NFE2L1 3' CCAATATATCTTCTCA 999 A CCAGTA
TGAGAA GA GTATTGG
||||| || |||||||
ACTCTT CT TATAACC
_ A____
GAM308 NLGN1 5' CCATTATACAGTCTTTCTCA 1592 CA GTAT
TGAGAAAGAC GTA TGG
||||||||| ||| |||
ACTCTTTCTG CAT ACC
A_ ATT_
GAM308 SLC21A2 3' ACTAACCCTGGTCTTTCCCA 1232 A ____
TG GAAAGACCAG TAGT
|| ||||||||| |||||

			AC CTTTCTGGTC ATCA	
			C CCA	
GAM308	FHR5	3'	ATCCAATACTAAATACCCCTTA 2166	AAAGACCAG
			TGAG TAGTATTGGAT	
			ATTC ATCATAACCTA	
			CCCATAA__	
GAM308	FLJ13710	3'	CTGGTGCTACTGGTCTTTCT 2091	TG
			AGAAAGACCAGTAGTAT G	
			TCTTTCTGGTCATCGTG C	
			GT	
GAM308	KIAA1155	3'	ATCACGGGCTAATAATCTTTCT 2628	CCAG ATTG
			CA TGAGAAAGA TAGT GAT	
			ACTCTTTCT ATCG CTA	
			AATA GGCA	
GAM308	SEF	3'	TCTCTCACTACCTTTCTCA 2860	ACCA ATT
			TGAGAAAG GTAGT GGA	
			ACTCTTTC CATCA TCT	
			____ CTC	
GAM308	TREX1	5'	ATCCAGTAATCCAGTCTCCCTC 2337	AA CAGTAG
			A TGAG AGAC TATTGGAT	
			ACTC TCTG ATGACCTA	
			CC ACCTA_	
GAM308	TRIM6	3'	ATCCAATACATATTTTTCTC 2366	CCA A
			GAGAAAGA GT GTATTGGAT	
			CTCTTTTT TA CATAACCTA	
			A__ _	
GAM308	VEST1	3'	ATTCTCTACCACTGCTCTTTCT 2349	C A TT
			CA TGAGAAAGA CAGT GTA GGAT	
			ACTCTTTCT GTCA CAT CTTA	
			C C CT	
GAM308	LOC149076	5'	ATGCCCACTGACCTTTTTCA 3128	AC A_
			TGAGAAAG CAGT GTAT	
			ACTTTTTTC GTCA CGTA	
			CA CC	
GAM308	LOC254043	3'	ATCTTTCTCTCTAGTCTTTCTC 3667	C T TATT
			A TGAGAAAGAC AG AG GGAT	
			ACTCTTTCTG TC TC TCTA	
			A _ TCTT	
GAM309	BUB3	3'	AAAGGTATTTGGGCAAAC 1149	A_ T
			GTTT TCA ATACCTTT	

			CAAA GGT TATGGAAA		
			CG T		
GAM309	CLCN6	3'	TAAAGGTATGTGCTATGATAAA 815	_____	III
			TTTATCATA TACCTTT A		
			AAATAGTAT ATGGAAA T		
			CGTGT III		
GAM309	CLCN6	3'	TAAAGGTATGTGCTATGATAAA 1957	_____	III
			TTTATCATA TACCTTT A		
			AAATAGTAT ATGGAAA T		
			CGTGT III		
GAM309	CLCN6	3'	TAAAGGTATGTGCTATGATAAA 1958	_____	III
			TTTATCATA TACCTTT A		
			AAATAGTAT ATGGAAA T		
			CGTGT III		
GAM309	CMAR	3'	AAAGGAAGTGATAAACTA 1193	ATA	
			TAGTTTATCAT CCTTT		
			ATCAAATAGTG GGAAA		
			AA_		
GAM309	CTPS	3'	AAAGGTATTTGGGAAACT 3441	AT T	
			AGTTT CA ATACCTTT		
			TCAA GT TATGGAAA		
			GG T		
GAM309	RB1	3'	AAAGGTGTATTTAAACTA 3505	TC	
			TAGTTTA ATATACCTTT		
			ATCAAAT TATGTGGAAA		
			T_		
GAM309	RP2	3'	AAAGGTATATGCAATGCTA 1339	TTAT	
			TAGT CATATACCTTT		
			ATCG GTATATGGAAA		
			TAAC		
GAM309	WHSC1	3'	AAAGGTATATGTGATAAAT 1394	—	
			GTTTATCAT ATACCTTT		
			TAAATAGTG TATGGAAA		
			TA		
GAM309	ARHGAP11A	3'	AAGGGTAGAGATAAACT 1546	ATA	
			AGTTTATC TACCTTT		
			TCAAATAG ATGGGAA		
			AG_		
GAM309	FLJ20533	3'	AAAGGTATGTGAATAAAT 1758	—	
			GTTTAT CATATACCTTT		

			TAAATA GTGTATGGAAA		
			A		
GAM309	MGC16063	3'	AAAGGCTTACTGATAAACT	2356	_ TA
			AGTTTATCA TA CCTTT		
			TCAAATAGT AT GGAAA		
			C TC		
GAM309	SEMA3C	3'	AAAGGTATAATTAAACT	1293	TCA
			AGTTTA TATACCTTT		
			TCAAAT ATATGGAAA		
			TA_		
GAM309	LOC135293	3'	AAGGTATAATAAACTG	3047	CA
			TAGTTTAT TATACCTT		
			GTCAAATA ATATGGAA		
			—		
GAM309	LOC153883	3'	AAAGGTATATTTGACTA	3182	TATC
			TAGTT ATATACCTTT		
			ATCAG TATATGGAAA		
			TT_		
GAM309	LOC199692	3'	GAGGGTGTAATAAACTG	2521	CA
			TAGTTTAT TATACCTTT		
			GTCAAATA ATGTGGGAG		
			—		
GAM310	MGC5242	5'	CCTTACAATCCGAGACTA	2042	—
			TGGTCTCGGATT AGG		
			ATCAGAGCCTAA TCC		
			CAT		
GAM310	LOC197259	3'	GCCAATCAAGACCAGAA	3422	CG A
			TTCTGGTCT GATT GGC		
			AAGACCAGA CTAA CCG		
			A_ _		
GAM311	CRYBA4	3'	AAACTCAAACGAATAAAAAAG	865	_ ATC
			CTTTTTTAT CGTT GGTTTT		
			GAAAAAATA GCAA TCAAAA		
			A AC_		
GAM311	UHL1	3'	GCTGATAAGATAAAAAA	1093	G
			TTTTTTATC TTATCGGT		
			AAAAAATAG AATAGTCG		
			—		
GAM311	BDG-29	3'	GAAAACCGTCTCATAACAAAAG	2944	_ CGTTAT
	G		CCTTTT TTAT CGGTTTTT		

			GGAAAA AATA GCCAAAAG		
			C CTCT__		
GAM311	ERG-1	5'	GAAATTTCAATGATAAAAAAGG 1972	ATC	
			CCTTTTTTATCGTT GGTTTT		
			GGAAAAAATAGTAA TTAAAG		
			CT_		
GAM311	LOC199837	5'	GAAAGAAGAAACAATAGAAAAG 3434	C A GG	
	G		CCTTTTTTAT GTT TC TTTTC		
			GGAAAAGATA CAA AG GAAAG		
			A _ AA		
GAM312	BHLHB3	3'	AAGTCCAAACTGATATATCCTA 2160	A	TTAAA
			TAG ATATATT GGACTT		
			ATC TATATAG CCTGAA		
			C TCAAA		
GAM312	CLN2	3'	AAGTCCTTCCAATTATATTT 735	T TA	
			GAATATA TT AAGGACTT		
			TTTATAT AA TTCCTGAA		
			T CC		
GAM312	ZFP36L1	3'	TCCATAGAATATATTCT 1165	AA	
			AGAATATATTTTA GGA		
			TCTTATATAAGAT CCT		
			A_		
GAM312	C8orf2	3'	TCCATTTAAAATACATTG 1361	A	_
			GAAT TATTTTAAA GGA		
			CTTA ATAAAATTT CCT		
			C A		
GAM312	DKFZP566K0524	3'	AAGGATTTAAAATATATTC 2854	GGA	
			GAATATATTTTAAA CTT		
			CTTATATAAAATTT GAA		
			AG_		
GAM312	FIGNL1	3'	TTTTTAAGAATATATTCTA 1980	A	
			TAGAATATATTTT AAGGA		
			ATCTTATATAAGA TTTT		
			A		
GAM312	FLJ10704	3'	TTTTTTAAAATATATTTTA 1796		
			TAGAATATATTTTAAAGGA		
			ATTTTATATAAAATTTT		
GAM312	HDAC9-PENDING	3'	TCTTTTAAAATACATTTTA 1528	A	
			TAGAAT TATTTTAAAGGA		

			ATTTTA ATAAAATTTTCT		
			C		
GAM312	KIAA1384	3'	AAGCCTAAAATATATTTTA 2695	AA	A
			TAGAATATATTTT AGG CTT		
			ATTTTATATAAAA TCC GAA		
			— —		
GAM312	SOX30	3'	TTTCTTAAAATATATTCTG 1346	AG	
			TAGAATATATTTTAA GA		
			GTCTTATATAAAATT TT		
			CT		
GAM312	LOC221810	3'	AGTCTTTAAAATATATTCTG 3625	G	
			TAGAATATATTTTAAAG ACT		
			GTCTTATATAAAATTC TGA		
			—		
GAM312	LOC255177	3'	AGTTCTTTAAAATATTCTA 3712	A	
			TAGAATAT TTTTAAAGGACT		
			ATCTTATA AAAATTTCTTGA		
			—		
GAM313	ADRA1A	3'	TTCCCATAGACACCCAGCCCAT 2327	CCA__	A
	AG		CTATGGGT TCTATG GAA		
			GATACCCG AGATAC CTT		
			ACCCAC C		
GAM313	ARF3	3'	TTCTCATAAATGGATCTG 845	C	
			TGGGTCCAT TATGAGAA		
			GTCTAGGTA ATACTCTT		
			A		
GAM313	C14orf1	3'	TCTCTGCTGCTGGACCCAAGA 1362	A	TCTAT_
			TCT TGGGTCCA GAGA		
			AGA ACCCAGGT CTCT		
			— CGTCGT		
GAM313	CTNNA2	3'	TTCTCATAAAATTGGGCACA 1108	G	TC__
			TG GTCCA TATGAGAA		
			AC CGGGT ATACTCTT		
			A TAAA		
GAM313	FAT2	3'	TTCTCATACCTGCCCACAG 829	A	CCATC
			CT TGGGT TATGAGAA		
			GA ACCCG ATACTCTT		
			C TCC__		
GAM313	GALNT3	3'	TTCAATGGACCCACAGG 1118	A	CTA
			TCT TGGGTCCAT TGAG		

GGA ACCCAGGTA ACTT
 C ____
 GAM313 HMG20A 3' TCTCATAGTATGCCCATA 1801 CCAT
 TATGGGT CTATGAGA
 ||||| |||||
 ATACCCG GATACTCT
 TAT_
 GAM313 HPCA 3' TCTCACACACACAGGCCCAT 903 CATCTA____
 AGA TCTATGGGTC TGAGA
 ||||| ||||
 AGATACCCGG ACTCT
 ACACACACAC
 GAM313 MTMR3 3' CTCACAGATGGATAAATG 1939 GG A
 TAT GTCCATCT TGAG
 || ||||| ||||
 GTA TAGGTAGA ACTC
 AA C
 GAM313 PIGR 3' CTCACATGGACCCAAGA 2955 A CTA
 TCT TGGGTCCAT TGAG
 || ||||| ||||
 AGA ACCCAGGTA ACTC
 _ C_
 GAM313 PIWIL1 3' TTCTCATAGATATTTTGTG 2959 GG TCC
 TAT G ATCTATGAGAA
 || | |||||
 GTG T TAGATACTCTT
 TT TA_
 GAM313 SORBS1 3' TTCTCATAGAACACCA 1625 _ CCA
 TGG GT TCTATGAGAA
 || | |||||
 ACC CA AGATACTCTT
 A ____
 GAM313 TOP3A 3' TTCTCATAGACGTCCTGAGA 1132 A TCCA
 TCT TGGG TCTATGAGAA
 || ||| |||||
 AGA GTCC AGATACTCTT
 _ TGC_
 GAM313 UC28 3' TTCTCAATCTTGAACATCATAGA 1951 C TCTA
 TCTATGGGT CA TGAGAA
 ||||| || |||||
 AGATACTCA GT ACTCTT
 A TCTA
 GAM313 ARL5 3' TTCTCATAGATTTTGTA 1406 GG TCC
 TAT G ATCTATGAGAA
 || | |||||
 ATG T TAGATACTCTT
 TT ____
 GAM313 DDM36 3' TCTCATAGGAGCATAGA 1932 GG ATC
 TCTATG TCC TATGAGA
 ||||| || |||||

			AGATAC AGG ATACTCT		
			G_ _		
GAM313	FLJ21596	3'	TCTCAGGGTGGGACCCATA	2093	_ A
			TATGGGTCC ATCT TGAGA		
			ATACCCAGG TGGG ACTCT		
			G _		
GAM313	FLJ22202	5'	TCCAGGAGATGGACCAACAGA	2102	ATG A_ A
			TCT GGTCCATCT TG GA		
			AGA CCAGGTAGA AC CT		
			CAA GG _		
GAM313	GPNMB	3'	TCTCATAAATGGGTGGGA	935	ATGGG C
			TCT TCCAT TATGAGA		
			AGG GGGTA ATACTCT		
			GT_ A		
GAM313	HSZFP36	3'	CAGGAGATGGACCCCAGA	2659	AT A_
			TCT GGTCCATCT TG		
			AGA CCCAGGTAGA AC		
			C_ GG		
GAM313	IPLA2(GAMMA)	3'	TTCTCATAAATGAAGGTCTGT	2577	GT_ C
			ATGG C CAT TATGAGAA		
			TGTC G GTA ATACTCTT		
			TG AA A		
GAM313	KIAA0648	3'	TTCTCATAGATAATCAAGA	3258	A GTCC
			TCT TGG ATCTATGAGAA		
			AGA ACT TAGATACTCTT		
			_ AA_		
GAM313	KIAA1239	3'	TTCATGTAACCCATAGA	2915	CCATC
			TCTATGGGT TATGAG		
			AGATACCCA GTACTT		
			AT_		
GAM313	KIAA1577	5'	TTCTCATGGGTACCCCAGA	2691	AT CC
			TCT GGGT ATCTATGAGAA		
			AGA CCCA TGGGTACTCTT		
			C_ _		
GAM313	KIAA1821	3'	CTCATCCTGTACCTATAGA	2926	C TCT
			TCTATGGGT CA ATGAG		
			AGATATCCA GT TACTC		
			T CC_		
GAM313	KIAA1853	5'	CTCAGGATGGACCCTCAGA	2857	AT A
			TCT GGTCCATCT TGAG		

AGA CCCAGGTAGG ACTC
 CT _
 GAM313 MGC3169 3' TCTCTGCCAGGACCCCATAGA 2051 _ ATCTAT
 TCTATGGG TCC GAGA
 ||||| ||| ||||
 AGATACCC AGG CTCT
 C ACCGT_
 GAM313 MST4 3' TTCATATGGACCCAGAGA 1696 A TC
 TCT TGGGTCCA TATGAG
 ||| ||||| |||||
 AGA ACCCAGGT ATAATT
 G _
 GAM313 PDE10A 3' ATTCTCACAGATCAGATCACTC 1321 ____ C_ A |||
 CATAGA TGG GTC ATCT TGAGAA T
 ||| ||| ||||| ||||| |
 ACC TAG TAGA ACTCTT A
 TCAC AC C |||
 GAM313 SKD3 3' TTCTAAGGGGAAGGGACCCATA 2170 A_ ATG_
 GA TCTATGGGTCC TCT AGAA
 ||||| ||| ||||
 AGATACCCAGG AGG TCTT
 GA GGAA
 GAM313 STX18 3' CTCATGGGCACTCACAGA 1714 A CCA
 TCT TGGGT TCTATGAG
 ||| ||||| |||||
 AGA ACTCA GGGTACTC
 C C_
 GAM313 LOC115811 5' CTCTGTGGACCTACAGA 2441 A CTAT
 TCT TGGGTCCAT GAG
 ||| ||||| |||
 AGA ATCCAGGTG CTC
 C T_
 GAM313 LOC131308 3' TTCCAGCCTGAACCCATGGA 3013 C TCTA A
 TCTATGGGT CA TG GAA
 ||||| || |||||
 AGGTACCCA GT AC CTT
 A CCG_ _
 GAM313 LOC139221 3' TCTCATAGATACTAGTTGA 3036 TATG CC
 TC GGT ATCTATGAGA
 || ||| |||||
 AG TCA TAGATACTCT
 TTGA _
 GAM313 LOC158490 5' TCTCATAGGACTGTCCTAGA 3220 T TCCA
 TCTA GGG TCTATGAGA
 |||| ||| |||||
 AGAT CCT GGATACTCT
 _ GTCA
 GAM313 LOC221466 5' CTCAGGATCCATAGA 3618 ATCTA
 TCTATGGGTCC TGAG
 ||||| |||

AGATACCTAGG ACTC

GAM313 LOC221540 3' TTCTCATAAATCCCCGCCCA 3621 CC__ C
TGGGT AT TATGAGAA
|||| |||||||
ACCCG TA ATACTCTT
CCCC A

GAM313 LOC222233 5' CTCAGCAGAGACAGACCCCAGA 3648 AT CA__ A_
TCT GGGTC TCT TGAG
||| |||| ||| ||||
AGA CCCAG AGA ACTC
C_ ACAG CG

GAM313 LOC255042 3' TTCTCACAGATGGGCAGCA 3671 G_ A
TG GTCCATCT TGAGAA
|| ||||||| |||||
AC CGGGTAGA ACTCTT
GA C

GAM313 LOC256117 3' CTCATTGAGACCCCATAGA 3705 _ CATCT
TCTATGGG TC ATGAG
||||||| || |||||
AGATACCC AG TACTC
C AGCT_

GAM313 LOC257545 3' TTCTCATAAATCCCCGCCCA 3747 CC__ C
TGGGT AT TATGAGAA
|||| |||||||
ACCCG TA ATACTCTT
CCCC A

GAM313 LOC257598 3' TTCTCATAAATCCCCGCCCA 3750 CC__ C
TGGGT AT TATGAGAA
|||| |||||||
ACCCG TA ATACTCTT
CCCC A

GAM314 CHAC 3' TGCCCATATGTCCATTTAT 1612 AGAT
ATAAGTGGACATAT GCA
||||||||||| |||
TATTTACCTGTATA CGT
CC__

GAM314 GGCX 3' CTGCACCCTGCCACTTGT 778 A TATAGA
ATAAGTGG CA TGCAG
||||||| || |||||
TGTTCAAC GT ACGTC
_ CCC__

GAM314 ITPKB 3' TCTGCATCTGTCCAC 911 TATA
GTGGACA GATGCAGA
||||||| |||||||
CACCTGT CTACGTCT

GAM314 KCNAB1 3' TCTAATGTTATGTCCACTTA 2584 ____
TAAGTGGACATA TAGA
||||||||||| ||||

ATTCACCTGTAT ATCT
 TGTA
 GAM314 KLRC4 5' CTGTCAAAATATACACCACTTA 1451 ACA GA_ _
 T ATAAGTGG TATA TG CAG
 ||||| ||| ||||
 TATTCACC ATAT AC GTC
 AC_ AAA T
 GAM314 MLF2 3' TCTGCATCTACTGACTTG 1212 _ ACATA
 TAAGT GG TAGATGCAGA
 ||||| || |||||
 GTTCA TC ATCTACGTCT
 G _
 GAM314 NR1I2 3' TCTGCATCCATTTGAACAC 1971 GA T A
 GTG CA AT GATGCAGA
 ||| ||| |||||
 CAC GT TA CTACGTCT
 AA T C
 GAM314 NR1I2 3' TCTGCATCCATTTGAACAC 1067 GA T A
 GTG CA AT GATGCAGA
 ||| ||| |||||
 CAC GT TA CTACGTCT
 AA T C
 GAM314 CEP3 3' TTCTACATCAGATGTTGTCACT 1304 _ ATA C
 TAT ATAAGTGG GACAT GATG AGAA
 ||||| |||| |||||
 TATTCAC TTGTA CTAC TCTT
 TG GA_ A
 GAM314 FHX 3' TCATGGATCATGTCCAC 1825 ATA G _
 GTGGACAT GAT CA GA
 ||||| ||| ||
 CACCTGTA CTA GT CT
 _ G A
 GAM314 FLJ10352 3' TTCTGCATCTACAACCAACAT 2233 GACATA_
 TTA TAAGTG TAGATGCAGAA
 ||||| |||||
 ATTTAC ATCTACGTCTT
 AACTCAAC
 GAM314 FLJ22127 3' TCGAGTCCATATGTCCAC 2008 A GCA
 GTGGACATAT GAT GA
 ||||| ||| ||
 CACCTGTATA CTG CT
 C AG_
 GAM314 GDAP1L1 3' TCTGCATCCATGCCAC 2043 A ATA
 GTGG CAT GATGCAGA
 ||| ||| |||||
 CACC GTA CTACGTCT
 _ C_
 GAM314 H-L(3)MBT 3' TCTGCTCTCTACCCACT 2230 ACA T T
 AGTGG TA AGA GCAGA
 ||||| ||| |||||

TCACC AT TCT CGTCT
 C__ C _
 GAM314 KIAA1340 3' TCTAAGCTATGCCCATTTAT 2846 A ____
 ATAAGTGG CATA TAGA
 ||||| ||| |||
 TATTTACC GTAT ATCT
 C CGA
 GAM314 KNSL7 3' TTCTGCATCCATATACACCCT 1905 T AC_ A
 AG GG ATAT GATGCAGAA
 || || ||| |||||
 TC CC TATA CTACGTCTT
 _ ACA C
 GAM314 P5-1 3' CTCCATTTATGTACCCAC 1322 AC C
 GTGG ATATAGATG AG
 ||| ||||| ||
 CACC TGTATTTAC TC
 CA C
 GAM314 PP1044 5' CTGCATCTTTACCTATATCCAT 1956 C T____
 TTA TAAGTGGA ATA AGATGCAG
 ||||| || |||||
 ATTTACCT TAT TCTACGTC
 A CCATT
 GAM314 SIRPB1 3' TGCATGTGTCCACTTA 1272 ATAG
 TAAGTGGA CAT ATGCA
 ||||| |||
 ATTCACCTGTG TACGT

 GAM314 LOC148811 3' CTGCATCTCTCCCCTTA 3126 T CATAT
 TAAG GGA AGATGCAG
 ||| || |||||
 ATTC CCT TCTACGTC
 C C____
 GAM314 LOC149711 3' TCCATATGTCTATCCACTTA 3315 ____ A
 TAAGTGGA CATAT GA
 ||||| ||| ||
 ATTCACCT GTATA CT
 ATCT C
 GAM314 LOC150630 5' CTGCATCTTCTGCCACT 3332 A TAT
 AGTGG CA AGATGCAG
 |||| || |||||
 TCACC GT TCTACGTC
 _ CT_
 GAM314 LOC150819 5' CTGCATTTTAGTCCAACCT 3333 _ ATAT
 AGT GGAC AGATGCAG
 || ||| |||||
 TCA CCTG TTTACGTC
 A AT_
 GAM314 LOC154877 3' TCTGCATCCATTCCACT 3373 CAT A
 AGTGGA AT GATGCAGA
 |||| || |||||

TCACCT TA CTACGTCT
 ____ C
 GAM314 LOC158327 3' TTCTGCAGGGACACCACTTAT 3216 ACATATAGA
 ATAAGTGG TGCAGAA
 ||||| |||||
 TATTCACC ACGTCTT
 ACAGGG____
 GAM314 LOC196540 3' TCTGCATCCATGTACTCC 3467 C_ A
 GGA ATAT GATGCAGA
 || ||| |||||
 CCT TGTA CTACGTCT
 CA C
 GAM314 LOC220394 5' TCTCAGAATATGTCCAT 3581 AGA C
 GTGGACATAT TG AGA
 ||||| || |||
 TACCTGTATA AC TCT
 AG_ _
 GAM314 LOC254428 3' CTGTTGACCCATGTCCACCTAT 3677 A ATAGAT
 ATA GTGGACAT GCAG
 || ||||| |||
 TAT CACCTGTA TGTC
 C CCCAGT
 GAM314 LOC92405 3' TTCTGTTACACATGTCTACTTA 2848 ATAGAT
 TAAGTGGACAT GCAGAA
 ||||| |||||
 ATTCATCTGTA TGTCTT
 CACAT_
 GAM315 PIGH 3' CAAGATCATAGTATTTTCAGTCA 1126 T _ GTA
 TG CT AAAT ATTATGATCTTG
 || ||| |||||
 AC GA TTTA TGATACTAGAAC
 T C ____
 GAM315 PRSC 3' CAAGATCATAATTTTATAGA 1313 AATGT
 TCTA AATTATGATCTTG
 ||| |||||
 AGAT TTAATACTAGAAC
 ATT_
 GAM315 PXMP4 3' CAAGATCATAGGCCTCAGAC 1370 AAATGTAA
 GTCT TTATGATCTTG
 ||| |||||
 CAGA GATACTAGAAC
 CTCCG____
 GAM316 C1orf1 5' TATGCTGACAGAAGAACCA 809 CC A A
 TGGTTCTTT GT CA CATA
 ||||| || |||
 ACCAAGAAG CA GT GTAT
 A_ _ C
 GAM316 LRAT 3' AGTATGCATACATAAAAGCAAC 2556 _ CC_ CAA
 CA
 TGGTTCTTT GTA CATACT
 ||||| ||| |||||

ACCAA GAAA CAT GTATGA
 C ATA AC_
 GAM316 MYBL1 3' AGTATGTTATACAAATGCCA 2679 TCTTTCC C
 TGGT GTA AACATACT
 |||| ||| |||||
 ACCG CAT TTGTATGA
 TAAA__ A
 GAM316 KIAA1028 3' TATGTCTGCATTGAAAAGAACC 3547 C TA_ _
 A TGGTTCTTT CG CA ACATA
 ||||| || |||
 ACCAAGAAA GT GT TGTAT
 A TAC C
 GAM316 MGC2488 3' TGTAGTGGAAAGAAGCAT 2045 G _
 ATG TTCTTTCCG TACA
 ||| ||||| |||
 TAC AAGAAAGGT ATGT
 G G
 GAM317 CX3CR1 3' ACTGCCTACTGCATCGAGTCA 2891 TCCCTTAA
 TGACTCG TAGGCAGT
 ||||| |||||
 ACTGAGC ATCCGTCA
 TACGTC__
 GAM317 WNT14 3' CTGCAAGGGACGAGTC 1014 AATAG
 GACTCGTCCCTT GCAG
 ||||| |||
 CTGAGCAGGGAA CGTC

 GAM317 FLJ20275 3' TACTGCCTTCATAAGATCAAGT 1745 CGTCC AT_
 CA TGACT CTTA AGGCAGTA
 |||| ||| |||||
 ACTGA GAAT TCCGTCAT
 ACTA_ ACT
 GAM317 FLJ22390 5' TACTGCCTATCAAACG 2002 CCC A
 CGT TT ATAGGCAGTA
 ||| ||| |||||
 GCA AA TATCCGTCAT
 _ C
 GAM318 LOC120864 5' CAAGGTCCAAACTGATATAA 2986 CGTAG
 TTGTATCAGTTT TCTTG
 ||||| |||
 AATATAGTCAAA GGAAC
 CCT__
 GAM319 KIAA0626 3' AACATCAGGGTGCAGAATTGAT 1954 C_ A_
 ATCGATTG CAT TGATGTT
 ||||| ||| |||||
 TAGTTAAG GTG ACTACAA
 AC GG
 GAM319 KIAA1239 3' AACATCATGATTATTGATG 2914 TCCCA
 CATCGAT TATGATGTT
 ||||| |||||

			GTAGTTA GTACTACAA		
			TTA__		
GAM319	LOC201475	5'	AACATCATATATTTTGATGTTA 3428		TTCCC
			TAACATCGA ATATGATGTT		
			ATTGTAGTT TATACTACAA		
			TTA__		
GAM320	CAPN2	3'	AAAACTTTATGAACTTCACCA 855 A _ AAA		
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM320	DAAM2	3'	AAAATTTTTCTAAAACTCCATC 3559 CG A		
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM320	SELE	3'	AAAACTCTCCTACACTTCCATT 747 _ C AAAA		
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM320	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570 C AAAA		
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM320	LOC222671	5'	GCTTCTACGACTCCGCCA 3582 A AAA		
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM320	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699 A _ A A		
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM320	LOC257615	5'	GCTTCTACGACTCCGCCA 3749 A AAA		
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM321	CAPN2	3'	AAAACTTTATGAACTTCACCA 855 A _ AAA		
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM321	DAAM2	3'	AAAATTTTTCTAAAACTCCATC 3559 CG A		
	A		TGATGGAGT TA AAAAGTTTT		

			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM321	SELE	3'	AAAACCTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM321	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM321	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM321	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A _ A A	
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM321	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM322	CAPN2	3'	AAAACCTTTATGAACTTCACCA 855	A _	AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM322	DAAM2	3'	AAAATTTTTCTAAAACTCCATC 3559	CG A	
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM322	SELE	3'	AAAACCTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM322	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM322	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		

			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM322	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A	_ A A
			TG TGGAGTC GT AA AAGTT			
			AC ACCTCAG CA TT TTAA			
			C	T C C		
GAM322	LOC257615	5'	GCTTCTACGACTCCGCCA	3749	A	AAA
			TG TGGAGTCGTA AAGT			
			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM323	CAPN2	3'	AAAACTTTATGAACTTCACCA	855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT			
			AC ACTTCA GTATT	TCAAAA		
			C	A _		
GAM323	DAAM2	3'	AAAATTTTTCTAAACTCCATC	3559		CG A
	A		TGATGGAGT TA AAAAGTTTT			
			ACTACCTCA AT TTTTAAAA			
			AA C			
GAM323	SELE	3'	AAAACTCTCCTACACTTCCATT	747		_ C AAAA
	A		TGATGGA GT GTA AGTTTT			
			ATTACCT CA CAT	TCAAAA		
			T _ CCTC			
GAM323	KIAA0475	3'	AAAACCTTGCAATTCCATCA	1570		C AAAA
			TGATGGAGT GTAA GTTTT			
			ACTACCTTA CGTT	CAAAA		
			_ C__			
GAM323	LOC222671	5'	GCTTCTACGACTCCGCCA	3582	A	AAA
			TG TGGAGTCGTA AAGT			
			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM323	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A	_ A A
			TG TGGAGTC GT AA AAGTT			
			AC ACCTCAG CA TT TTAA			
			C	T C C		
GAM323	LOC257615	5'	GCTTCTACGACTCCGCCA	3749	A	AAA
			TG TGGAGTCGTA AAGT			
			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM324	CAPN2	3'	AAAACTTTATGAACTTCACCA	855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT			

			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM324	DAAM2	3'	AAAATTTTCTAAAACTCCATC 3559	CG	A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM324	SELE	3'	AAAACCTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM324	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C _		
GAM324	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM324	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM324	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM325	CAPN2	3'	AAAACCTTTATGAACTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM325	DAAM2	3'	AAAATTTTCTAAAACTCCATC 3559	CG	A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM325	SELE	3'	AAAACCTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM325	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		

			ACTACCTTA CGTT CAAAA		
			_ C_		
GAM325	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C_		
GAM325	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM325	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C_		
GAM326	CAPN2	3'	AAAACTTTATGAACTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM326	DAAM2	3'	AAAATTTTTCTAAAACTCCATC 3559		CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM326	SELE	3'	AAAACTCTCCTACACTTCCATT 747		_ C AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM326	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C_		
GAM326	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C_		
GAM326	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM326	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		

			AC GCCTCAGCAT	TTCG		
			C	C__		
GAM327	CAPN2	3'	AAAAC	TTTATGAACTTCACCA	855	A _ AAA
				TG TGGAGT CGTAA AGTTTT		
				AC ACTTCA GTATT TCAAAA		
			C	A		
GAM327	DAAM2	3'	AAAAT	TTTTTCTAAAACTCCATC	3559	CG A
	A			TGATGGAGT TA AAAAGTTTT		
				ACTACCTCA AT TTTTAAAA		
				AA C		
GAM327	SELE	3'	AAAAC	TCTCCTACACTTCCATT	747	_ C AAAA
	A			TGATGGA GT GTA AGTTTT		
				ATTACCT CA CAT TCAAAA		
				T _ CCTC		
GAM327	KIAA0475	3'	AAAAC	CTTGCATTCCATCA	1570	C AAAA
				TGATGGAGT GTAA GTTTT		
				ACTACCTTA CGTT CAAAA		
				_ C__		
GAM327	LOC222671	5'	GCTTCTACGACTCCGCCA	3582	A	AAA
				TG TGGAGTCGTA AAGT		
				AC GCCTCAGCAT TTCG		
			C	C__		
GAM327	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A	_ A A
				TG TGGAGTC GT AA AAGTT		
				AC ACCTCAG CA TT TTTAA		
			C	T C C		
GAM327	LOC257615	5'	GCTTCTACGACTCCGCCA	3749	A	AAA
				TG TGGAGTCGTA AAGT		
				AC GCCTCAGCAT TTCG		
			C	C__		
GAM328	CAPN2	3'	AAAAC	TTTATGAACTTCACCA	855	A _ AAA
				TG TGGAGT CGTAA AGTTTT		
				AC ACTTCA GTATT TCAAAA		
			C	A		
GAM328	DAAM2	3'	AAAAT	TTTTTCTAAAACTCCATC	3559	CG A
	A			TGATGGAGT TA AAAAGTTTT		
				ACTACCTCA AT TTTTAAAA		
				AA C		
GAM328	SELE	3'	AAAAC	TCTCCTACACTTCCATT	747	_ C AAAA
	A			TGATGGA GT GTA AGTTTT		

			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM328	KIAA0475	3'	AAAACCTTGCATTCCATCA	1570	C AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM328	LOC222671	5'	GCTTCTACGACTCCGCCA	3582	A AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM328	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A _ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM328	LOC257615	5'	GCTTCTACGACTCCGCCA	3749	A AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM329	CAPN2	3'	AAAACCTTTATGAACTTCACCA	855	A _ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM329	DAAM2	3'	AAAATTTTTCTAAACTCCATC	3559	CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM329	SELE	3'	AAAACCTCTCCTACACTTCCATT	747	_ C AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM329	KIAA0475	3'	AAAACCTTGCATTCCATCA	1570	C AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM329	LOC222671	5'	GCTTCTACGACTCCGCCA	3582	A AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM329	LOC254901	5'	AATTTCTTCACTGACTCCACCA	3699	A _ A A
			TG TGGAGTC GT AA AAGTT		

			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM329	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM330	CAPN2	3'	AAAACCTTTATGAACTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM330	DAAM2	3'	AAAATTTTTCTAAACTCCATC 3559		CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM330	SELE	3'	AAAACCTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM330	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C__		
GAM330	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM330	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM330	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C__		
GAM331	ITGB7	5'	AGAGAAAGTCTGACTTGCCCCA 783	AAAA_	TTAT
	C		GT AAGTT CTTTCTCT		
			CA TTCAG GAAAGAGA		
			CCCCG TCT_		
GAM331	RPP30	3'	AGAGAAAGACAACTGTTCTGCG 1297	A A	TTA
			CGTA AA AGTT TCTTTCTCT		

GCGT TT TCAA AGAAAGAGA
 C G C__
 GAM331 FLJ13263 3' AGAGAAAGATTTTAGCTTTT 2139 TT_
 AAAAGTT ATCTTTCTCT
 ||||| |||||
 TTTTCGA TAGAAAGAGA
 TTT
 GAM331 FLJ23074 5' AGAGAAAGACAAGGGTTT 2133 G A
 AAA TTTT TCTTTCTCT
 ||| ||| |||||
 TTT GGAA AGAAAGAGA
 G C
 GAM331 GTF2A2 3' AGAAAAAATATGACTTTTTTAC 1119 T C_
 GTAAAAAAGTT TAT TTTCT
 ||||| ||| |||||
 CATTTTTTCAG ATA AAAGA
 T AA
 GAM331 IMP-2 3' AGAGAAAGCAGGCTTTTCTA 1308 A TAT
 TA AAAAGTTT CTTTCTCT
 || ||||| |||||
 AT TTTTCGGA GAAAGAGA
 C C_
 GAM331 KIAA0212 3' AGAAAGGTAAATCTTTTTAC 1518 A T
 GTAAAAA G TTTATCTTTCT
 ||||| |||||
 CATTTTT C AAATGGAAAGA
 _T
 GAM331 OSBPL2 5' AGAGAAAGTTTGTAATAATTCCT 1566 AAA ____
 TAC GTAA AGTTTTAT CTTTCTCT
 ||| ||||| |||||
 CATT TTAAATG GAAAGAGA
 CC_ TTT
 GAM331 OSBPL2 5' AGAGAAAGTTTGTAATAATTCCT 2482 AAA ____
 TAC GTAA AGTTTTAT CTTTCTCT
 ||| ||||| |||||
 CATT TTAAATG GAAAGAGA
 CC_ TTT
 GAM331 RBM9 3' AGAAAGAATACTTTTTTAT 1489 TTTA
 GTAAAAAAGT TCTTTCT
 ||||| |||||
 TATTTTTTCA AGAAAGA
 TA_
 GAM331 LOC254826 3' AGAGAAAGTCTTGCTTTTT 3732 TTTAT
 AAAAAGT CTTTCTCT
 ||||| |||||
 TTTTTCG GAAAGAGA
 TTCT_
 GAM332 DSC3 3' TAAATCTATGTGTTTTAGACT 871 AGT A
 TA TAAGTT AATACATA ATTTTA
 ||||| ||||| |||||

			ATTCAG TTGTGTAT TAAAAT		
			ATT C		
GAM332	DSC3	3'	TAAAATCTATGTGTTTTAGACT 2060	AGT	A
	TA		TAAGTT AATACATA ATTTTA		
			ATTCAG TTGTGTAT TAAAAT		
			ATT C		
GAM332	FLJ20366	3'	AAGTTTACATGTACTAACTTA 1751	ATACA	
			TAAGTTAGTA TAAATTT		
			ATTCAATCAT ATTTGAA		
			GTAC_		
GAM333	CAPN2	3'	AAAACTTTATGAACTTCACCA 855	A _ AAA	
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM333	DAAM2	3'	AAAATTTTTCTAAACTCCATC 3559	CG A	
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM333	SELE	3'	AAAACTCTCCTACACTTCCATT 747	_ C AAAA	
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM333	KIAA0475	3'	AAAACCTTGCAATTCCATCA 1570	C AAAA	
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C_		
GAM333	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A AAA	
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C_		
GAM333	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A _ A A	
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM333	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A AAA	
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C_		
GAM334	CAPN2	3'	AAAACTTTATGAACTTCACCA 855	A _ AAA	
			TG TGGAGT CGTAA AGTTTT		

			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM334	DAAM2	3'	AAAATTTTCTAAACTCCATC 3559	CG	A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM334	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM334	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C _		
GAM334	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM334	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM334	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM335	CAPN2	3'	AAACTTTATGAACTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM335	DAAM2	3'	AAAATTTTCTAAACTCCATC 3559	CG	A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM335	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM335	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		

			ACTACCTTA CGTT CAAAA		
			_ C_		
GAM335	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C_		
GAM335	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM335	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C_		
GAM336	CAPN2	3'	AAAACTTTATGAACTTCACCA 855	A	_ AAA
			TG TGGAGT CGTAA AGTTTT		
			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM336	DAAM2	3'	AAAATTTTTCTAAAACTCCATC 3559		CG A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM336	SELE	3'	AAAACTCTCCTACACTTCCATT 747		_ C AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM336	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C_		
GAM336	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C_		
GAM336	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTTAA		
			C T C C		
GAM336	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		

AC GCCTCAGCAT TTCG
 C C__
 GAM337 FGF2 3' ATATTTTGTGGCTGCTTTT 884 T_
 AAAAAAGT TTACAAAATAT
 ||||| |||||
 TTTTTCG GGTGTTTTTATA
 TC
 GAM337 MPHOSPH1 3' ATATTTTATAAGGCTTTTTT 1670 C
 AAAAAAGTTTAA AAAAATAT
 ||||| |||||
 TTTTTCGGAAT TTTTATA
 A
 GAM337 FLJ11274 3' ATATCTTGTAGTAGCTTTTTT 1820 _ A
 TA TAAAAAAGTT TTACAAA ATAT
 ||||| ||||| |||
 ATTTTTTTCGA GATGTTT TATA
 T C
 GAM337 FLJ31101 3' ATATTTTGTAAATGTATTTG 1771 AAAA
 T ATAAA GTTTTACAAAAATAT
 ||| |||||
 TGTTC TAAATGTTTTTATA
 ATG_
 GAM337 GPT2 3' ATATTTTGTACAATTGCTTT 2417 T____
 TTT AAAAAAGT TTACAAAATAT
 ||||| |||||
 TTTTTCG AATGTTTTTATA
 TTAAC
 GAM337 RMP 3' TTTTGTAAAACTTTTTTTTC 2430 T
 A AAAAAAAGTTTTACAAAA
 | |||||
 C TTTTTTTCAAAATGTTTT
 T
 GAM337 RMP 3' TTTTGTAAAACTTTTTTTTC 1059 T
 A AAAAAAAGTTTTACAAAA
 | |||||
 C TTTTTTTCAAAATGTTTT
 T
 GAM337 SOX6 3' ATATTTTGTCTTACTTTTTTT 2328 TTT
 AAAAAAAGT ACAAAAATAT
 ||||| |||||
 TTTTTTCA TGTTTTTATA
 TTC
 GAM337 LOC136288 3' ATATTTCTGAGGCTTTTTTTGT 3018 CAA
 ATAAAAAAGTTTAA AAATAT
 ||||| |||||
 TGTTTTTTTCGGAGT TTTATA
 C_
 GAM338 AICDA 3' AGAAAGAGAACAATATTT 1922 TTTA
 AAATATT TTCTCTTCT
 ||||| |||||

			TTTATAA AAGAGAAAGA	
			C__	
GAM338	AS3	3'	AGAAAGATTTAAAGTATTTTA 1652	TATTC
			TAAAATATTTT TCTTTCT	
			ATTTTATGAAA AGAAAGA	
			TTT__	
GAM338	EPM2A	3'	AGAAAGAGAAGTGTTTT 1234	TTTTA
			AAAATAT TTCTCTTTCT	
			TTTTGTG AAGAGAAAGA	

GAM338	HRH1	3'	AGAAAGAGAAATGAAATATTTT 780	TA
			AAAATATTTT TTCTCTTTCT	
			TTTTATAAAG AAGAGAAAGA	
			TA	
GAM338	MAPK14	3'	GAGAAAGGGCAAATTATTTTA 818	T TATT
			TAAAATA TTT CTCTTTCTC	
			ATTTTAT AAA GGGAAAGAG	
			T C__	
GAM338	MAPK14	3'	GAGAAAGGGCAAATTATTTTA 2465	T TATT
			TAAAATA TTT CTCTTTCTC	
			ATTTTAT AAA GGGAAAGAG	
			T C__	
GAM338	MAPK14	3'	GAGAAAGGGCAAATTATTTTA 2466	T TATT
			TAAAATA TTT CTCTTTCTC	
			ATTTTAT AAA GGGAAAGAG	
			T C__	
GAM338	NOTCH2	3'	GAGAATTAAAATATTTTA 2058	T
			TAAAATATTTT ATTCTC	
			ATTTTATAAAA TAAGAG	
			T	
GAM338	SIM1	3'	GAGAAAGAGAGAGATA 1181	TAT
			TATTTT TCTCTTTCTC	
			ATAGAG AGAGAAAGAG	

GAM338	C11orf25	3'	AAAGAGAAAAATATTTTA 2193	TAT
			TAAAATATTTT TCTCTT	
			ATTTTATAAAA AGAGAAA	

GAM338	DKFZP564D116	3'	GAAAAGCAATAAAAATATTTTA 2938	_ C
			TAAAATATTTTATT CT TTTC	

ATTTTATAAAAATAA GA AAAG
 C _
 GAM338 DSCR6 3' GAGAAAGAGAAGGTCTATGTCA 1866 A TTTTA
 A ATAT TTCTCTTTCTC
 ||||| |||||
 A TGTA AAGAGAAAGAG
 C TCTGG
 GAM338 FLJ10006 3' GAGAAAGAAGATATTTTA 3152 A
 TAAAATATTTTT TTCTC
 ||||| |||||
 ATTTTATAGAAG AAGAG
 A
 GAM338 HTPAP 3' GAGAATAAAAAGATTTTA 2255 A
 TAAAAT TTTTATTCTC
 ||||| |||||
 ATTTTA AAAATAAGAG
 G
 GAM338 KIAA0979 3' AGAAAGATTTAAAGTATTTTA 1601 TATTC
 TAAAATATTTT TCTTTCT
 ||||| |||||
 ATTTTATGAAA AGAAAGA
 TTT_
 GAM338 KIAA1634 3' GAGAATAAAACTATTTTA 2657 T
 TAAAATA TTTTATTCTC
 ||||| |||||
 ATTTTAT AAAATAAGAG
 C
 GAM338 PTD012 3' GAGATTGGGAACAAAAATAT 1465 A TT
 ATATTTTT TTCTC TCTC
 ||||| |||||
 TATAAAAA AAGGG AGAG
 C TT
 GAM338 SAMHD1 3' AGAAAGAGAAAGAAATAT 2593 A
 ATATTTTT TTCTCTTCT
 ||||| |||||
 TATAAAGA AAGAGAAAGA
 -
 GAM338 LOC196758 3' GAGAAAGAGCAGGTGAAATATT 3410 TATT_
 TT AAAATATTTT CTCTTTCTC
 ||||| |||||
 TTTTATAAAG GAGAAAGAG
 TGGAC
 GAM338 LOC219790 3' GAGAATAAAAATAATTTA 3520 A
 TAAA TATTTTTATTCTC
 ||| |||||
 ATTT ATAAAAATAAGAG
 A
 GAM339 CAPN2 3' AAAACTTTATGAACTTCACCA 855 A _ AAA
 TG TGGAGT CGTAA AGTTTT
 || ||||| |||||

			AC ACTTCA GTATT TCAAAA		
			C A _		
GAM339	DAAM2	3'	AAAATTTTCTAAACTCCATC 3559	CG	A
	A		TGATGGAGT TA AAAAGTTTT		
			ACTACCTCA AT TTTTAAAA		
			AA C		
GAM339	SELE	3'	AAACTCTCCTACACTTCCATT 747	_ C	AAAA
	A		TGATGGA GT GTA AGTTTT		
			ATTACCT CA CAT TCAAAA		
			T _ CCTC		
GAM339	KIAA0475	3'	AAAACCTTGCATTCCATCA 1570	C	AAAA
			TGATGGAGT GTAA GTTTT		
			ACTACCTTA CGTT CAAAA		
			_ C _		
GAM339	LOC222671	5'	GCTTCTACGACTCCGCCA 3582	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM339	LOC254901	5'	AATTTCTTCACTGACTCCACCA 3699	A	_ A A
			TG TGGAGTC GT AA AAGTT		
			AC ACCTCAG CA TT TTAA		
			C T C C		
GAM339	LOC257615	5'	GCTTCTACGACTCCGCCA 3749	A	AAA
			TG TGGAGTCGTA AAGT		
			AC GCCTCAGCAT TTCG		
			C C _		
GAM340	ADCY6	3'	TTGTACAATATTTTGTACAAAG 1617	G	TTCAC
	A		TCTTTG TACAAAAT ACAA		
			AGAAAC ATGTTTTA TGTT		
			_ TAACA		
GAM340	ADCY6	3'	TTGTACAATATTTTGTACAAAG 1933	G	TTCAC
	A		TCTTTG TACAAAAT ACAA		
			AGAAAC ATGTTTTA TGTT		
			_ TAACA		
GAM340	APBB2	5'	TGAGCTTTGTACCAAAGA 2946	AT	
			TCTTTGGTACAAA TTCA		
			AGAAACCATGTTT GAGT		
			C _		
GAM340	ATP8B2	3'	TGATTTTATACCAAAGA 2716	C	TT
			TCTTTGGTA AAAA TCA		

			AGAAACCAT TTTT AGT	
			A T_	
GAM340	CEACAM1	3'	TGTGTGAACTAGCAAAGA 848	G CAAAAT
			TCTTTG TA TTCACACA	
			AGAAAC AT AAGTGTGT	
			G C_____	
GAM340	CHST1	3'	TGTGATATTTCTTTGTGCCAAA 1046	___ T
			TTTGGTACAAA AT TCACA	
			AAACCGTGTTT TA AGTGT	
			CTT T	
GAM340	FBXL7	3'	TGCGTGTTTTCCACCAAAGA 1425	AC TTT A
			TCTTTGGT AAAA CAC CA	
			AGAAACCA TTTT GTG GT	
			CC ___ C	
GAM340	HOXC9	3'	TGCGTGCGAGATTTTGTAC 2592	_ A
			GTACAAAATTT CAC CA	
			CATGTTTTAGA GTG GT	
			C C	
GAM340	IGF1	3'	TGTGGCATTGTACCAA 763	ATT
			TTTGGTACAAA TCACA	
			AAACCATGTTT GGTGT	
			AC_	
GAM340	ITGAL	3'	TGTGAAATTCTGTCCAAA 907	T A
			TTTGG ACA AATTCACA	
			AAACC TGT TTAAAGTGT	
			_ C	
GAM340	LBR	3'	TGTA CTGGATTGCACCAAGGA 2522	A AAT C_
			TCTTTGGT CAA TTCA ACA	
			AGGAACCA GTT AGGT TGT	
			C ___ CA	
GAM340	MIP	3'	TGTGTGAAATCTTTCAAG 1399	TACAAA
			TTTGG ATTCACACA	
			GA ACT TAAAGTGTGT	
			TTC_____	
GAM340	RLN2	3'	TGTTGGTTGTACCAA 1175	AATT C
			TTTGGTACAA TCA ACA	
			AAACCATGTT GGT TGT	

GAM340	SART2	3'	TGATTTTCATACCAAAGA 1444	CA TT
			TCTTTGGTA AAA TCA	

			AGAAACCAT TTT AGT	
			AC T_	
GAM340	TPK1	3'	AAATTTTGCTACCAAAGA 1987	_
			TCTTTGGTA CAAAATT	
			AGAAACCAT GTTTTAAA	
			C	
GAM340	TRIP12	3'	TGTGTGAAATTTAAAAAAGG 1094	GGTACA
			TCTTT AAATTTACACACA	
			GGAAA TTAAAGTGTGT	
			AAA_	
GAM340	BRD3	3'	GTGTGAGATTCGTACCGAAGA 1398	AA
			TCTTTGGTAC AATTTACACAC	
			AGAAGCCATG TTAGAGTGTG	
			C_	
GAM340	FLJ13397	3'	GTGTGAAATTTACTAGCAAA 2116	G CA
			TTTG TA AAATTTACACAC	
			AAAC AT TTAAAGTGTG	
			G CA	
GAM340	FLJ22202	3'	TGTATCATTTTGTACCAAA 2103	TTC
			TTTGGTACAAAAT ACA	
			AAACCATGTTTTA TGT	
			CTA	
GAM340	GROS1	3'	TGTGTAGACAACCAAAGA 1986	ACAAAATT _
			TCTTTGGT TC ACACA	
			AGAAACCA AG TGTGT	
			AC_____ A	
GAM340	KIAA0981	3'	TGTGTAAAACTGCCAAGGA 2598	CAAAA C
			TCTTTGGTA TTT ACACA	
			AGGAACCGT AAA TGTGT	
			C_____ A	
GAM340	KIAA1243	3'	TGTGACATGACCAAAGA 2978	A AAATT
			TCTTTGGT CA TCACA	
			AGAAACCA GT AGTGT	
			_ AC_	
GAM340	KIAA1462	3'	TTGTGTGAGAGGAACCCAAAGA 3524	TACAAAA
			TCTTTGG TTTCACACAA	
			AGAAACC AGAGTGTGTT	
			CAAGG_	
GAM340	MGC1136	3'	TTGTGTGAAACCCCTAGCATAG 2041	T G CAAAA
	A		TCT TG TA TTTCACACAA	

			AGA AC AT AAAGTGTGTT		
			T G CCCC_		
GAM340	MSTP043	3'	TGTCTTTATTTTTACCAAAGA 2223	C	TTC_
			TCTTTGGTA AAAAT ACA		
			AGAAACCAT TTTTA TGT		
			_ TTTC		
GAM340	Nup43	3'	TGTGCAAAATTTTAGTATCAGA 2075	_	CA
			TTTGGTAC AAAATTT CACA		
			AGACTATG TTTTAAA GTGT		
			A AC		
GAM340	RPS6KA4	3'	TGTGCAATTACGTCCACCAAAG 1072	_	AA T
	A		TCTTTGGT AC AATT CACA		
			AGAAACCA TG TTAA GTGT		
			CC CA C		
GAM340	SLC17A6	3'	TGAAACTTGTGCCACAGA 1911	T	AA
			TCT TGGTACAA TTTCA		
			AGA ACCGTGTT AAAGT		
			C C_		
GAM340	TERA	3'	TGTATGAATAGTACCAAAG 1949	AAAAT	C
			CTTTGGTAC TTCA ACA		
			GAAACCATG AAGT TGT		
			AT_ A		
GAM340	VAV3	3'	TTGTGTAGAGTTCTAATACCAA 1273	CAA_	TC
	AGA		TCTTTGGTA AATT ACACAA		
			AGAAACCAT TTGA TGTGTT		
			AATC GA		
GAM340	LOC120892	3'	TGCAATTTTTTTTACCAAAGA 2987	C_	T
			TCTTTGGTA AAAATT CA		
			AGAAACCAT TTTTAA GT		
			TTT C		
GAM340	LOC155434	3'	TTGTGTGATTTTCGTACCAAA 3376	A	TT
			TTTGGTAC AAA TCACACAA		
			AAACCATG TTT AGTGTGTT		
			C _		
GAM340	LOC169966	3'	ATTTTGCCCTTTACCAAAGA 3252	_____	
			TCTTTGGTA CAAAAT		
			AGAAACCAT GTTTTA		
			TTCC		
GAM340	LOC221272	3'	TGTCTGCTCTGTACCAGAGA 3616	AAATTT	C
			TCTTTGGTACA CA ACA		

AGAGACCATGT GT TGT
 CTC__ C
 GAM340 LOC221968 3' TTGTGTGAAATTTTGTGCGAA 3569 GT
 TTTG ACAAATTTTCACACAA
 ||| |||||
 AAGC TGTTTTAAAGTGTGTT

 —
 GAM340 LOC86651 5' TTGTGTGAAAGATGTTTCATAC 2830 CA —
 CAAGGA CTTTGGTA AAAT TTCACACAA
 ||||| ||| |||||
 GGAACCAT TTTG AAGTGTGTT
 AC TAGA
 GAM340 LOC90322 3' GAGATTCCATACTAAAGA 2632 CAA
 TCTTTGGTA AATTTC
 ||||| |||||
 AGAAATCAT TTAGAG
 ACC
 GAM341 MYO1E 5' ATGGAGTCCCCTCTAGGGTT 1168 ATC A A
 GACC GA GG GACTCCAT
 ||| ||| |||||
 TTGG CT CC CTGAGGTA
 GAT C _
 GAM341 ROCK2 3' ATGAAGTCTTTTAACAGTCTC 2737 CATCGA C
 GAGAC AGGAGACT CAT
 |||| ||||| |||
 CTCTG TTTTCTGA GTA
 ACAA__ A
 GAM341 MGC15937 5' GAGTTTCTTCTTCAAGGTCTCA 2383 ATC —
 TGAGACC GAAGGAGA CTC
 ||||| ||||| |||
 ACTCTGG CTTCTTCT GAG
 AA_ TT
 GAM341 STK16 5' GAGCTCTTCGGTAGCCTCA 2937 ACC G A
 TGAG ATCGAAG AG CTC
 ||| ||||| |||
 ACTC TGGCTTC TC GAG
 CGA — —
 GAM341 LOC148029 5' GGAGTCTCCATCCTCA 3116 ACCATC A
 TGAG GA GGAGACTCC
 ||| ||| |||||
 ACTC CT CCTCTGAGG
 — A
 GAM341 LOC169436 5' TGGAGTTCAATGAGCTCA 3261 AC C AGGAG
 TGAG CAT GA ACTCCA
 ||| ||| ||| |||||
 ACTC GTA CT TGAGGT
 GA A —
 GAM341 LOC256267 3' ATGGAGTCTCCCTCTGTC 3713 CATC A
 GAC GA GGAGACTCCAT
 ||| ||| |||||

			CTG CT CCTCTGAGGTA		
			T__ C		
GAM341	LOC257426	3'	GAGTCCTTCGGTGGCCTCA 2755	A	GA
			TGAG CCATCGAAGGA CTC		
			ACTC GGTGGCTTCCT GAG		
			C _		
GAM341	LOC92466	3'	ATGGAGTCTCCCTCTGTC 2858	CATC	A
			GAC GA GGAGACTCCAT		
			CTG CT CCTCTGAGGTA		
			T__ C		
GAM342	MME	3'	AAAAAAAGTTACAGAAATA 785	AA	
			TATTTTGTGTA ACTTTTTTT		
			ATAAAGACAT TGAAAAAAA		
			_		
GAM342	MME	3'	AAAAAAAGTTACAGAAATA 1377	AA	
			TATTTTGTGTA ACTTTTTTT		
			ATAAAGACAT TGAAAAAAA		
			_		
GAM342	MME	3'	AAAAAAAGTTACAGAAATA 1378	AA	
			TATTTTGTGTA ACTTTTTTT		
			ATAAAGACAT TGAAAAAAA		
			_		
GAM342	MME	3'	AAAAAAAGTTACAGAAATA 1379	AA	
			TATTTTGTGTA ACTTTTTTT		
			ATAAAGACAT TGAAAAAAA		
			_		
GAM342	DKFZP434C212	3'	AAAAAGTACACAGAAATATT 2832	AAA	
			AATATTTTGT ACTTTTT		
			TTATAAAGACA TGAAAAA		
			CA_		
GAM342	FLJ11275	3'	TAAAATGGGATTTATAAAAATA 1821	A	TT
		TT	AATATTTTGTAAA CT TTTTA		
			TTATAAAAATATTT GG AAAAT		
			A GT		
GAM342	GOLPH3	3'	TAAAAAAGTTTTACTGCCATA 1981	TTTT	
		TT	AATAT GTAAACTTTTTTTA		
			TTATA CATTTTGAAAAAAT		
			CCGT		
GAM342	KIAA0563	5'	TAAAAAAGGAGCAAAAGTAT 1565	AAAA	
			ATATTTTGT CTTTTTTA		

			TATGAAAACG GAAAAAAAT	
			AG__	
GAM342	TAF2	3'	AGAAAGTTTGACAAAAATA 997	A
			TATTTTTGT AAACTTTT	
			ATAAAAACA TTTGAAAGA	
			G	
GAM342	LOC147071	5'	TAAAAAAGGAGCAAAAGTAT 2965	AAAA
			ATATTTTTGT CTTTTTTA	
			TATGAAAACG GAAAAAAAT	
			AG__	
GAM342	LOC147639	5'	AAAAGTGCTGCAAAATATT 3110	AA
			AATATTTTGT ACTTTT	
			TTATAAAAACGT TGAAAA	
			CG	
GAM342	LOC201173	5'	TAAAAAAGGAGCAAAAGTAT 3405	AAAA
			ATATTTTTGT CTTTTTTA	
			TATGAAAACG GAAAAAAAT	
			AG__	
GAM342	LOC201220	5'	TAAAAAAGGAGCAAAAGTAT 3406	AAAA
			ATATTTTTGT CTTTTTTA	
			TATGAAAACG GAAAAAAAT	
			AG__	
GAM343	MME	3'	AAAAAAAGTTACAGAAATA 785	AA
			TATTTTTGTA ACTTTTTT	
			ATAAAGACAT TGAAAAAAA	
			—	
GAM343	MME	3'	AAAAAAAGTTACAGAAATA 1377	AA
			TATTTTTGTA ACTTTTTT	
			ATAAAGACAT TGAAAAAAA	
			—	
GAM343	MME	3'	AAAAAAAGTTACAGAAATA 1378	AA
			TATTTTTGTA ACTTTTTT	
			ATAAAGACAT TGAAAAAAA	
			—	
GAM343	MME	3'	AAAAAAAGTTACAGAAATA 1379	AA
			TATTTTTGTA ACTTTTTT	
			ATAAAGACAT TGAAAAAAA	
			—	
GAM343	DKFZP434C212	3'	AAAAAGTACACAGAAATATT 2832	AAA
			AATATTTTGT ACTTTT	

			TTATAAAGACA TGAAAAA		
			CA_		
GAM343	FLJ11275	3'	TAAAATGGGATTTATAAAAATA 1821	A	TT
		TT	AATATTTTTGTAAA CT TTTTA		
			TTATAAAAATATTT GG AAAAT		
			A GT		
GAM343	GOLPH3	3'	TAAAAAAGTTTTACTGCCATA 1981	TTTT	
		TT	AATAT GTAAACTTTTTTTA		
			TTATA CATTTTGAAAAAAT		
			CCGT		
GAM343	KIAA0563	5'	TAAAAAAGGAGCAAAAGTAT 1565	AAAA	
			ATATTTTGT CTTTTTTA		
			TATGAAAACG GAAAAAAT		
			AG_		
GAM343	TAF2	3'	AGAAAGTTTGACAAAATA 997	A	
			TATTTTGT AAACTTTT		
			ATAAAAACA TTTGAAAGA		
			G		
GAM343	LOC147071	5'	TAAAAAAGGAGCAAAAGTAT 2965	AAAA	
			ATATTTTGT CTTTTTTA		
			TATGAAAACG GAAAAAAT		
			AG_		
GAM343	LOC147639	5'	AAAAGTGCTGCAAAAATATT 3110	AA	
			AATATTTTGTA ACTTTT		
			TTATAAAAACGT TGAAAA		
			CG		
GAM343	LOC201173	5'	TAAAAAAGGAGCAAAAGTAT 3405	AAAA	
			ATATTTTGT CTTTTTTA		
			TATGAAAACG GAAAAAAT		
			AG_		
GAM343	LOC201220	5'	TAAAAAAGGAGCAAAAGTAT 3406	AAAA	
			ATATTTTGT CTTTTTTA		
			TATGAAAACG GAAAAAAT		
			AG_		
GAM344	MARK1	3'	TATAATAAACATGATTGCTTA 1857	TA	TAC
		A	TTA CGATC GTTTTATTATA		
			AAT GTTAG CAAAATAATAT		
			TC TA_		
GAM345	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_	TAA
			TCAGAAAG AGGTT TATTTT		


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AGTCTTTT TTCGA ATAAAA
      A TC_
GAM345 KERA 3' AAAATATTGAATGCTTTCT 1349 AG
      AGAAAG GTTTAATATTTT
      ||||| |||||
      TCTTTC TAAGTTATAAAA
      G_
GAM345 PPP1R12A 3' AAAATACTACATCTTTCTGG 931 G TTAA
      TCAGAAAGA GT TATTTT
      ||||| || |||||
      GGTCTTTCT CA ATAAAA
      A TC__
GAM345 S100B 3' AAAATTGAAAACCTCTTTC 1284 AAT
      GAAAGAGGTTT ATTTT
      ||||| |||||
      CTTTCTCCAAA TAAAA
      AGT
GAM345 DKFZP564I0422 3' AAAATATTGCATTCTTCTGAT 2196 A GTT
      ATCAGAA GAG TAATATTTT
      ||||| ||| |||||
      TAGTCTT CTT GTTATAAAA
      _ AC_
GAM345 EML4 3' AAAATGTTTCCTCTTTCT 1876 TTT
      AGAAAGAGG AATATTTT
      ||||| |||||
      TCTTTCTCC TTGTAAAA
      T__
GAM345 FLJ21657 3' AAAATATTTTACTCTGCCTGAT 1990 AA GTTT
      ATCAG AGAG AATATTTT
      |||| ||| |||||
      TAGTC TCTC TTATAAAA
      CG ATT_
GAM345 KIAA1054 3' AAAATGGTACCTCTTTC 2820 TTAA
      GAAAGAGGT TATTTT
      ||||| |||||
      CTTTCTCCA GTAAAA
      TG__
GAM345 SEMA3E 5' AAAATACAGCTTCTTCCTGA 1431 A TAA
      TCAG AAGAGGTT TATTTT
      ||| ||||| |||||
      AGTC TTCTTCGA ATAAAA
      C C__
GAM345 LOC130507 3' AAAATATTAAGATACTTTCTG 3011 AGG_
      CAGAAAG TTTAATATTTT
      ||||| |||||
      GTCTTTC GAATTATAAAA
      AATA
GAM345 LOC148145 5' AAAATATTAAACCTGGACCTGA 3296 AAAG
      T ATCAG AGGTTTAATATTTT
      |||| |||||

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			TAGTC TCCAAATTATAAAA		
			CAGG		
GAM346	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_	TAA
			TCAGAAAG AGGTT TATTTT		
			AGTCTTTT TTCGA ATAAAA		
			A TC_		
GAM346	KERA	3'	AAAATATTGAATGCTTTCT 1349	AG	
			AGAAAG GTTTAATATTTT		
			TCTTTC TAAGTTATAAAA		
			G_		
GAM346	PPP1R12A	3'	AAAATACTACATCTTTCTGG 931	G	TTAA
			TCAGAAAGA GT TATTTT		
			GGTCTTTCT CA ATAAAA		
			A TC__		
GAM346	S100B	3'	AAAATTGAAAACCTCTTTC 1284	AAT	
			GAAAGAGGTTT ATTTT		
			CTTTCTCCAAA TAAAA		
			AGT		
GAM346	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT 2196	A	GTT
			ATCAGAA GAG TAATATTTT		
			TAGTCTT CTT GTTATAAAA		
			_ AC_		
GAM346	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT	
			AGAAAGAGG AATATTTT		
			TCTTTCTCC TTGTAAAA		
			T_		
GAM346	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA	GTTT
			ATCAG AGAG AATATTTT		
			TAGTC TCTC TTATAAAA		
			CG ATT_		
GAM346	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA	
			GAAAGAGGT TATTTT		
			CTTTCTCCA GTAAAA		
			TG_		
GAM346	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A	TAA
			TCAG AAGAGGTT TATTTT		
			AGTC TTCTTCGA ATAAAA		
			C C_		
GAM346	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_	
			CAGAAAG TTTAATATTTT		

			GTCTTTC GAATTATAAAA		
			AATA		
GAM346	LOC148145	5'	AAAATATTAAACCTGGACCTGA	3296	AAAG
		T	ATCAG AGGTTTAATATTTT		
			TAGTC TCCAAATTATAAAA		
			CAGG		
GAM347	DKK1	3'	AAAATACTAGCTTATTTTCTGA	1417	_ TAA
			TCAGAAAG AGGTT TATTTT		
			AGTCTTTT TTCGA ATAAAA		
			A TC_		
GAM347	KERA	3'	AAAATATTGAATGCTTTCT	1349	AG
			AGAAAG GTTTAATATTTT		
			TCTTTC TAAGTTATAAAA		
			G_		
GAM347	PPP1R12A	3'	AAAATACTACATCTTTCTGG	931	G TTAA
			TCAGAAAGA GT TATTTT		
			GGTCTTTCT CA ATAAAA		
			A TC__		
GAM347	S100B	3'	AAAATTGAAAACCTCTTTC	1284	AAT
			GAAAGAGGTTT ATTTT		
			CTTTCTCCAAA TAAAA		
			AGT		
GAM347	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT	2196	A GTT
			ATCAGAA GAG TAATATTTT		
			TAGTCTT CTT GTTATAAAA		
			_ AC_		
GAM347	EML4	3'	AAAATGTTTCCTCTTTCT	1876	TTT
			AGAAAGAGG AATATTTT		
			TCTTTCTCC TTGTAAAA		
			T_		
GAM347	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT	1990	AA GTTT
			ATCAG AGAG AATATTTT		
			TAGTC TCTC TTATAAAA		
			CG ATT_		
GAM347	KIAA1054	3'	AAAATGGTACCTCTTTC	2820	TTAA
			GAAAGAGGT TATTTT		
			CTTTCTCCA GTAAAA		
			TG_		
GAM347	SEMA3E	5'	AAAATACAGCTTCTTCCTGA	1431	A TAA
			TCAG AAGAGGTT TATTTT		

		AGTC TTCTTCGA ATAAAA	
		C C__	
GAM347	LOC130507 3'	AAAATATTAAGATACTTTCTG 3011	AGG_
		CAGAAAG TTTAATATTTT	
		GTCTTTC GAATTATAAAA	
		AATA	
GAM347	LOC148145 5'	AAAATATTAAACCTGGACCTGA 3296	AAAG
	T	ATCAG AGGTTTAATATTTT	
		TAGTC TCCAAATTATAAAA	
		CAGG	
GAM348	DKK1 3'	AAAATACTAGCTTATTTTCTGA 1417	_ TAA
		TCAGAAAG AGGTT TATTTT	
		AGTCTTTT TTCGA ATAAAA	
		A TC_	
GAM348	KERA 3'	AAAATATTGAATGCTTTCT 1349	AG
		AGAAAG GTTTAATATTTT	
		TCTTTC TAAGTTATAAAA	
		G_	
GAM348	PPP1R12A 3'	AAAATACTACATCTTTCTGG 931	G TTAA
		TCAGAAAGA GT TATTTT	
		GGTCTTTCT CA ATAAAA	
		A TC__	
GAM348	S100B 3'	AAAATTGAAAACCTCTTTC 1284	AAT
		GAAAGAGGTTT ATTTT	
		CTTTCTCCAAA TAAAA	
		AGT	
GAM348	DKFZP564I0422 3'	AAAATATTGCATTCTTCTGAT 2196	A GTT
		ATCAGAA GAG TAATATTTT	
		TAGTCTT CTT GTTATAAAA	
		_ AC_	
GAM348	EML4 3'	AAAATGTTTCCTCTTTCT 1876	TTT
		AGAAAGAGG AATATTTT	
		TCTTTCTCC TTGTAAAA	
		T__	
GAM348	FLJ21657 3'	AAAATATTTTACTCTGCCTGAT 1990	AA GTTT
		ATCAG AGAG AATATTTT	
		TAGTC TCTC TTATAAAA	
		CG ATT_	
GAM348	KIAA1054 3'	AAAATGGTACCTCTTTC 2820	TTAA
		GAAAGAGGT TATTTT	

			CTTTCTCCA	GTAAAA		
			TG__			
GAM348	SEMA3E	5'	AAAATACAGCTTCTTCCTGA	1431	A	TAA
			TCAG AAGAGGTT TATTTT			
			AGTC TTCTTCGA ATAAAA			
			C C__			
GAM348	LOC130507	3'	AAAATATTAAGATAACTTTCTG	3011	AGG_	
			CAGAAAG TTTAATATTTT			
			GTCTTTC GAATTATAAAA			
			AATA			
GAM348	LOC148145	5'	AAAATATTAACCTGGACCTGA	3296	AAAG	
		T	ATCAG AGGTTTAATATTTT			
			TAGTC TCCAAATTATAAAA			
			CAGG			
GAM349	DKK1	3'	AAAATACTAGCTTATTTTCTGA	1417	_ TAA	
			TCAGAAAG AGGTT TATTTT			
			AGTCTTTT TTCGA ATAAAA			
			A TC_			
GAM349	KERA	3'	AAAATATTGAATGCTTTCT	1349	AG	
			AGAAAG GTTTAATATTTT			
			TCTTTC TAAGTTATAAAA			
			G_			
GAM349	PPP1R12A	3'	AAAATACTACATCTTTCTGG	931	G TTAA	
			TCAGAAAGA GT TATTTT			
			GGTCTTTCT CA ATAAAA			
			A TC__			
GAM349	S100B	3'	AAAATTGAAAACCTCTTTC	1284	AAT	
			GAAAGAGGTTT ATTTT			
			CTTTCTCCAAA TAAAA			
			AGT			
GAM349	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT	2196	A GTT	
			ATCAGAA GAG TAATATTTT			
			TAGTCTT CTT GTTATAAAA			
			_ AC_			
GAM349	EML4	3'	AAAATGTTTCCTCTTTCT	1876	TTT	
			AGAAAGAGG AATATTTT			
			TCTTTCTCC TTGTAAAA			
			T__			
GAM349	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT	1990	AA GTTT	
			ATCAG AGAG AATATTTT			

			TAGTC TCTC	TTATAAAA		
			CG ATT_			
GAM349	KIAA1054	3'	AAAATGGTACCTCTTTC	2820		TTAA
			GAAAGAGGT TATTTT			
			CTTTCTCCA GTAAAA			
			TG__			
GAM349	SEMA3E	5'	AAAATACAGCTTCTTCCTGA	1431	A	TAA
			TCAG AAGAGGTT TATTTT			
			AGTC TTCTTCGA ATAAAA			
			C C__			
GAM349	LOC130507	3'	AAAATATTAAGATAACTTTTCTG	3011		AGG_
			CAGAAAG TTTAATATTTT			
			GTCTTTC GAATTATAAAA			
			AATA			
GAM349	LOC148145	5'	AAAATATTAACCTGGACCTGA	3296		AAAG
	T		ATCAG AGGTTTAATATTTT			
			TAGTC TCCAAATTATAAAA			
			CAGG			
GAM350	DKK1	3'	AAAATACTAGCTTATTTTCTGA	1417	_	TAA
			TCAGAAAG AGGTT TATTTT			
			AGTCTTTT TTCGA ATAAAA			
			A TC_			
GAM350	KERA	3'	AAAATATTGAATGCTTTTCT	1349	AG	
			AGAAAG GTTTAATATTTT			
			TCTTTC TAAGTTATAAAA			
			G_			
GAM350	PPP1R12A	3'	AAAATACTACATCTTTCTGG	931		G TTAA
			TCAGAAAGA GT TATTTT			
			GGTCTTTCT CA ATAAAA			
			A TC__			
GAM350	S100B	3'	AAAATTGAAAACCTCTTTC	1284		AAT
			GAAAGAGGTTT ATTTT			
			CTTTCTCCAAA TAAAA			
			AGT			
GAM350	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT	2196		A GTT
			ATCAGAA GAG TAATATTTT			
			TAGTCTT CTT GTTATAAAA			
			_ AC_			
GAM350	EML4	3'	AAAATGTTTCCTCTTTCT	1876		TTT
			AGAAAGAGG AATATTTT			

		TCTTTCTCC TTGTA AAA		
		T__		
GAM350	FLJ21657 3'	AAAATATTTTACTCTGCCTGAT 1990	AA	GTTT
		ATCAG AGAG AATATTTT		
		TAGTC TCTC TTATAAAA		
		CG ATT_		
GAM350	KIAA1054 3'	AAAATGGTACCTCTTTC 2820	TTAA	
		GAAAGAGGT TATTTT		
		CTTTCTCCA GTAAAA		
		TG__		
GAM350	SEMA3E 5'	AAAATACAGCTTCTTCCTGA 1431	A	TAA
		TCAG AAGAGGT TATTTT		
		AGTC TTCTTCGA ATAAAA		
		C C__		
GAM350	LOC130507 3'	AAAATATTAAGATAACTTTCTG 3011	AGG_	
		CAGAAAG TTTAATATTTT		
		GTCTTTC GAATTATAAAA		
		AATA		
GAM350	LOC148145 5'	AAAATATTAAACCTGGACCTGA 3296	AAAG	
	T	ATCAG AGGTTTAATATTTT		
		TAGTC TCCAAATTATAAAA		
		CAGG		
GAM351	DKK1 3'	AAAATACTAGCTTATTTTCTGA 1417	_	TAA
		TCAGAAAG AGGTT TATTTT		
		AGTCTTTT TTCGA ATAAAA		
		A TC_		
GAM351	KERA 3'	AAAATATTGAATGCTTTCT 1349	AG	
		AGAAAG GTTTAATATTTT		
		TCTTTC TAAGTTATAAAA		
		G_		
GAM351	PPP1R12A 3'	AAAATACTACATCTTTCTGG 931	G	TTAA
		TCAGAAAGA GT TATTTT		
		GGTCTTTCT CA ATAAAA		
		A TC__		
GAM351	S100B 3'	AAAATTGAAAACCTCTTTC 1284	AAT	
		GAAAGAGGTTT ATTTT		
		CTTTCTCCAAA TAAAA		
		AGT		
GAM351	DKFZP564I0422 3'	AAAATATTGCATTCTTCTGAT 2196	A	GTT
		ATCAGAA GAG TAATATTTT		

			TAGTCTT CTT GTTATAAAA		
			_ AC_		
GAM351	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT	
			AGAAAGAGG AATATTTT		
			TCTTTCTCC TTGTAAAA		
			T__		
GAM351	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA GTTT	
			ATCAG AGAG AATATTTT		
			TAGTC TCTC TTATAAAA		
			CG ATT_		
GAM351	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA	
			GAAAGAGGT TATTTT		
			CTTTCTCCA GTAAAA		
			TG__		
GAM351	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A TAA	
			TCAG AAGAGGTT TATTTT		
			AGTC TTCTTCGA ATAAAA		
			C C__		
GAM351	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_	
			CAGAAAG TTTAATATTTT		
			GTCTTTC GAATTATAAAA		
			AATA		
GAM351	LOC148145	5'	AAAATATTAAACCTGGACCTGA 3296	AAAG	
			T ATCAG AGGTTTAATATTTT		
			TAGTC TCCAAATTATAAAA		
			CAGG		
GAM352	DKK1	3'	AAAATACTAGCTTATTTTCTGA 1417	_ TAA	
			TCAGAAAG AGGTT TATTTT		
			AGTCTTTT TTCGA ATAAAA		
			A TC_		
GAM352	KERA	3'	AAAATATTGAATGCTTTCT 1349	AG	
			AGAAAG GTTTAATATTTT		
			TCTTTC TAAGTTATAAAA		
			G_		
GAM352	PPP1R12A	3'	AAAATACTACATCTTTCTGG 931	G TTAA	
			TCAGAAAGA GT TATTTT		
			GGTCTTTCT CA ATAAAA		
			A TC__		
GAM352	S100B	3'	AAAATTGAAAACCTCTTTC 1284	AAT	
			GAAAGAGGTTT ATTTT		

			CTTTCTCCAAA TAAAA		
			AGT		
GAM352	DKFZP564I0422	3'	AAAATATTGCATTCTTCTGAT 2196	A	GTT
			ATCAGAA GAG TAATATTTT		
			TAGTCTT CTT GTTATAAAA		
			_ AC_		
GAM352	EML4	3'	AAAATGTTTCCTCTTTCT 1876	TTT	
			AGAAAGAGG AATATTTT		
			TCTTTCTCC TTGTAAAA		
			T_		
GAM352	FLJ21657	3'	AAAATATTTTACTCTGCCTGAT 1990	AA	GTTT
			ATCAG AGAG AATATTTT		
			TAGTC TCTC TTATAAAA		
			CG ATT_		
GAM352	KIAA1054	3'	AAAATGGTACCTCTTTC 2820	TTAA	
			GAAAGAGGT TATTTT		
			CTTTCTCCA GTAAAA		
			TG_		
GAM352	SEMA3E	5'	AAAATACAGCTTCTTCCTGA 1431	A	TAA
			TCAG AAGAGGTT TATTTT		
			AGTC TTCTTCGA ATAAAA		
			C C_		
GAM352	LOC130507	3'	AAAATATTAAGATAACTTTCTG 3011	AGG_	
			CAGAAAG TTTAATATTTT		
			GTCTTTC GAATTATAAAA		
			AATA		
GAM352	LOC148145	5'	AAAATATTAACCTGGACCTGA 3296	AAAG	
			T ATCAG AGGTTTAATATTTT		
			TAGTC TCCAAATTATAAAA		
			CAGG		
GAM353	EFG1	3'	TGTCTATCTCAACTCTATT 3661	ATC TC	
			AATAGAGTT GAT AGACA		
			TTATCTCAA CTA TCTGT		
			CT_ _		
GAM353	PHYH	3'	TCTGCTATAACTCTTTCA 1281	T	CGATT
			TGAA AGAGTTAT CAGA		
			ACTT TCTCAATA GTCT		
			_ TC_		
GAM353	SLC6A3	3'	TGTCTGTTGACCAATCTCTATT 795	TTA_	TT
	CA		TGAATAGAG TCGA CAGACA		

			ACTTATCTC	AGTT	GTCTGT	
			TAACC	___		
GAM353	H2AV	3'	TGCCTGACAATTAGCTCTATTC	2447	TCGAT	A
	A		TGAATAGAGTTA	TCAG	CA	
			ACTTATCTCGAT	AGTC	GT	
			TAAC	_	C	
GAM353	HMP19	3'	GTCTGAACCGATATTTCT	3408	T	A
			AGAG	TATCG	TTCAGAC	
			TCTT	ATAGC	AAGTCTG	
			T	C		
GAM353	KIAA1726	3'	TGTCTGAAAGCAACCCTACTC	2786	A	A ATCGA
			GA	TAG	GTT TTCAGACA	
			CT	ATC	CAA AAGTCTGT	
			C	C	CGA	
GAM354	SOX11	3'	GTCTCACTGTTTGATCAAACCTT	992	A	ATTTTT
	CT		AGAGGTTT	AT	GTGAGAC	
			TCTTCAA	TA	CACTCTG	
			C	GTTTGT		
GAM354	CAP350	3'	TCTTGTAATAGTTAAACCTC	1554	ATT	TG
			GAGGTTTAAT	TTG	AGA	
			CTCCAAATTG	AAT	TCT	
			AT	_	GT	
GAM354	DKFZP564A022	3'	TCTCACAAATATAAAACC	2174	A	TT
			GTTTT	ATATT	TGTGAGA	
			CCAAA	TATAA	ACACTCT	
			A	_		
GAM354	FLJ11730	3'	CTCACAAAGATAAACATC	2005	G	TAA
			GA	GTT	TATTTTTGTGAG	
			CT	CAA	ATAGAAACACTC	
			A	_		
GAM354	FLJ20686	5'	CTCACAGTCCTACTGAACCTC	1765	A	TTT
			GAGGTTTA	TA	TTGTGAG	
			CTCCAAGT	AT	GACACTC	
			C	CCT		
GAM354	FRSB	3'	GTCCCAGGGGAGATATTAGACCT	1236	G	A
	CT		AGAGGTTTAATATTTTT	TG	GAC	
			TCTCCAGATTATAGAGG	AC	CTG	
			G	C		
GAM354	KIAA1600	3'	ACAAAAAGACTAAACCTCT	2919	ATA	
			AGAGGTTTA	TTTTTGT		

			TCTCCAAAT AAAAACA		
			CAG		
GAM354	LOC124801	3'	GTCTCACATTTGCCCCAAACCT 2996		AATATTTT
		C	GAGGTTT TGTGAGAC		
			CTCCAAA ACACTCTG		
			CCCGGTTT		
GAM354	LOC221035	3'	TCCCAGTATTAAACCT 3593		TTTTG A
			AGGTTTAATAT TG GA		
			TCCAAATTATG AC CT		
			_____ C		
GAM354	LOC51611	3'	CGAAAATTAAACCTCT 1653		AT
			AGAGGTTTAAT TTTTG		
			TCTCCAAATTA AAAGC		

GAM355	AXUD1	3'	TTTATTCCATTTCTCTCT 2309		GA
			AGAGAGAAA GAATAAA		
			TCTCTCTTT CTTATTT		
			AC		
GAM355	BSN	3'	ATTTTCTTTTGTTTCTCTCT 1024		G T
			AGAGAGAAA AGAA AAAAAT		
			TCTCTCTTT TTTT TTTTAA		
			G C		
GAM355	DPYSL2	3'	AATATTTTCGTGTCTGTCTCTC 822		A GA TA
		T	AGAGAGA AGA A AAAATATT		
			TCTCTCT TCT T TTTTATAA		
			G G_ GC		
GAM355	EVA1	3'	AATGTGTTTACTCTCTTTCCCTT 1250	A	A A
		C	GAG GAAAGAGA TAAA ATATT		
			CTT CTTTCTCT ATTT TGTAA		
			C C G		
GAM355	PTMS	3'	TTTGCTCTCTTTCTCCCT 959	A	A
			AG GAGAAAGAGA TAAA		
			TC CTCTTTCTCT GTTT		
			C C		
GAM355	SELE	3'	TTTTGTGGCTTTCTTTCT 748		AGA
			AGAGAGAAAG ATAAAA		
			TCTTTCTTTC TGTTTT		
			GG_		
GAM355	SLC7A6	3'	AATATTTTGTACCTTTCTCCT 1076	A	AGA
			AG GAGAAAG ATAAAAATATT		

			TC CTCTTTC TGT TTTTATAA		
			— CA_		
GAM355	TGFR2	5'	TTTCTTCTAGTTCTTTCT 1003	AG	T
			AGAGAGAA AGAA AAA		
			TCTTTCTT TCTT TTT		
			GA C		
GAM355	DKFZP586N0721	5'	TTTTATTCCCTTTCCTCT 1627	A	A
			AGAG GAAAG GAATAAAA		
			TCTC CTTTC CTTATTTT		
			— C		
GAM355	DKFZp761J139	5'	TTTATTCTCTCTGTCTCT 2242	GAA	
			AGAGA AGAGAATAAA		
			TCTCT TCTCTTATTT		
			GTC		
GAM355	FLJ10468	3'	TTTTATTCTCCTTTC 1779	AAA	
			GAGAG GAGAATAAAA		
			CTTTC CTCTTATTTT		
			—		
GAM355	FLJ20485	3'	AATATTTTTTAAAATCTCCTTTC 1874	AAA	A_
			T AGAGAG GAGA TAAAAATATT		
			TCTTTC CTCT ATTTTATAA		
			— AAA		
GAM355	H2BFQ	3'	ATATTTACTCTTTCTGTC 2523	G	AATAA
			GA AGAAAGAG AAATAT		
			CT TCTTTCTC TTTATA		
			G A_		
GAM355	KIAA0077	3'	TTTTATTCTCTCTCCCTT 2774	A	A
			AGAG GA AGAGAATAAAA		
			TTTC CT TCTCTTATTTT		
			C C		
GAM355	KIAA0295	3'	TTTTTTCCCTTTCTCTCT 2807	A	T
			AGAGAGAAAG GAA AAA		
			TCTCTCTTTC CTT TTT		
			C T		
GAM355	KIAA0828	3'	AATATTTTGCCTTCTTTCTTTC 3195	AATA	
			T AGAGAGAAAGAG AAAATATT		
			TCTTTCTTTCTT TTTTATAA		
			CCG_		
GAM355	KIAA1203	3'	AATATTTTATTCTTGAGTTAT 2921	GAGAAA	
			CT AGA GAGAATAAAAAATATT		

			TCT TTCTTATTTTATAA		
			ATTGAG		
GAM355	OSBPL8	3'	TTTTTATTATCCTCCTCTCT 1928	AAA G	
			AGAGAG GA AATAAAAA		
			TCTCTC CT TTATTTT		
			CTC A		
GAM355	PAK6	3'	AATATTTT TAGATTCTTGCT 1897	_ A AA	
	C		GAG AGAA GAG TAAAAATATT		
			CTC TCTT CTT ATTTTATAA		
			G _ AG		
GAM355	POLR3F	3'	AATATTTTCACTGTTCTTCTT 2547	A A ____	
	TCT		AGAGAGAA G GAATA AAAATATT		
			TCTTTCTT C CTTGT TTTTATAA		
			_ _ CAC		
GAM355	RNF11	3'	TTTATTCTCTTTCTTCT 1495	G	
			AGA AGAAAGAGAATAAA		
			TCT TCTTTCTCTTATTT		
			-		
GAM355	SLC16A6	5'	TTTATTCTCTTCCCTTCT 1143	AGA	
			AGAG AAGAGAATAAA		
			TCTT TTCTCTTATTT		
			CCC		
GAM355	LOC144321	3'	TTTTATTCCCTTCTCTC 3267	A A	
			GAGAGAA G GAATAAAA		
			CTCTCTT C CTTATTTT		
			_ C		
GAM355	LOC150951	5'	ATATTTTATTTTCTTCCT 3336	A	
			AG AAGAGAATAAAAATAT		
			TC TTCTTTTATTTTATA		
			C		
GAM355	LOC199920	5'	AATATTTTATTCTTTGATTCT 3435	AA	
	T		GAGAG AGAGAATAAAAATATT		
			TTCTT TTTCTTATTTTATAA		
			AG		
GAM355	LOC256435	3'	AATATTTTAAATGTTGTCTCT 3675	AAGAGAA	
	CT		AGAGAGA TAAAAATATT		
			TCTCTCT ATTTTATAA		
			GTTGTAA		
GAM356	ADAMTS5	3'	TATTTTCACAAC TACTTTCTCT 1352	_ AATA_	
	CT		AGAGAGAAAG AG AAAATA		

TCTCTCTTTC TC TTTTAT
 A AACAC
 GAM356 ADAT1 3' TATTCCCAGCCTTTCTTTCTTC 1404 A____
 GAAGAGAGAAAG GAATA
 ||||| ||||
 CTTCTTTCTTTC CTTAT
 CGACC
 GAM356 ADCY2 3' TTTTATTTTCCTGTCTTC 2711 G AAA
 GAAGA AG GAGAATAAAA
 |||| || |||||
 CTTCT TC CTTTTATTTT
 G ____
 GAM356 AHR 3' ATTTTGTACTCTCTTC 840 _ A
 GAAGAGAG AA GAGAAT
 ||||| || |||||
 CTTCTCTC TT TTTTAA
 A G
 GAM356 BSN 3' ATTTTCTTTTGTCTCTCT 1025 G T
 AGAGAGAAA AGAA AAAAAT
 ||||| ||| |||||
 TCTCTCTTT TTTT TTTTAA
 G C
 GAM356 BSN 3' TCTCCCCCTTTCTCTCTTC 1026 ____
 GAAGAGAGAAA GAGA
 ||||| |||
 CTTCTCTCTTT CTCT
 CCCC
 GAM356 C7 3' TATTCCTTATTTCTCTTT 756 _ A
 GAAGAGAGA AAG GAATA
 ||||| ||| |||||
 TTTCTCTTT TTC CTTAT
 A _
 GAM356 CFTR 3' TATTCCTTTTCTCTCCTC 753 A _
 GA GAGAGAAAGAG AATA
 || ||||| |||||
 CT CTCTCTTTTTC TTAT
 C C
 GAM356 CHD2 3' ATATTTTTCTGATCCCCACT 813 AA____ GAAT_ |||
 CTCTCTTC AGA GA AAAAATA T
 || || ||||| |
 TCT CT TTTTAT A
 CACCCC AGTCT |||
 GAM356 CKN1 3' TATTTTATTCTTTCTTC 703 AG
 GAAGAGAGAA AGAATA
 ||||| |||||
 CTTCTTTCTT TTTTAT
 A_
 GAM356 CTH 5' TGTTCTTTTCCTCTCTTC 867 A
 GAAGAGAG AAGAGAATA
 ||||| |||||

			CTTCTCTC TTTTCTTGT		
			C		
GAM356	EVA1	3'	ATTTTATTTTATGTCTCTC 1251	AA_	
			GAGAGA GAGAATAAAAAT		
			CTCTCT TTTTATTTTTA		
			GTA		
GAM356	FBXL11	3'	TTGTTCCCCCTCTCTCTT 1426	AAGA	
			GAAGAGAGA GAATAA		
			TTTCTCTCT CTTGTT		
			CCCC		
GAM356	GATA3	3'	TATTTTCCTTCTCTCTC 893	A A	
			GA GAGAGAA GAGAATA		
			CT CTCTCTT CTTTAT		
			_ C		
GAM356	GDI2	5'	TTTTCCTCTCTTTCTCTT 832	AT	
			GAGAGAAAGAGA AAAA		
			TTCTCTTCTCT TTTT		
			CC		
GAM356	HD	3'	ATTCTCCCTTCTCTCTT 899	A_	
			GAAGAGAGAA GAGAAT		
			TTTCTCTCTT CTCTTA		
			CC		
GAM356	HTR2C	3'	TATTTTGTCTCTCCCTCCCTTC 781	A AAA A	
			GAAG GAG GAGA TAAAAATA		
			CTTC CTC CTCT GTTTTAT		
			C C_ C		
GAM356	LGR6	3'	TTCTCTTCCCCTCTCTTC 3302	A_	
			GAAGAGAG AAGAGAA		
			CTTCTCTC TTCTCTT		
			CCC		
GAM356	LRP8	3'	TCTCTTATTTCTCTTTTC 2326	---	
			GAAGAGAGAA AGAGA		
			CTTTTCTCTT TCTCT		
			TAT		
GAM356	LRP8	3'	TCTCTTATTTCTCTTTTC 1139	---	
			GAAGAGAGAA AGAGA		
			CTTTTCTCTT TCTCT		
			TAT		
GAM356	MEF2C	5'	TTTTTTTTCTCTCTCTCTCT 926	_ A T	
	C		GA AGAGAGA AGAGAA AAAAA		

			CT TCTCTCT TCTCTT TTTT		
			C C T		
GAM356	MSR1	3'	TATTTTGGTTTCTCTCT 929	—	
			AGAGAGAAA GAGAATA		
			TCTCTCTTT TTTTAT		
			GG		
GAM356	PCDH11X	3'	TATTTTCACATTTTCTCTCT 2299	—	
			AGAGAGAAA GAGAATA		
			TCTCTCTTT CTTTAT		
			TACA		
GAM356	PCDH11X	3'	TATTTTCACATTTTCTCTCT 2301	—	
			AGAGAGAAA GAGAATA		
			TCTCTCTTT CTTTAT		
			TACA		
GAM356	PCDH11Y	3'	TATTTTCACATTTTCTCTCT 2303	—	
			AGAGAGAAA GAGAATA		
			TCTCTCTTT CTTTAT		
			TACA		
GAM356	PCMT1	3'	TATCTTCTGCTCTTTCTTC 1205	A_ GA	
			GAAGAGAGA AGA ATA		
			CTTCTTTCT TCT TAT		
			CG TC		
GAM356	PCNA	3'	TATTTTTTTTCTCTATTC 939	G	
			GAA AGAGAAAGAGAATA		
			CTT TCTCTTTTTTTTAT		
			A		
GAM356	PRELP	3'	ATTCGTTTTCTCTCTCTC 950	_ A	
			GA AGAGAGAAAG GAAT		
			CT TCTCTCTTTT CTTA		
			C G		
GAM356	PTMS	3'	TTTGCTCTCTTTCTCCCT 958	A A	
			AG GAGAAAGAGA TAAA		
			TC CTCTTTCTCT GTTT		
			C C		
GAM356	SLC4A4	3'	TATTTTATTCTCTTAAGTCTT 1054	GAGA	
	T		GAAGA AAGAGAATAAAAATA		
			TTTCT TTCTCTTATTTTAT		
			GAA_		
GAM356	TRPS1	5'	TATTCCTTTCTCTTTCTCTCT 1471	TAA	
			AGAGAGAAAGAGAA AAATA		

			TCTCTCTTTCTCTT TTTAT	
			TCC	
GAM356	ARS2	5'	TTTTGTTTCGCCTCTCTTC 1650	AAAGA
			GAAGAGAG GAATAAAA	
			CTTCTCTC CTTGTTTT	
			CG__	
GAM356	BRD4	3'	TATTTTAAATTCTCTCTTC 2368	A_
			GAAGAGAGAA GAGAATA	
			CTTCTCTCTT TTTTAT	
			AA	
GAM356	CAPN13	3'	TATTTTACCTGCCTCTCTTC 2485	AA __
			GAAGAGAG AG AGAATA	
			CTTCTCTC TC TTTTAT	
			CG CA	
GAM356	CECR6	3'	TTACCCTCTCCTCTCTTC 2218	AA AA
			GAAGAGAG AGAG TAA	
			CTTCTCTC TCTC ATT	
			C_ CC	
GAM356	DKFZP434I0714	5'	TTTTTGTTTTTCCCCCTCTTC 3362	AGAAA
			GAAGAG GAGAATAAAAA	
			CTTCTC TTTTGTTTTT	
			CCCC_	
GAM356	DKFZP564G092	5'	TATTCCTCTTTCTTTTC 1639	A A
			GAAGAGAGA AG GAATA	
			CTTTTCTTT TC CTTAT	
			C _	
GAM356	DKFZp564K142	3'	TATCCTCTTAACCTTCTCTTC 2231	A__ A
			GAAGAGAG AAGAG ATA	
			CTTCTCTT TTCTC TAT	
			CCAA C	
GAM356	DKFZp566D234	3'	TATTTTTTTTCTCTGTC 2612	AG
			GA AGAGAAAGAGAATA	
			CT TCTCTTTTTTTTAT	
			G_	
GAM356	DKFZP566I1024	3'	TTTAAATCTATTCTCTC 2878	_ GAA
			GAGAGAA AGA TAAAA	
			CTCTCTT TCT ATTTT	
			A AAA	
GAM356	EPI64	3'	TATTTTGACATCTCTCTCTT 3681	A GAATA
	C		GAAGAGAGA AGA AAAATA	

CTTCTCTCT TCT TTTTAT
 C ACAG_
 GAM356 FLJ00012 3' TATTTTATCTCTATCTCCT 2985 A A A
 AG GAGA AGAGA TAAAAATA
 || ||| |||| |||||
 TC CTCT TCTCT ATTTTAT
 _ A _
 GAM356 FLJ10460 3' ATTTTATTCTACCTTTC 1778 AAAG
 GAGAG AGAATAAAAAT
 |||| | |||||
 CTTTC TCTTATTTTA
 CA_
 GAM356 FLJ10687 3' TTTATTCATTTCTCTCCTC 1793 A GA
 GA GAGAGAAA GAATAAA
 || ||||| |||||
 CT CTCTCTTT CTTATTT
 C A_
 GAM356 FLJ10738 3' TATTTTACTCTCCCTCTTC 1799 AGAAA A
 GAAGAG GAGA TAAAAATA
 |||| | |||||
 CTTCTC CTCT ATTTTAT
 C_ C
 GAM356 FLJ13158 3' TTCTCTCCCTTTCTCTTC 2109 A_
 GAAGAGAGA AGAGAA
 ||||| |||||
 CTTCTCTTT TCTCTT
 CCC
 GAM356 FLJ20294 5' TATTCCTGTCTCCTCTTT 1747 _ A A
 GAAGAG AGA AG GAATA
 |||| | || |||||
 TTTCTC TCT TC CTTAT
 C G _
 GAM356 FLJ21657 3' TATTCTACTTCTCTCTTC 1991 AG
 GAAGAGAGAA AGAATA
 ||||| |||||
 CTTCTCTCTT TCTTAT
 CA
 GAM356 GT650 3' TATTTCTGATTCTCCCTCTCTT 2341 AAA AA_
 C GAAGAGAG GAGAAT AAATA
 ||||| |||| | |||||
 CTTCTCTC CTCTTA TTTAT
 C_ GTC
 GAM356 HEY2 3' TATTCTCTTTTTTTTCTC 1420 AG
 GA AGAGAAAGAGAATA
 || ||||| |||||
 CT TTTTTTTCTCTTAT
 CT
 GAM356 HIC2 3' ATTTTTTTTTCTCTCTCTTTTC 2717 A T
 GAAGAGAGA AGAGAA AAAAAT
 ||||| |||| | |||||

			CTTTTCTCT TCTTTT TTTTTA		
			C _		
GAM356	HOOK3	3'	ATTTTGAGGACTTTTTCTCTCT 2249	AATA_	
			AGAGAGAAAGAG AAAAT		
			TCTCTCTTTTC TTTTA		
			AGGAG		
GAM356	IL1RAPL1	5'	TATTCTTATTTTCCCCTCTCTT 1488	AAA A	
		T	GAAGAGAG GAGAATAA AATA		
			TTTCTCTC CTTTATT TTAT		
			CC_ C		
GAM356	KALI	3'	TTTTGTTCTTGTCCCTCTC 2347	AAA_	
			GAGAG GAGAATAAAA		
			CTCTC TTCTTGTTTT		
			CCTG		
GAM356	KIAA0077	3'	TTTTATTCTCTCTCCCTTT 2773	A AA	
			GAAG GAGA GAGAATAAAA		
			TTTC CTCT CTCTTATTTT		
			C _		
GAM356	KIAA0089	3'	ATTTTGTAGCCTCTTTTCTCTTC 2873	A AA	
			GAAGAGAGAA GAG TAAAAAT		
			CTTCTCTTTT CTC ATTTTTA		
			_ CG		
GAM356	KIAA0286	3'	TATTTTCACCCTCTTTTC 2814	AAA	
			GAAGAGAG GAGAATA		
			CTTTTCTC CTTTAT		
			CCA		
GAM356	KIAA0295	3'	TTTTTCCCTTTCTCTCT 2808	A T	
			AGAGAGAAAG GAA AAA		
			TCTCTCTTTC CTT TTT		
			C T		
GAM356	KIAA0342	3'	TATTCTCATTACTTCTCTTT 2890	_ _ A	
			GAAGAGA G AA GAGAATA		
			TTTCTCT C TT CTCTTAT		
			T A A		
GAM356	KIAA0564	3'	TATTTTATTTTCTCCCTGCTC 2743	_ AA	
			GAG AG AGAGAATAAAAATA		
			CTC TC TCTTTATTTTAT		
			G CC		
GAM356	KIAA0630	3'	TATTTTAAAAAGTCTTTCTCT 3465	GAAT_	
		CT	AGAGAGAAAGA AAAAATA		

			TCTCTCTTTCT	TTTTAT		
			GAAAAT			
GAM356	KIAA0662	3'	TGTTCTCTCTCTCTTT	3215	A	
			GAAGAGAGA AGAGAATA			
			TTTCTCTCT TCTCTTGT			
			C			
GAM356	KIAA0830	3'	TTTGCTTCTCTTTCTCCT	2866	A	—
			AG GAGAAAGAGAA TAAA			
			TC CTCTTTCTCTT GTTT			
			— C			
GAM356	KIAA0964	3'	ATTCTTATGTTTTTCTCTTTTC	1579	GA	A
			GAAGAGAGAAAGA ATAA AAT			
			CTTTTCTCTTTT TATT TTA			
			G_ C			
GAM356	KIAA1076	3'	TATTTTTTGCTTTTCTCTC	2723	AGAAT	
			GAGAGAAAG AAAAATA			
			CTCTCTTTC TTTTAT			
			GT__			
GAM356	KIAA1181	3'	ATTCCTCTTCCTCTCTTC	2817	A	—
			GAAGAGAG AAGAG AAT			
			CTTCTCTC TTCTC TTA			
			C C			
GAM356	KIAA1319	3'	TATTTTTGTCTTCTTCCTTTC	1925	A	GA
			GAGAG AAGA ATAAAAATA			
			CTTTC TTCT TGTTTTTAT			
			C TC			
GAM356	KIAA1522	3'	ATTCTCTGACCTTTCTCTCT	2708		_____
			AGAGAGAA AGAGAAT			
			TCTCTCTT TCTCTTA			
			TCCAG			
GAM356	KIAA1906	3'	ATTTTTATTCTCTGCTT	2971	AA	
			GAG AGAGAATAAAAAAT			
			TTC TCTCTTATTTTAA			
			G_			
GAM356	MAPK6	5'	TATTTTTCTTCTCCCTTT	952	A	AG
			GAAG GAGAA AGAATA			
			TTTC CTCTT TTTTAT			
			C CT			
GAM356	MGC13138	3'	TATTTTTATTCTTGTGACCCTC	2332	AGAAA_	
			GAG GAGAATAAAAAATA			

			CTC TTCTTATTTTAT		
			CCAGTG		
GAM356	MGC2742	5'	TATTTCTTTTCTCTCTC 2040	AG	
			GAAGAGAGAAAG AATA		
			CTTCTCTCTTTT TTAT		
			CT		
GAM356	MGC32043	3'	TATTCCTGTTTCTCTTT 2486	_ A	
			GAAGAGAGAA AG GAATA		
			TTTCTCTTTT TC CTTAT		
			G _		
GAM356	NFAT5	3'	TATTCCTTTTCTCTTC 2452	A	
			GAAGAGAGAAAG GAATA		
			CTTCTCTTTTTC CTTAT		
			C		
GAM356	OSBPL8	3'	TTTTTATTATCCTCCTCTCTTC 1929	AAA G	
			GAAGAGAG GA AATAAAAA		
			CTTCTCTC CT TTATTTT		
			CTC A		
GAM356	RAB10	3'	TGTTCTGCTTTTCCTCCTC 3337	A AG _	
			GA GAG AAAG AGAATA		
			CT CTC TTTC TCTTGT		
			C CT G		
GAM356	RANBP1	3'	TATTTTCTTTTCCTCTCTTT 969	—	
			GAAGAGAG AAAGAGAATA		
			TTTCTCTC TTTCTTTTAT		
			CT		
GAM356	RASSF2	3'	TATTTTCACAATCCTCTCTTC 1537	AAA__	
			GAAGAGAG GAGAATA		
			CTTCTCTC CTTTTAT		
			CTAACA		
GAM356	STK22D	3'	TATTTTCATCAGCTTCTTCTCT 2226	AG AATA__	
	CT		AGAGAGAA AG AAAATA		
			TCTCTCTT TC TTTTAT		
			CT GACTAC		
GAM356	SYNJ2	3'	ATTTTtaggTTTCTCTTC 2606	AGAGAA	
			GAAGAGAGAA TAAAAAT		
			CTTCTCTTTT ATTTTA		
			GG__		
GAM356	TBLR1	3'	TATTCTTTTTTTCCCTTC 2079	A	
			GAAG GAGAAAGAGAATA		

			CTTC CTTTTTTTCTTAT		
			C		
GAM356	TM9SF1	3'	TATTGCTGTTCTCTCCCTTTCT 1296	AA	AA
		TC	GAAGAGAG AGAGAATA AATA		
			CTTCTTTC TCTCTTGT TTAT		
			CC CG		
GAM356	ULK2	3'	TATTCTATCCTCTCCTCTTC 1523	_	AAG_
			GAAGAG AGA AGAATA		
			CTTCTC TCT TCTTAT		
			C CCTA		
GAM356	UNC5D	3'	TTATTCTTTCTTCCTCTTC 2393	A	_
			GAAGAG GAA AGAGAATAA		
			CTTCTC CTT TTTCTTATT		
			_ C		
GAM356	LOC121219	5'	TTATTAACCTCTTCTCTCTTT 2988	A	_
			GAAGAGAGAA GAG AATAA		
			TTTCTCTCTT CTC TTATT		
			C AA		
GAM356	LOC128077	3'	ATTTGTTTTCTCTTTCTTTCCT 3006	A	TAA
		C	GA GAGAGAAAGAGAA AAAT		
			CTCTTTCTTTCTCTT TTTA		
			C TTG		
GAM356	LOC143451	3'	TTCTCTCCTTCTCTCTTC 3058	_	
			GAAGAGAGAA AGAGAA		
			CTTCTCTCTT TCTCTT		
			CC		
GAM356	LOC145125	3'	TTCTCTCCTTCTCTCTTC 3075	_	
			GAAGAGAGAA AGAGAA		
			CTTCTCTCTT TCTCTT		
			CC		
GAM356	LOC149351	3'	ATTTTTCAGATCTTTCTCTTT 3131		GAAT
			AGAGAGAAAGA AAAAAT		
			TTTCTCTTTCT TTTTAA		
			AGAC		
GAM356	LOC149722	5'	TATTCTTTCTTTCTCTTC 3312	A	
			GAAGAGAGA AGAGAATA		
			CTTCTCTTT TTTCTTAT		
			C		
GAM356	LOC149837	5'	TATTCCTGTCTTTCTCTCT 3318	_	
			AGAGAGAAAGA GAATA		

		TCTCTCTTTCT CTTAT		
		GTC		
GAM356	LOC150054 3'	TATTCTGTCTTTCTCCTC 3323	—	—
		GAG AGAAAGA GAATA		
		CTC TCTTTCT CTTAT		
		C GT		
GAM356	LOC150150 5'	TTTTGTGCCTCTCTTTCTTC 3324	AA	A_
		GAAGAGAGA GAG ATAAAA		
		CTTCTTTCT CTC TGTTTT		
		— CG		
GAM356	LOC150225 3'	TATTTTGTTCCTCTTC 3327	A	G
		GAAGAG GAAA AGAATA		
		CTTCTC CTTT TTTTAT		
		C G		
GAM356	LOC152816 3'	TATTTTATCCTCAACCTCTT 3364	AAA	A
		GAGAG GAG ATAAAAATA		
		TTCTC CTC TATTTTAT		
		CAA C		
GAM356	LOC155038 3'	ATTGCGTTTCTCTTTCTCCTTC 3198	A	TAAA
		GAAG GAGAAAGAGAA AAT		
		CTTC CTCTTTCTCTT TTA		
		— TGCG		
GAM356	LOC158629 3'	TATTTTCTTTCCCTCTC 3394	A	A
		GA GAG GAAAGAGAATA		
		CT CTC CTTTCTTTTAT		
		— C		
GAM356	LOC158943 3'	TATTTTCTTTTCTCTCTT 2572	—	
		GAAGAGAG AAAGAGAATA		
		TTTCTCTC TTTCTTTTAT		
		CT		
GAM356	LOC170082 3'	ATTCTTTTCCCCTCTCTTTC 3254	—	
		GAAGAGAGA AAGAGAAT		
		CTTTTCTCT TTTCTTA		
		CCCC		
GAM356	LOC199920 5'	TATTTTATTCTTTGATTCTTC 3436	AGAA	
		GAAGAG AGAGAATAAAAATA		
		CTTCTT TTTCTATTTTAT		
		AG_		
GAM356	LOC219667 3'	ATTTTGTATCTCTCTTC 3516	AAGAG	
		GAAGAGAGA AATAAAAAT		

		CTTCTCTCT	TTGTTTTTA	
		A_____		
GAM356	LOC220279 5'	TATTTTCTTCCCCTACCTCTCT	3653	A_____
	TC	GAAGAGAG	AAGAGAATA	
		CTTCTCTC	TTCTTTTAT	
		CATCCCC		
GAM356	LOC221830 3'	TATTTTCTTTTCTTTCTTC	3567	—
		GAAGAGAGAAA	GAGAATA	
		CTTCTTTCTTT	CTTTTAT	
		T		
GAM356	LOC222166 3'	ATTTTACCTTCTCTCTTT	3635	AG_
		GAAGAGAGAA	AGAAT	
		TTTCTCTCTT	TTTTA	
		CCA		
GAM356	LOC254440 3'	TTCTCTCCTTCTCTCTTC	3729	—
		GAAGAGAGAA	AGAGAA	
		CTTCTCTCTT	TCTCTT	
		CC		
GAM356	LOC51123 3'	ATTTTTATGCTGTTCCCTCTT	2571	A AG A
		AAGAG GAA	AG ATAAAAAT	
		TTCTC CTT	TC TATTTTTA	
		C G_ G		
GAM356	LOC51596 5'	TATTTTCCAAGTTTCTCTCTC	1651	A _____
		GA GAGAGAAA	GAGAATA	
		CT CTCTCTTT	CTTTTAT	
		— GAAC		
GAM356	LOC84570 5'	TTTCGTTTTTCCTCTCTCTTC	2257	AA TA
		GAAGAGAGA	GAGAA AAA	
		CTTCTCTCT	CTTTT TTT	
		C_ GC		
GAM356	LOC92710 5'	TATTTTATGCCTCTGTCTC	2885	A A_
		GAGA AGAG	ATAAAAATA	
		CTCT TCTC	TATTTTAT	
		G CG		
GAM357	FANCF 3'	GTCCCTTTAAAGCATTGA	1997	ATATAT
		TCAATGTTTTAAA	GGAC	
		AGTTACGAAATTT	CCTG	
		C_____		
GAM357	GPR65 5'	TCCACCCTTTAAAGCATTGA	2544	A TATA
		TCAATGTTTT AAA	TGGA	

			AGTTACGAAA TTT ACCT		
			A CCC_		
GAM357	LMNB1	3'	TGTCCATACACTTTGTTGCA 1226	TT	ATA
			TGT TAAA TATGGACA		
			ACG GTTT ATACCTGT		
			TT CAC		
GAM357	MEN1	5'	CATAATATTTTAAAACATT 3600		_
			AATGTTTTTAAAATAT ATG		
			TTACAAAATTTTATA TAC		
			A		
GAM357	PLAG1	3'	TGTCCATATACCAGATTTAAAA 944	A	A____
	TATT		AATGTTTTTAAA TATATGGACA		
			TTATAAAATTT ATATACCTGT		
			AGACC		
GAM357	S100A11	3'	TGTCAC TTTTTTAAAACATGA 1231	A	TATATG
			TCA TGTTTTTAAAA GACA		
			AGT ACAAATTTT CTGT		
			_ TTCA_		
GAM357	SLC9A6	3'	TCCAGTTAGAACATTGA 1290		AATATA
			TCAATGTTTTTAA TGGA		
			AGTTACAAGATT ACCT		
			G_____		
GAM357	SOD2	3'	TCCATATACTTTGGGGACTTG 766	T	TA _
			CAA GTTT AAA TATATGGA		
			GTT CAGG TTT ATATACCT		
			_ GG C		
GAM357	BIRC2	5'	TATATTTTAAAACATTGA 2784		T
			TCAATGTTTTTAAAA ATATG		
			AGTTACAAAATTTT TATAT		
			-		
GAM357	CXorf1	5'	TGTCCATAGAAAAAATATT 1145		AAAATA
			AATGTTTT TATGGACA		
			TTATAAAA ATACCTGT		
			AAG_____		
GAM357	KIAA0367	3'	TGTCCCACAATGCCTAAAACAT 2787		AAATATAT_
	TGA		TCAATGTTTTTA GGACA		
			AGTTACAAAAT CCTGT		
			CCGTAACAC		
GAM357	KIAA1321	3'	TCCTTGAGCTTTAAAGCATTGA 2627		ATATAT
			TCAATGTTTTTAAA GGA		

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AGTTACGAAATTT CCT
CGAGTT
GAM357 KIAA1718 3' TGTATTTTAAAATATTGA 2686
TCAATGTTTTAAAATATA
|||||
AGTTATAAAATTTTATGT

GAM357 KIAA1789 5' TGTCCCTGCCCTAGAAACATTG 2781 AAAATATAT
A TCAATGTTTT GGACA
||||| |||
AGTTACAAAG CCTGT
ATCCCGTC_
GAM357 PRO2964 3' CAAGTATTTTAAAACACTG 1842 A A
CA TGTTTTAAAATAT TG
|| ||||| ||
GT ACAAATTTTATG AC
C A
GAM357 SLC17A6 3' TGTCCATACACAGAAACAT 1912 AAAATA
ATGTTTT TATGGACA
||||| |||||
TACAAAG ATACCTGT
ACAC_
GAM357 TRAF3 5' CATTTTATTTTAAAACGTTGA 2542 T_
TCAATGTTTTTAAAATA ATG
||||| |||
AGTTGCAAAATTTTAT TAC
TT
GAM357 LOC151361 3' TGTCTGTGTTTTTAAAAC 3344 T
GTTTTAAAA ATATGGACA
||||| |||||
CAAAATTTT TGTGTCTGT
-
GAM357 LOC158714 3' TCCACACATTTAAAACATTGA 3224 ATATA
TCAATGTTTTTAAA TGGA
||||| |||
AGTTACAAAATTT ACCT
ACAC_
GAM357 LOC219667 3' TATACCTTAGAACATTGA 3518 AA
TCAATGTTTTTAA TATA
||||| |||
AGTTACAAGATT ATAT
CC
GAM357 LOC91565 3' TCCATTTTAAAACATT 2749 ATAT
AATGTTTTTAAA ATGGA
||||| |||
TTACAAAATTT TACCT
-
GAM358 EHF 3' ATATTGTAGAAGGAAACACCAA 1411 T GGA
TTGGT GT TCTTCTACAATAT
|||| || |||||

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			AACCA CA GGAAGATGTTATA	
			_ AA_	
GAM358	C9orf5	3'	ATATTGCAAAAACTACAGCTA 2225	ATCTTCTA
	A		TTGGTTGTGG CAATAT	
			AATCGACATC GTTATA	
			AAAAAAC_	
GAM358	KIAA1546	3'	TTGAAAAGACCACAACCAA 2805	A CTA
			TTGGTTGTGG TCTT CAA	
			AACCAACACC AGAA GTT	
			_ AA_	
GAM358	LOC253263	3'	TGAGAAAAACCCACAATAA 3724	ATC_ A
			TTGGTTGTGG TTCT CA	
			AATCAACACC AAGA GT	
			CAAA _	
GAM359	BRCA1	3'	GCCATGAGCACAAAAATTATGGT 1380	AGGGTA
	A		TATCATAA TGCTCATGGC	
			ATGGTATT ACGAGTACCG	
			AAAAC_	
GAM359	BRCA1	3'	GCCATGAGCACAAAAATTATGGT 1381	AGGGTA
	A		TATCATAA TGCTCATGGC	
			ATGGTATT ACGAGTACCG	
			AAAAC_	
GAM359	BRCA1	3'	GCCATGAGCACAAAAATTATGGT 1382	AGGGTA
	A		TATCATAA TGCTCATGGC	
			ATGGTATT ACGAGTACCG	
			AAAAC_	
GAM359	BRCA1	3'	GCCATGAGCACAAAAATTATGGT 1383	AGGGTA
	A		TATCATAA TGCTCATGGC	
			ATGGTATT ACGAGTACCG	
			AAAAC_	
GAM359	BRCA1	3'	GCCATGAGCACAAAAATTATGGT 1384	AGGGTA
	A		TATCATAA TGCTCATGGC	
			ATGGTATT ACGAGTACCG	
			AAAAC_	
GAM359	BRCA1	3'	GCCATGAGCACAAAAATTATGGT 1385	AGGGTA
	A		TATCATAA TGCTCATGGC	
			ATGGTATT ACGAGTACCG	
			AAAAC_	
GAM359	BRCA1	3'	GCCATGAGCACAAAAATTATGGT 1386	AGGGTA
	A		TATCATAA TGCTCATGGC	

			ATGGTATT	ACGAGTACCG		
			AAAAC_			
GAM359	BRCA1	3'	GCCATGAGCACAAAATTATGGT	1387	AGGGTA	
	A		TATCATAA	TGCTCATGGC		
			ATGGTATT	ACGAGTACCG		
			AAAAC_			
GAM359	BRCA1	3'	GCCATGAGCACAAAATTATGGT	1388	AGGGTA	
	A		TATCATAA	TGCTCATGGC		
			ATGGTATT	ACGAGTACCG		
			AAAAC_			
GAM359	BRCA1	3'	GCCATGAGCACAAAATTATGGT	1389	AGGGTA	
	A		TATCATAA	TGCTCATGGC		
			ATGGTATT	ACGAGTACCG		
			AAAAC_			
GAM359	BRCA1	3'	GCCATGAGCACAAAATTATGGT	1391	AGGGTA	
	A		TATCATAA	TGCTCATGGC		
			ATGGTATT	ACGAGTACCG		
			AAAAC_			
GAM359	PPP1CB	3'	GCCATTTGACACCCTTTATGAT	949	ATGCTC	
	G		TATCATAAAGGGT	ATGGC		
			GTAGTATTTCCCA	TACCG		
			CAGTT_			
GAM359	TRPS1	3'	CATGCACACCCTCTCTGATA	1470	TAA	A TC
			TATCA	AGGGT TGC ATG		
			ATAGT	TCCCA ACG TAC		
			CTC	C _		
GAM359	FLJ23323	3'	GCCATGAATGGTGCCCTT	2077	GC_	
			AAGGGTAT	TCATGGC		
			TTCCCGTG	AGTACCG		
			GTA			
GAM359	KIAA0057	3'	CCACAAGCATACCTATTAAGA	1421	A A	CA
			TC TAA	GGGTATGCT TGG		
			AG ATT	TCCATACGA ACC		
			A A	AC		
GAM359	LOC145439	5'	GCCATGAGCTGCATCTTTAT	3079	_	T
			ATAAAGG	GTA GCTCATGGC		
			TATTTCT	CGT CGAGTACCG		
			A _			
GAM360	DKFZP434G1411	3'	TAGGTTGATACATGTATCA	3554	AA	
			TGATACATGTATTAA	TA		

			ACTATGTACATAGTT AT		
			GG		
GAM360	DKFZP564I052	3'	GAAAGTATTCCTATCATGTAT 2760	T TAA	
			ATACATG AT AATACTTTC		
			TATGTAC TA TTATGAAAG		
			_ TCC		
GAM360	KLHL8	3'	AAAGTATTTGTTACATAATCA 2639	AC TTA	
			TGAT ATGTA AAATACTTT		
			ACTA TACAT TTTATGAAA		
			A_ TG_		
GAM360	XLKD1	3'	AAAGTGCCATTAACAAATGTAT 1323	GTA AA_	
	CA		TGATACAT TTAA TACTTT		
			ACTATGTA AATT GTGAAA		
			AAC ACC		
GAM360	LOC51003	3'	GAGGCACTTAATACATGTAT 1658	AATA	
			ATACATGTATTAA CTT		
			TATGTACATAATT GAG		
			CACG		
GAM361	GCNT2	5'	TCTCGGGATGAAACGGAATCGA 831	_____ A	
			TCGATTCCGT CC AGA		
			AGCTAAGGCA GG TCT		
			AAGTAG C		
GAM361	BLP1	3'	TTACCTTGACAGACGGAATGA 2222	G _ A	
			TC ATTCCGTC CAAG TGA		
			AG TAAGGCAG GTTC ATT		
			_ AC C		
GAM361	BLP1	3'	TTACCTTGACAGACGGAATGA 2371	G _ A	
			TC ATTCCGTC CAAG TGA		
			AG TAAGGCAG GTTC ATT		
			_ AC C		
GAM361	LOC143914	5'	TCACTCAAACGGAATCGA 3062	CCA A	
			TCGATTCCGT AG TGA		
			AGCTAAGGCA TC ACT		
			AAC _		
GAM361	LOC253891	5'	CACTGGGACGGAATCGG 3654	A A	
			TCGATTCCGTCC AG TG		
			GGCTAAGGCAGG TC AC		
			G _		
GAM362	ADSS	3'	GAAACAAATGATGAAAACAT 2925	CCTGTT	
			ATGT TCATTTGTTTC		

			TACA AGTAAACAAAG		
			AAAGT_		
GAM362	CASP6	3'	GAAACAAAATCCTCAGGAAATT 2305	G	TTTCA
	A		TAAT TCCTG TTTGTTTC		
			ATTA AGGAC AAACAAAG		
			A TCCTA		
GAM362	CASP6	3'	GAAACAAAATCCTCAGGAAATT 810	G	TTTCA
	A		TAAT TCCTG TTTGTTTC		
			ATTA AGGAC AAACAAAG		
			A TCCTA		
GAM362	CKTSF1B1	3'	AAGTGGATAAACAGAACATT 1445	C	C TG
			AATGT CTGTTT ATT TTT		
			TTACA GACAAA TAG GAA		
			A _ GT		
GAM362	F2R	3'	AAACAATGCAGTACAGGACAT 879	TTCAT_	
			ATGTCCTGT TTGTTT		
			TACAGGACA AACAAA		
			TGACGT		
GAM362	GPRK7	3'	GGAAACAAATGTTTCTGACATT 2476	CTGTTT	
			AATGTC CATTTGTTTCC		
			TTACAG GTAAACAAAGG		
			TCTTT_		
GAM362	NLGN1	3'	AAACAAATGAGATGGAC 1591	T	
			GTCC GTTTCATTTGTTT		
			CAGG TAGAGTAAACAAA		
			_		
GAM362	APC10	5'	GGAAACTGTAACAGGACATT 1574	T TTT	
			AATGTCCTGTT CA GTTTCC		
			TTACAGGACAA GT CAAAGG		
			T _		
GAM362	C20orf139	3'	GGAACAAAAACAGGACATTA 3319	CAT	
			TAATGTCCTGTTT TTGTTTC		
			ATTACAGGACAAA AACAAAGG		
			_		
GAM362	FLJ11186	3'	GAAGCCCGAAACAAGACATTA 1818	C	ATTT
			TAATGTC TGTTTC GTTTC		
			ATTACAG ACAAAG CGAAG		
			A CC_		
GAM362	FLJ22116	5'	GGAATTGCGGAAAACAGGAC 2073	CA	_
			GTCCTGTTT TTTGT TTCC		

CAGGACAAA AGGCG AAGG
 — TT
 GAM362 FLJ32978 3' AAACAAATGAAATCAACA 2487 CCT
 TGT GTTTCATTTGTTT
 ||| |||||
 ACA TAAAGTAAACAAA
 AC_

GAM362 KIAA1164 3' GGAAACAAAACAAAAC 2862 CC CA_
 GT TGTTC TTTGTTTCC
 || |||| |||||
 CA ACAA AAACAAAGG
 AA ACA

GAM362 KIAA1762 3' AAAGAGAGAAACGGACA 2668 T A G
 TGTCC GTTTC TTT TTT
 |||| |||| ||| ||
 ACAGG CAAAG AGA AAA
 — — G

GAM362 KIAA1918 5' GAAAGGAGACAGAACATTA 2969 C ATTTG
 TAATGT CTGTTTC TTTC
 ||||| ||||| |||
 ATTACA GACAGAG AAAG
 A G____

GAM362 POPX1 3' GGAAACAACTTCAGGTCA 1583 T TTCA
 TG CCTG TTTGTTTCC
 || |||| |||||
 AC GGAC AAACAAAGG
 T TTC__

GAM362 PRO0800 3' AAACAAAGAGACAGGAATTA 1852 G A
 TAAT TCCTGTTTC TTTGTTT
 |||| ||||| |||||
 ATTA AGGACAGAG AAACAAA

GAM362 LOC142779 3' GGAGTAACAAAATAGGACATTA 3050 CATT _
 TAATGTCCTGTTT TGTT TCC
 ||||| |||| |||
 ATTACAGGATAAA ACAA AGG
 — TG

GAM362 LOC143274 5' GGAAACAAACAAAAGGA 3053 G CA
 TCCT TTT TTTGTTTCC
 |||| ||| |||||
 AGGA AAA AAACAAAGG
 — AC

GAM362 LOC154089 3' AAACAAATACTGAGACAG 3186 _
 CTGTTTCA TTTGTTT
 ||||| |||||
 GACAGAGT AAACAAA
 CAT

GAM362 LOC169679 3' AGCATATGAAGACAGGACAT 3404 _ T
 ATGTCCTGTTT CAT TGTT
 ||||| ||| |||

TACAGGACAGA GTA ACGA
A T
GAM362 LOC202052 5' GAAACAAATACCCAGAAGACA 3484 _ TTTC
TGTC CTG ATTTGTTTC
||||| ||| |||||
ACAG GAC TAAACAAAG
AA CCA_
GAM362 LOC256021 3' GAAACGAGAACAATGACATTA 3708 C_ CAT
TAATGTC TGTTT TTGTTTC
||||| ||||| |||||
ATTACAG ACAAG AGCAAAG
TA _
GAM362 LOC91650 5' AAACAAAACATCTCAGGACAT 2765 TTTCA_
ATGTCCTG TTTGTTT
||||| |||||
TACAGGAC AAACAAA
TCTACA
GAM362 LOC91752 5' AAGTCAAATAAAACAGGACA 2777 C _
TGTCTGTTT ATTTG TTT
||||||| ||||| |||
ACAGGACAAA TAAAC GAA
A T
GAM363 ARCN1 3' CCCATTTCTTCCAGTCA 844 GAAGT CA
TGATTGGA AGGAAA GG
||||| ||||| ||
ACTGACCT TCCTTT CC
_ AC
GAM363 CTSK 3' TCCTACTTTGCTTCTCTCCACC 736 AT _
CA TG TGGAGA AGTAGGA
|| ||||| |||||
AC ACCTCT TCATCCT
CC CTTCGTT
GAM363 HMG20A 3' TCCTATTTCCCTGCCATCA 1800 T_ A
TGAT GG GAAGTAGGA
||| || |||||
ACTA CC CTTTATCCT
CCGT _
GAM363 PRDM2 3' TCCTGTTTCCCACCCAG 1415 AGAA A
TTGG GT GGAAACAGGA
||| || |||||
GACC CA CCTTTGTCCT
_ C
GAM363 RNMT 3' CTGCCTATCCTCTCCGATCA 1060 A_ AAA
TGATTGGAGA GTAGG CAGG
||||||| ||||| |||
ACTAGCCTCT TATCC GTCC
CC _
GAM363 SCAP1 3' TCCCACCTCCCTACTTCTGCCA 1052 _ AAACA
TGG AGAAGTAGG GGA
||| ||||| |||

			ACC TCTTCATCC	CCT		
			G	CTCAC		
GAM363	USH3A	5'	CCTATTTTATTTCTCCATCA	2355	T	AAC
			TGAT GGAGAAGTAGGA	AGG		
			ACTA CCTCTTTATTTT	TCC		
			—	A—		
GAM363	VAT1	3'	TCCTGTTTCCCACCTCCTTCTC	1292	TA—	
	C		GGAGAAG	GGAAACAGGA		
			CCTCTTC	CCTTTGTCCT		
			CTCCAC			
GAM363	AIF1	5'	CCTGCTGAAAACCCTCCAGTCA	2297	A—	
			TGATTGGAG	AGTAGG		
			ACTGACCTC	TCGTCC		
			CCAAAAG			
GAM363	CPLX1	3'	CCTGTTTCTCCTCCATTCA	1317	T	AAGTA
			TGA TGGAG	GGAAACAGG		
			ACT ACCTC	TCTTTGTCC		
			T	C—		
GAM363	CXYorf1	3'	CCTGTTCCTCCACCTCCCGGCTC	3228	—	A A A A
			GA TTGG GA GT GG AACAGG			
			CT GGCC CT CA CC TTGTCC			
			C	— C C C		
GAM363	FLJ12221	3'	CCCACCCTTGCTCTCCAATTA	2637	A	AAACA
			TGATTGGAGA GTAGG	GG		
			ATTAACCTCT CGTTC	CC		
			—	CCAC—		
GAM363	FLJ20207	3'	CCTGCCCTGCTTCCCCACCCA	1741	AT A	AAA
			TG TGG GAAGTAGG	CAGG		
			AC ACC CTTCGTCC	GTCC		
			CC C	C—		
GAM363	FLJ22215	3'	CCTGCCCTTACCCTGTTCTCC	3715	—	AAA
			GGAGAA	GTAGG CAGG		
			CCTCTT	CATCC GTCC		
			GTCC	CCC		
GAM363	FLJ31547	3'	TCCATAATTTCTCCCGCAATC	2511	—	A—
	A		TGATT	GGAGAAGT GGA		
			ACTAA	CCTCTTTA CCT		
			CGC	ATAC		
GAM363	HSCBCIP1	3'	TCCTACCTATGTCTTCTCCAAT	3449	—	AAAC
			ATTGGAGAAG	TAGG AGGA		

			TAACCTCTTC ATCC TCCT		
			TGT A__		
GAM363	KIAA0515	5'	TCCTACCAGAACTCCTCCGATC 2670	A A__	AAAC
		A	TGATTGGAG AGT GG AGGA		
			ACTAGCCTC TCA CC TCCT		
			C AGA A__		
GAM363	KIAA1514	3'	CCTGCTCAACTTCTCCA 1877	A AAA	
			TGGAGAAGT GG CAGG		
			ACCTCTTCA CT GTCC		
			A C__		
GAM363	KIAA1553	3'	TCCTCACTTCTCCATCCA 3544	AT	_
			TG TGGAGAAGT AGGA		
			AC ACCTCTTCA TCCT		
			CT C		
GAM363	KIAA1656	3'	CCCACTTCCTTCCAGTCA 2730	_	A
			TGATTGGA GAAGT GG		
			ACTGACCT CTTCA CC		
			TC C		
GAM363	KIAA1877	3'	CCTACCTTATTTCTCCAGCCA 2741	AT	AAAC
			TG TGGAGAAGTAGG AGG		
			AC ACCTCTTTATTC TCC		
			CG CA__		
GAM363	MTCH1	3'	CCCGTCTACCCCTCCAGTCA 1493	AA	AAACA
			TGATTGGAG GTAGG GG		
			ACTGACCTC CATCT CC		
			CC GC__		
GAM363	N-PAC	3'	CCGCCCTCACCCCTCCAATC 2902	AA _	AAACA
			GATTGGAG GT AGG GG		
			CTAACCTC CA TCC CC		
			CC C CG__		
GAM363	SEMA4B	5'	CCTGTTTCCACCTCC 2839	AA A	
			GGAG GT GGAAACAGG		
			CCTC CA CCTTTGTCC		
			_ C		
GAM363	SPRY1	3'	CCTGTTTCCACCTTCTCT 2709	TA_	
			GGAGAAG GGAAACAGG		
			TCTCTTC CCTTTGTCC		
			CAC		
GAM363	WS-3	5'	CCTGCCAGGCTCTCCAATC 1312	A A_	AAA
			GATTGGAGA GT GG CAGG		

		CTAACCTCT CG CC GTCC			
		_ GA _			
GAM363	LOC123242 5'	TCTGTACCTTCTCCATCCA 3030	AT		TAGGAA
		TG TGGAGAAG ACAGG			
		AC ACCTCTTC TGTCT			
		CT CA_			
GAM363	LOC127702 3'	CCTGCCCACAACCTTCTCCAAAC 3024	A		A_ AAA
	A	TG TTGGAGAAGT GG CAGG			
		AC AACCTCTTCA CC GTCC			
		A ACA C_			
GAM363	LOC146745 5'	TCCTGCCACCATTCTCCAACC 3099	A		A AAA
	A	TG TTGGAGAAGT GG CAGGA			
		AC AACCTCTTTA CC GTCCT			
		C _ ACC			
GAM363	LOC147791 3'	CCCATTCCCTAACCTCCAATC 3294		AAG	A CA
		GATTGGAG TAGG AA GG			
		CTAACCTC ATCC TT CC			
		CA_ C AC			
GAM363	LOC196892 3'	TCCTGGTGATTCTTCTCCAATC 3417			TAGGAAA
	A	TGATTGGAGAAG CAGGA			
		ACTAACCTCTTC GTCCT			
		TTAGTG_			
GAM363	LOC200093 3'	CCTGTTCCCCACCTCCCGGCTC 2648	_	A A A A	
		GA TTGG GA GT GG AACAGG			
		CT GGCC CT CA CC TTGTCC			
		C _ C C C			
GAM363	LOC201243 5'	TCCTGCCACCATTCTCCAACC 3426	A		A AAA
	A	TG TTGGAGAAGT GG CAGGA			
		AC AACCTCTTTA CC GTCCT			
		C _ ACC			
GAM363	LOC219404 3'	CCTGCTCCCTACTTCCTGGCA 3606	A TG A		AAA
		TG T G GAAGTAGG CAGG			
		AC G C CTTTCATCC GTCC			
		_ GT _ CTC			
GAM363	LOC222066 3'	TCCTGCAAACCACCTTCTCCAA 3574		TA	AAA_
	TCA	TGATTGGAGAAG GG CAGGA			
		ACTAACCTCTTC CC GTCCT			
		CA AAAC			
GAM363	LOC253001 5'	TCTGTACCTTCTCCATCCA 3698	AT		TAGGAA
		TG TGGAGAAG ACAGG			

AC ACCTCTTC TGTCT

CT CA_____

GAM363 LOC91040 3' CCTGTTCCCCACCTCCCGGCTC 2700 _ A A A A

GA TTGG GA GT GG AACAGG

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CT GGCC CT CA CC TTGTCC

C _ C C C